9th world one health CONGRESS

LISBON
PORTUGAL
4-7 SEPTEMBER 2026

PROGRAM AND ABSTRACTBOOK

Under the patronage of

unesco

2024 · 2033
International Decade of Sciences for Sustainable Development

Contents

General Information
- Welcome Message from the Congress Chairs
- Committees
- Congress program at a glance
- Venue floor plan
- Important information for oral presentations
- Posters
- Conference information
- General information
- About the Global One Health Community
- Commitment to environmental sustainability
- Availability of recordings and proceedings after the Congress
- Sponsors

Complete Program

Oral Abstracts
- Climate change, Environment, Ecosystems Health - session 1
- Knowledge, Education & Communities
- Pathogens, Microbiome, & Intervention Strategies
- Governance, Policy & Legal Frameworks
- Food Systems, Agriculture & Plant Health
- One Health Implementation & Financing
- Biosecurity, biosafety, global health security
- The critical role of the private sector and civil society in One Health implementation
- Biodiversity, Wildlife & Pathogen Interfaces - session 1
- Antimicrobial resistance - session 1
- Data, Technology & Innovative Analytics
- Biodiversity, Wildlife & Pathogen Interfaces - session 2
- Preparedness, Resilience & Economic Evaluation
- Climate change, Environment, Ecosystems Health - session 2
- Antimicrobial resistance - session 2
- Antimicrobial resistance - session 3
- Late Breakers: novel and outstanding discoveries
- Late Breakers: novel and outstanding discoveries

Poster Abstracts

Poster zone 1 – Olive Tree
Poster zone 1 – Sardines
Poster zone 2 – Olive Tree
Poster zone 2 – Sardines
Poster zone 3 – Olive Tree
Poster zone 3 – Sardines
Poster zone 4 – Olive Tree
Virtual posters

Welcome Message from the Congress Chairs

It is our pleasure, on behalf of the Global One Health Community, to welcome you to the**9th World One Health Congress** in Lisbon, Portugal. This year marks an important milestone, as the World One Health Congress returns to Europe for the first time since the 3rd Congress was held in Amsterdam in 2015. Bringing together the international One Health community in Europe provides a timely opportunity to strengthen international collaboration while highlighting the region's contributions to advancing integrated approaches to human, animal, plant and environmental health. At a time when interconnected health challenges continue to transcend borders, our collective commitment to One Health has never been more important.

As the world's largest gathering dedicated to One Health, this Congress brings together researchers, policymakers, healthcare professionals, veterinarians, environmental scientists, public health experts, industry leaders, international organisations and civil society to exchange knowledge, build partnerships, and shape solutions to the world's most pressing health challenges. The program has been developed with the recommendations and key outcomes of the **8th World One Health Congress** in Cape Town (South Africa) firmly in mind, ensuring continuity of discussions while addressing emerging priorities and future opportunities. We have designed a program that promotes scientific excellence, interdisciplinary dialogue and meaningful engagement between science and policy.

The Congress features two complementary abstract-driven tracks: the **Scientific Sessions (SCS)**, showcasing cutting-edge research across the One Health spectrum, and the **Science Policy Interface Sessions (SPI)**, which bridge scientific evidence with policy development and implementation. Complementing these tracks are **Workshops**, selected through an open call, providing highly interactive opportunities for participants to exchange expertise, develop practical skills and foster collaboration. The program also includes inspiring **PlenarySessions**, **Keynotes**, **PartnerSessions**, **SideEvents**, and **PosterSessions**, where hundreds of peer-reviewed scientific abstracts will be presented, reflecting the breadth, diversity and strength of the global One Health community.

Supporting the next generation of One Health leaders is one of our core priorities. Through our **Early Career Scientists Fund** and **Low- and Lower-Middle-Income Countries (LMIC) Fund**, we are committed to broadening participation and enabling talented researchers from around the world to contribute to and benefit from this global exchange of knowledge. Their ideas, perspectives, and discoveries are essential to advancing One Health for future generations.

We are equally committed to ensuring that the Congress reflects the principles of **environmental sustainability**. From minimizing single-use plastic and food waste, to making use of a digital program and minimizing any printed material, we continue to implement measures aimed at reducing the environmental footprint of the event while encouraging participants to adopt sustainable practices throughout the Congress.

Finally, we extend our sincere gratitude to everyone who has contributed to making this Congress possible. We warmly thank the members of the **Scientific Program Committee**, and members of the **Local Partner Committee**, our Local PCO Leading, all our abstract reviewers, speakers, supporters, instructional partners, technical and logistics teams, the catering team, the volunteers and the many individuals whose expertise and dedication have shaped this outstanding event.

Last but not least, we thank the Lisbon Congress Center, and the vibrant city of Lisbon for hosting us here over the next four days.

Dear participants, colleagues, and friends, **we wish you all an inspiring, interactive and fruitful Congress** and thank you for being here to make this 9th edition a great success!

Ab OSTERHAUS
Co-founder global One Health Community, RIZ Hannover, Germany

John MACKENZIE
Co-founder global One Health Community, Curtin University, Australia

Dominique CHARRON
Ontario Veterinary College, University of Guelph, Canada

Jomana MUSMAR
Founder and Senior Consultant, Advisors of Global Health, United States of America

Committees

Congress chairs

Ab OSTERHAUS
Co-founder global One Health Community, RIZ Hannover, Germany

John MACKENZIE
Co-founder global One Health Community, Curtin University, Australia

Dominique CHARRON
Ontario Veterinary College, University of Guelph, Canada

Jomana MUSMAR
Founder and Senior Consultant, Advisors of Global Health, United States of America

International Organizing Committee

Ab OSTERHAUS
Co-founder global One Health Community, RIZ Hannover, Germany

John MACKENZIE
Co-founder global One Health Community, Curtin University, Australia

Aida BAKRI
Global One Health Community

Annick HAUCHART MANNAERTS
Global One Health Community

Dagmar DE GRAEF
Global One Health Community

Local Partner Committee

Adriano A. BORDALO
ICBAS - University of Porto

Alice MATOS
Veterinários Sem Fronteiras Portugal (VSF Portugal)

ANA DOMINGOS
University NOVA of Lisboa, Institute of Hygiene and Tropical Medicine

Begoña PEREZ-CABEZAS
ICBAS-UP

Carlos DAS NEVES
European Food Safety Authority

Catarina LAVRADOR
University of Évora

Júlio CARVALHO
Portuguese Army

Margarida PIRES SIMÕES
University of Évora

Ricardo MEXIA
National Health Institute Doutor Ricardo Jorge

Ricardo SOARES MAGALHAES
The University of Queensland

Scientific Program Committee

Amina BENYAHIA
WHO

ANA DOMINGOS
University NOVA of Lisboa, Institute of Hygiene and Tropical Medicine

Carlos DAS NEVES
European Food Safety Authority

Chadia WANNOUS
World Organisation for Animal Health (WOAH)

Daniel BAUSCH
National University of Singapore

Dominique CHARRON
University of Guelph

Walter Ian LIPKIN
Columbia University

Jomana MUSMAR
AMR Strategic Coalition

Jonathan RUSHTON
University of Edinburgh

Julian BLANC
UNEP

Junxia SONG
FAO

Lawrence MADOFF
University of Massachusetts Chan Medical School

Linfa WANG
Duke-NUS Medical School

Marietjie VENTER
University of the Witwatersrand

Natalia CEDIEL
Universidad de la Salle

Peter DASZAK
Nature Health Global

Rebecca KATZ
Georgetown University

Ricardo MEXIA
National Health Institute Doutor Ricardo Jorge

Ricardo SOARES MAGALHAES
The University of Queensland

Ron FOUCHIER
Erasmus MC

Salome BUKACHI
University of Nairobi

Thomas METTENLEITER
Friedrich-Loeffler-Institut

Tiggy GRILLO
Wildlife Health Australia

Tracey GOLDSTEIN
Colorado State University

Congress program at a glance

Get an overview of the program, filter by day, track and room on our program at a glance page.
To see full details of each session, you will need to be registered and logged in.

9th WORLD One health CONGRESS

FRIDAY 4 SEPTEMBER 2026

Time	Auditorium I	Auditorium II	Room 1.05 · 45 pax	Room 1.06 · 45 pax	Room 1.07 · 45 pax	Room 1.08 · 50 pax	Room 1.10 · 50 pax
07:30–19:00	REG02 **Registration desk open & Poster mounting**						
08:30–10:00	PLE01 **Plenary opening and keynotes** · Auditorium I						
10:00–11:00	SPS01 **Partner Session organized by Global Affairs Canada: Multisectoral Collaboration to Counter Deliberate Biothreats** · Auditorium I						
11:00–11:30	RB01 **Refreshment break** · Foyer D & Pavillon 4						
11:30–13:00	SCS01 **Climate change, Environment, Ecosystems Health (1)**	SPI01 **Knowledge, Education & Communities**		WS02 WORKSHOP: One Health in Social-Ecological Systems research methods	WS03 WORKSHOP: Building Skills for Community-Engaged One Health Research	SPI02 Taming the Resistant: A One Health Policy Pathway for the fight against AMR	WS01 WORKSHOP: Virtual Deployment: Simulating Rapid Response Mobile Laboratory Operations and Diagnostic Workflows Using Virtual Reality
13:00–14:00	LUN01 **Welcome Lunch & networking** · Foyer D & Pavillon 4						
14:00–15:30	SCS02 **Pathogens, Microbiome, & Intervention Strategies**	SPI03 **Governance, Policy & Legal Frameworks**	SPI16 Financing One Health: Sourcing Funding, Structuring Investments, and Involving Private Sector Partners	WS05 WORKSHOP: Empowering Youth for Antimicrobial Resistance Action: Capacity Building and Community Engagement Approaches within a One Health Framework		SPI04 From International Instruments to On-the-Ground Imple-mentation: Wildlife Health, Surveillance, and One Health Risk Reduction	WS07 WORKSHOP: Simulating One Health in Action: A Card Game for Transdiscipli-nary Zoonotic Outbreak Re-sponse, Policy Decision-Mak-ing, and Systems-Level Collaboration
15:30–16:00	RB02 **Refreshment break** · Foyer D & Pavillon 4						
16:00–17:30	SCS03 **Food Systems, Agriculture & Plant Health**	SPI05 **One Health Im-plementation & Financing**	SCS04 REVEAL: Rodent Ecology and Viral Emergence: Anthropogenic Links. Understanding rodent-borne viruses in a changing world	SPI06 Strengthening One Health Governance for Antimicrobial Resistance: Latest Evidence and Case Studies	SPI09 One Health in Higher Education and University-led Networks	SCS06 Moving Upstream: Exposome-Informed One Health	
17:40–18:30	SCS07 **Biosecurity, biosafety & global health security**	SPI07 **The critical role of the private sector & civil society in One Health imple-mentation**	SPI08 Developing One Health Competencies for Tomorrow: The FAO/WHO/WOAH Joint One Health Learning Taskforce in Action		SPI10 Closing the gap between One Health policy commitments and ground-level action: lessons from dog-mediated rabies elimination	SCS05 Antimicrobial Resistance Data Systems and Informatics Solutions across Africa and Asia-Pacific	
18:30–19:30	RB03 **Welcome reception & networking** · Foyer D & Pavillon 4						

9th WORLD one health CONGRESS

SATURDAY 5 SEPTEMBER 2026

Time	Auditorium I	Auditorium II	Room 1.05 - 45 pax	Room 1.06 - 45 pax	Room 1.07 - 45 pax	Room 1.08 - 50 pax	Room 1.10 - 50 pax
08:00–08:50	SPS02 **Company and organization lectures** · Auditorium I						
09:00–10:30	PLE02 **Plenary: One Health Governance — where does the EU stand?** · Auditorium I						
10:30–11:00	RB04 **Refreshment break** · Foyer D & Pavillon 4						
11:00–12:30	SCS09 **Biodiversity, Wildlife & Pathogen Interfaces (1)**	SPI12 **Structuring One Health cooperation among EU Agencies**	WS06 WORKSHOP: Practical AI for One Health Surveillance: A Beginner-Friendly Introduction to Zoonotic Disease Analysis	WS08 WORKSHOP: Species distribution modelling for emerging infectious diseases		11:00–11:40 SPI11 One Health in humanitarian contexts: climate change, conflict & forced migration 11:50–12:30 SPI13 The Future of Global Health Cooperation: Risks, Resilience & Reform	WS09 WORKSHOP: From Evidence to Action: How to Bridge the Gap Between Scientists and Decision-Makers to Solve Global One Health Challenges
12:30–14:00	LUN02 **Lunch break** · Foyer D & Pavillon 4						
12:45–13:45	SPS07 **Partner session organized by Prezode and the World Bank: From Response to Prevention: Financing and Partnerships for Sustainable One Health Impact**	SPS03 **The socio-economic value of disease prevention: vaccines in the real world**					
14:00–15:30	SCS10 **Antimicrobial resistance (1)**	SPI14 **Bridging Policy-to-Practice: Implementing the One Health Joint Plan of Action at National Level**	WS11 Strengthening One Health Response by applying the 7-1-7 Framework to Timeliness Analysis: an Interactive Training	WS22 WORKSHOP: Networking as a Driver of One Health Operationali-zation: Lessons learned and beyond		SPI15 From Governance Analysis to Practice: Integrating the Environmental Dimension into National One Health AMR Strategies	WS19 WORKSHOP: A One Health Framework for Biosecurity on Islands
15:30–16:00	RB05 **Refreshment break** · Foyer D & Pavillon 4						
16:00–17:30	SCS11 **Data, Technology & Innovative Analytics**	SPI17 **Operationalizing One Health: Translating Enablers, Dismantling Barriers and Aligning Global Policy**	SPI Operation-alizing One Health: Translating Enablers into Practice, Dismantling Barriers and Aligning Global Policy	SCS12 Zoonotic Threats in a Changing World: Ad-vanced Tools, Laboratory Capacity Build-ing and Part-nerships for Early Detec-tion and Rapid Response	SCS18 Restoring nature, reducing risk: ecosystem-based approaches to zoonotic disease prevention		WS14 Workshop: The One Health Mural: An Interactive Systems-Think-ing Tool to Strengthen Multisectoral Understanding and Action on Complex Health Challenges
17:30–19:00	POS01 **Poster presentations & refreshments — session 1 (Olive Tree)** · Foyer D & Pavillon 4						

9th WORLD one health CONGRESS

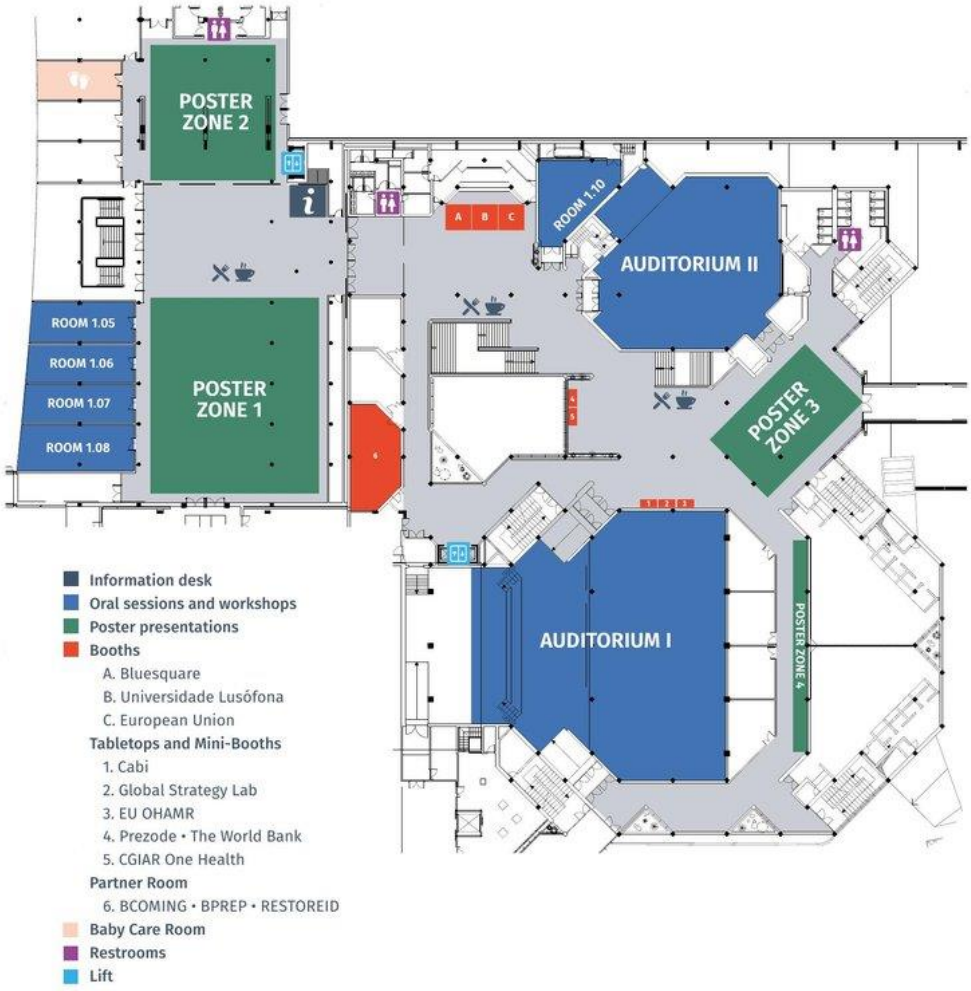
SUNDAY 6 SEPTEMBER 2026

Time	Auditorium I	Auditorium II	Room 1.06 · 45 pax	Room 1.07 · 45 pax	Room 1.08 · 50 pax	Room 1.10 · 50 pax
08:00–08:50	SCS13 **Biodiversity, Wildlife & Pathogen Interfaces (2)**	SPS04 **Partner Session organized by IDC: Breath & Beyond: The IDC - A Model for Interdisciplinary Research Collaboration**		SPI19 Bridging Biosecurity Gaps in Africa: Strengthening Links to Global Mechanisms through SIMBA, the UNSGM, and the BWC	SCS14 One Health Surveillance in a Changing Climate: Data-Driven Solutions for Resilient Systems	
09:00–10:30	PLE03 **Plenary session and keynotes** · Auditorium I					
10:30–11:00	RB06 **Refreshment break** · Foyer D & Pavillon 4					
11:00–12:30	SCS15 **Preparedness, Resilience & Economic Evaluation**	SPI20 **From Indicators to Preparedness - Strengthening Operational One Health Systems through Food, Agriculture, and Security Integration**	WS15 WORKSHOP: Bridging Disciplines – Integrating Ecological Principles into One Health Disease Research and Practice	WS17 WORKSHOP: Introducing the NEOH One Health Core Competencies: An Interactive Workshop for Strengthening Transdisciplinary Practice	SPI21 Operationalizing One Health Prevention: Building Science–Society–Policy Interfaces from Local Action to Global Governance	WS16 WORKSHOP: The 18-Month AMR Action Sprint: A One Health Policy Simulation
12:30–14:00	LUN03 **Lunch break** · Foyer D & Pavillon 4					
12:45–13:45	SPS05 **Partner Session organized by ESWI: The Ongoing H5N1 Panzootic: A Continuing Threat to Animals and Humans** · Auditorium II					
14:00–15:30	SCS16 **Climate change, Environment, Ecosystems Health (2)**	*14:00–14:40* SPI22 Advancing gender transformative One Health approaches: how can we ensure equity, diversity and inclusion in policy and practices? *14:50–15:30* SPI24 Inclusive One Health in Practice: Integrating Environment, Data, and Community Knowledge to Improve Health Outcomes in the Global South		WS13 WORKSHOP: One Health Communication: How to introduce One Health to new audiences	SCS08 One Health Approaches to Pathogen Surveillance, Intervention, and Prevention Strategies	WS18 WORKSHOP: Transformative One Health Training: Learning Together
15:30–16:00	RB07 **Refreshment break** · Foyer D & Pavillon 4					
16:00–17:30	SCS17 **Antimicrobial resistance (2)**	*16:00–16:40* SPI25 **Biodiversity and Health: The science, policy, and implementation of biodiversity action as a One Health measure** *16:50–17:30* SCS19 **Advanced tools and instruments for the detection and characterization of viral zoonoses in wildlife**	WS21 WORKSHOP: Quantifying, interpreting, visualizing and validating the climate-driven transmission suitability of mosquito-borne viruses		SPI26 Multi-Dimensional One Health Approach to Mitigating Mental Health Challenges in Africa	WS25 WORKSHOP: Meaningful and Inclusive Engagement of People and Communities in One Health Implementation Session
17:30–19:00	POS02 Poster presentations & refreshments — session 2 (Sardines) · Foyer D & Pavillon 4					

Venue floor plan

Zoom in on our venue floorplan.

9th WORLD one health CONGRESS



Important information for oral presentations

All oral presentations must adhere to the unique script they have received ahead of the Congress, as their given time limits can vary from session to session. Please respect the allocated time for your presentation. Due to the multi-track nature of the Congress and the movement of attendees between tracks, it is imperative that sessions remain on schedule.

Presenters are expected to be in their designated room **5 minutes before their session** starts.

The presentations in **Auditorium I and II** are managed centrally, so presenters must upload their Powerpoint files to the virtual platform at least 48 hours before their session.

For presentations in **rooms 1.05, 1.06, 1.07, 1.08 and 1.10**, a HDMI connection will be available in each room, enabling speakers to connect their personal computers directly to the AV system.

All Congress sessions will be recorded and available for viewing on-demand after the Congress. Footage may also be used for global One Health Community educational purposes.

This information pertains to presentations in Auditorium I and II rooms only:

Presentations for sessions taking place in Auditorium I and II must be uploaded to the Congress virtual platform at least **48 hours prior to the session**. No edits or updates will be accepted on the day of your session. The use of personal laptops to present during sessions in Auditorium I and II is not permitted.

Presentations are uploaded on the relevant page for that session. You must click on the specific abstract/part of the session you will be presenting. You can easily view and access your sessions through your own account page**.** Detailed guidance for how to upload your presentation to the virtual platform can be found here.

Presentations must be in **widescreen (16:9)** format, with a maximum file size of **50 MB**. Only **Microsoft PowerPoint (.ppt or .pptx)** files are accepted.

If you experience difficulties uploading your powerpoint presentation, please contact the helpdesk on the virtual platform.

If you are delivering a presentation in Auditorium I or II, you can download our guidelines for uploading your presentation to the virtual platform.

Posters

Accepted posters have been allocated to one of three groups:

• Live poster presentation - Olive Trees session (Saturday 5 September)

• Live poster presentation - Sardines session (Sunday 6 September)

• Virtual poster presentation (online)

Virtual posters must be uploaded to the virtual Congress platform by **28 August 2026**. Accepted live posters can also be uploaded onto the virtual platform, in addition to the live presentation. Please don't miss the 28 August deadline after which the congress chairs will make their decisions on which posters will be presented during the poster peeks. More information on how to upload your poster can be found here.

Information for live poster presentations

Live posters have been assigned to one of these two presentation sessions:

• Olive Trees - **Saturday 5 September from 17.30 to 19.00**

• Sardines - **Sunday 6 September from 17.30 to 19.00**.

Posters have been allocated to these sessions using the following icons:

You are welcome to attend and interact with the poster presenters on both of these occasions. The poster areas are also open for viewing throughout official Congress hours.

Poster set-up

Posters can be set-up on Thursday 3 September between 17.00 and 20.00 or on Friday 4 September during the scheduled coffee and refreshment breaks in the Congress program. Poster tubes must not be left behind anywhere.

Posters must be dismantled on Monday 7 September between 12.30 (start of lunch) and 15.40 (end of the final break). All posters remaining after this time will be disposed of.

A dedicated poster panel will be assigned to each presenter. Each panel will include a header sticker displaying the poster number, a QR code to view your digital poster, and the symbol indicating your allocated poster presentation session (olive trees or sardines). Please ensure your printed poster matches the assigned poster number on-site.

Only paper posters are allowed. Fabric posters are not permitted. Mounting materials will be available in the poster area, and staff will be present to assist if needed. Posters must be A0 size (1189 x 841 mm) and in portrait format.

Presenters are responsible for arranging and collecting their own printed poster.

Need to print your poster locally in Lisbon? A nearby print shop is available approximately 1 km (13-minute walk) from the congress venue (CCL):

• Publiforce: Rua Artur Lamas 2-B, 1300-075 Lisbon, Portugal, https://publiforce.pt Approximate price: A0 poster (250 g paper) — €25 + VAT

Poster areas

There are four poster areas within the Congress center. A map of the poster areas can be found below.

Throughout the poster areas, posters will be arranged in numerical order, starting at poster area 1. The numbers will continue to increase in the direction indicated by the arrow in the diagram.

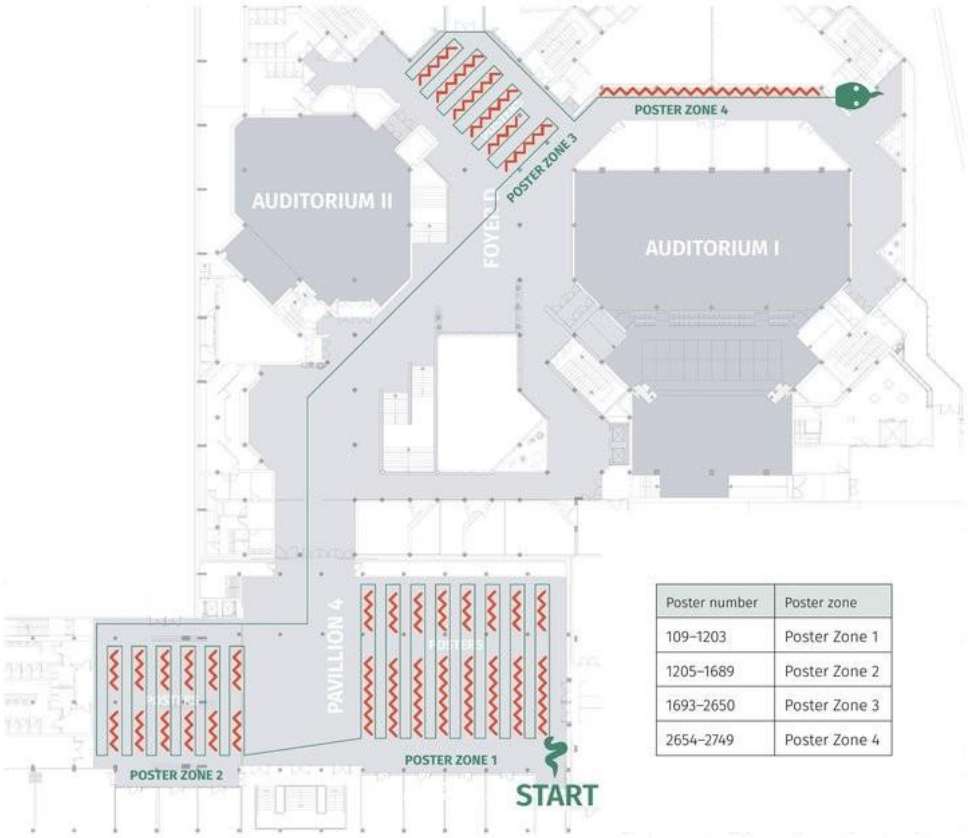
• Poster number 109–1203 - Poster Zone 1

• Poster number 1205–1689 - Poster Zone 2

• Poster number 1693–2650 - Poster Zone 3

• Poster number: 2654–2749 - Poster Zone 4

9th WORLD one health CONGRESS



Poster number	Poster zone
109–1203	Poster Zone 1
1205–1689	Poster Zone 2
1693–2650	Poster Zone 3
2654–2749	Poster Zone 4

Conference information

Participant badges

For security and organisational reasons, participants must wear their congress badges at all times when visiting the Lisbon Congress Center (CCL).

Badges are collected from the Congress Registration Desk. **Please bring your registration confirmation email with you when you come to pick up your badge.**

Registration

The Congress Registration Desk is located on the ground floor of the conference center, and is open at the following times:

• Thursday 3 September 17.00-20.00

• Friday 4 September 07.30-19.00

Participants registering after 4 September must collect their badges at the Congress Information Desk on the first floor in Pavilion 4.

Information Desk

The congress team is ready to assist you throughout the 9th World One Health Congress. The Congress Information Desk is located on the first floor of the conference center, in Pavilion 4.

The Congress Information Desk is open:

• Thursday 3 September: 17.00-20.00

• Friday 4 September to Sunday 6 September: 07:30-19.00

• Monday 7 September: 07:30-17:00

In case of emergency outside of office hours, and only during Congress days from 4 to 7 September (in case of emergency only): contact Elina Martin +371 2639 43 48

WOHC2026 Virtual platform

We have created a dedicated virtual platform for WOHC2026: https://wohc2026.globalohc.org. Register for the virtual platform to view the Congress program, upload accepted posters and presentations, connect with other participants, and more.

Please note that the virtual platform is separate from the conftool platform where you registered for the Congress.

To register on the virtual platform:

• Log in with the **same email address used to register for the Congress.**

• A login code will be sent directly to your inbox.

The virtual platform includes an online helpdesk for all web-related support. Please use the online helpdesk for any assistance with uploading posters and presentations, resolving login issues, and addressing any other technical concerns. We aim to reply to all helpdesk queries as soon as we can during business hours (WEST).

The virtual platform will remain open until the end of the year, so you can continue to view session recordings, digital posters, and stay connected with other participants after the Congress.

Session Capacity

Please note the maximum capacity of the session rooms:

• Auditorium I - 1500 people

• Auditorium II - 380 people

• Rooms 1.08 and 1.10 - 50 people

• Rooms 1.05, 1.06 and 1.07 - 45 people

It is not possible to exceed the stated capacity for each room. Once a room reaches its capacity for that session, the door will be closed and no further entry will be permitted. We encourage you to **arrive at the room for your chosen session 10 minutes before the session starts**, to ensure that you secure a seat.

Language

The official language of the congress is English. No translation will be provided.

Please note, however, that the side event “The Integration of One Health Approaches in Tropical Medicine” taking place on 3 September, will be held only in Portuguese as a special Lusophone Workshop.

Venue

The 9th World One Health Congress will take place at the Lisbon Congress Center (CCL), Portugal’s premier venue for international conferences and events. The CCL offers state-of-the-art facilities, spacious auditoriums, and modern exhibition areas, providing the perfect setting for global discussions on One Health. Easily accessible from Lisbon’s historic city center and major transport hubs, the venue is surrounded by the city’s rich cultural heritage, vibrant atmosphere, and renowned gastronomy. Whether engaging in scientific sessions or networking with peers, attendees will experience a world-class event in one of Europe’s most dynamic capitals.

The congress will take place on the first floor of the venue, bringing together plenary sessions, breakout rooms and poster areas in one central and easily accessible space.

Address of the venue: Praça das Indústrias 1, 1300-307, Lisbon, Portugal

Wifi

A free, high speed WiFi connection is available throughout the venue for visitors to use. You can use the following details to connect:

WiFi Network: WOHC2026Password: WOHCLisbon2026

Filming and photography

During the congress, videos and photographs will be taken. Pictures and footage shall be used for Global One Health Community activities and educational purposes.

Code of Conduct

The Global One Health Community (GOHC) is guided by the highest professional and ethical standards and is committed to providing a collegial, respectful, and harassment-free Congress to all delegates regardless of race, ethnicity, gender identity or expression, sexual orientation, physical ability, nationality, age, socioeconomic status, and belief. We expect all attendees to foster the exchange of scientific ideas, opinions, and expertise through open and respectful dialogues and to create a safe, inclusive, collaborative, and positive experience for everyone at the Congress and all Congress related events. We expect Congress participants to display respectful behavior at all times. Participants asked to stop any harassing behavior are expected to comply immediately. 9th World One Health Congress organizers will not tolerate scientific misconduct nor harassment of any sort and reserve the right to take any action they deem appropriate, including warning the offender or expulsion from the Congress with no refund.

General information

Credit cards and debit cards

Major credit card brands, namely MasterCard and Visa, are widely accepted in Lisbon. American Express is accepted by some large hotels and shops, but has limited use overall.

Credit or debit card payments will be accepted in most places, but this is not guaranteed or mandatory.

Please check with your bank to understand if there will be any fees on payments or cash withdrawals in Portugal. Banco Montepio and Multibanco ATMs can be found close to the Congress center, including here.

Disability access

If you have any disabilities that may require additional help, please email the congress secretariat, elina.martin@globalohc.org, who will be able to help you with your request.

Emergency

The main emergency number in Portugal is **112**. It is free to call, available 24 hours a day, and connects you to medical, police, and fire services.

Pharmacies

Pharmacies can be found close to the Congress Center:

Farmácia Correia de Azevedo, Rua Luís de Camões, 42-B, Alcântara

- Phone: (+351) 213 638 625
- Open: 09:00 - 19:00

Farmácia Sepol, Calçada da Boa-Hora, 94-A, 1300-096, Lisboa

- Phone: (+351) 937897528
- Open: 09:00 - 19:30 (13:00 on Saturdays, closed on Sundays)

Baby Care Room

A dedicated baby care room offering facilities for parents can be found in room 1.02.

Smoking

Smoking (including vaping and the use of e-cigarettes) is not allowed within the Congress center.

Taxis and public transport

Taxis and public transport options can be found around the Congress Center. If you are arriving by car, CCL is accessible via the A5, A2 and the Ponte 25 de Abril (The April 25th Bridge). The Congress Center has an underground parking garage and an uncovered car park with 1,100 spaces with autonomous management (paid). Taxi apps like Bolt and Uber are available, in addition to traditional licensed taxi services.

Public transport options from the city center include: Tram 15E (from Cais do Sodré station, towards Algés); Bus 732 (from Marquês de Pombal or Avenida da Liberdade); and Bus 728 (Praça do Comércio).

Travelling between Lisbon Airport and the Congress Center

Humberto Delgado Airport is located 12 km from the Lisbon Congress Center (20 minute drive). Transport options from the airport include:

- Taxi - You can find taxis queueing outside the departures and arrivals terminals. Taxi apps like Bolt and Uber are also available, and there is a dedicated area at the airport for picking up passengers with orders on online reservation platforms. This area is located on P2, Level 2, on the arrivals level.
- Bus - At the airport, you can take the bus 722 (towards Restauradores) until Avenida João XXI/Praça de Londres. There change to the bus 756 (towards Rua Junqueira - Centro Congressos), which is the last stop. Then, walk 2 minutes to the Congress Center.
- Metro + Tram/Bus - Take the red line from Aeroporto station to Alameda station, then change to the green line and get off at Cais do Sodré station (last stop). Take the tram 15E (towards Algés) or the bus 728 (towards Restelo) and get off at Rua Junqueira - Centro Congressos. Then, walk 2 minutes to the Congress Center.

For returning to the airport, official guidance recommends arriving at least **3 hours before your flight,** as Lisbon Airport may experience longer-than-usual waiting times.

Please note that while we have provided suggestions and advice, we cannot take responsibility for your journeys to and from the Congress.

Water

Water refill stations will be located throughout the Congress Center. The tap water in Lisbon is regularly tested and safe to drink.

Tipping

Tipping at bars and restaurants is not mandatory or expected in Portugal, but small tips are appreciated.

About the Global One Health Community

The 9th World One Health Congress is organized by the Global One Health Community, a unique, independent and global community that brings together One Health voices from around the world. Our mission is to build bridges and strengthen communication between science and policy in a rapidly changing world. More information on GOHC can be found at globalohc.org.

We are honored that the 9th World One Health Congress has received the official patronage of UNESCO, and is also an endorsed initiative under the International Decade of Sciences for Sustainable Development.

Commitment to environmental sustainability

GOHC has implemented a range of practices to minimize the environmental footprint of the 9th World One Health Congress. Paper usage has been reduced to an absolute minimum. GOHC has introduced a fully electronic registration and abstract management system, with email used for communication with delegates, faculty, and committee members. To save paper and printing, the congress Abstract Book and full Program Book are available exclusively in electronic format. Water refill stations will be located throughout the Congress Center, encouraging the use of reusable bottles to minimize waste of single use plastics and beverage packaging.

GOHC calls upon its participants to help us make the 9th World One Health Congress a more sustainable event. All feedback and suggestions are highly appreciated.

Availability of recordings and proceedings after the Congress

Following the 9th World One Health Congress, the proceedings will be published in One Health Outlook, a part of Springer Nature. A report of the Science Policy Interface track will also be made available at globalohc.org.

All Congress sessions will be recorded and available for viewing on-demand after the Congress. Footage may also be used for global One Health Community educational purposes.

The virtual platform will remain open until the end of the year for all live and On Demand participants, offering access to session recordings, participant profiles, digital posters, and more.

Sponsors

In partnership with Canada
GORDON AND BETTY MOORE FOUNDATION
IDC
Boehringer Ingelheim
Ceva
ESWI
SCIENTISTS FIGHTING INFLUENZA AND OTHER ACUTE RESPIRATORY VIRUSES
dgav
Direção Geral de Alimentação e Veterinária
sanofi
PREZODE
Preventing zoonotic disease emergence
WORLD BANK GROUP
BLUESQUARE
LUSÓFONA
fmv
BCOMING
BE PREP
RESTOREID
Healthier landscapes for a stronger future
CALOUSTE GULBENKIAN FOUNDATION
CABI
Global Strategy Lab
NORTH AMERICA ONE HEALTH UNIVERSITY NETWORK
One Health Outlook
OH AMR
CGIAR
ILRI
Centres of Excellence
U.PORTO
ICBAS
SCHOOL OF MEDICINE AND BIOMEDICAL SCIENCES
One Health Commission
UNIVERSIDADE DE ÉVORA
VSF
World Organisation for Animal Health
UPPARTNER
Supported by
visit Portugal

Complete Program

All times are in WEST. This schedule may still change; the most recent version is available at wohc2026.globalohc.org.

Thu 3 Sep 2026

09:00 - 18:00 **SE**

SE01 Side Event: One Health in tropical settings - training day for Lusophone countries - in Portuguese · Institute of Hygiene and Tropical Medicine

Fri 4 Sep 2026

08:30 - 10:00 **PLE**

PLE01 Plenary opening and keynotes · Auditorium I

Chairs: *Ab OSTERHAUS · John MACKENZIE · Jomana MUSMAR · Dominique CHARRON*

- Welcome address by the congress chairs — *Ab OSTERHAUS*
- UNESCO: Advancing One Health through Science for Sustainable Development — *Shaofeng HU*
- Health Beyond Boundaries: Realizing the Promise of One Health — *Emmanuelle SOUBEYRAN*
- Advancing the European Health Union through One Health — *Sandra GALLINA*
- Copenhagen, Lyon, Lisbon: Carpe diem Europe — *Carlos DAS NEVES*
- Feedback from the Lyon Summit and actions spanning from it — *Anne-Françoise BERTHON*
- From Science to Strategy: Ireland's EU Presidency Vision for One Health — *Mary HORGAN*

10:00 - 11:00 **SPS**

SPS01 Partner Session organized by Global Affairs Canada: Multisectoral Collaboration to Counter Deliberate Biothreats · Auditorium I

Chairs: *Keith HAMILTON*

- Panel discussion — *Trevor SMITH*

11:00 - 11:30 *Refreshment break*

11:30 - 13:00 **SCS**

SCS01 Climate change, Environment, Ecosystems Health - session 1 · Auditorium I

Chairs: *Julian BLANC · Rumbidzai GONDO*

- Climate-driven Expansion of Vibrio vulnificus: Global Genomics Reveals Environmentally Persistent Pathogenic Lineages — *Anders DALSGAARD*
- Flooding the frontlines: Consequences of summer inundation on the ecology of mosquito-borne diseases — *Reina SIKKEMA*
- Analysis of the 2025 Chikungunya Outbreak in Foshan, China, from a One Health Perspective — *Yuan ZHANG*
- Climate Change and expanding sandfly activity in Sicily over ten years of surveillance within a One Health Framework — *Maria Liliana DI PASQUALE*
- When extreme heat fuels infection: Machine Learning Evidence from Hospital Admissions in Portugal (2000–2018) — *Maria Miguel OLIVEIRA*
- One Health and the Climate Agenda in Brazil: Integrating the Triple Planetary Crisis into Health Governance, Equity, and Strategic Response toward COP30 — *David SOEIRO-BARBOSA*

SPI

SPI01 Knowledge, Education & Communities · Auditorium II

Chairs: *Salome BUKACHI · Abdoul Kader ILBOUDO*

- Insights from the Collaborative One Health Research Initiative on Epidemics Across Africa and Latin America — *Stéphanie MALTAIS*
- A One Health Curriculum Self-Assessment Checklist for Evaluating Competency Integration in Higher Education — *Katie NOLAN*
- Development and Implementation of the Field Training for the Wildlife and Environment Sector Professionals – the Compliment to FETP and FETPV — *Jonathan SLEEMAN*
- Community One Health Units: A gender responsive One Health approach to zoonotic diseases control in Burkina Faso — *Abdoul Kader ILBOUDO*
- Grounding Ethics in Climate Change and Health Research: A collaborative study triangulating perspectives of the communities, researchers and ethical committees — *Soledad COLOMBE*
- Evaluating the Value of One Health: Results from the Quadripartite Online Course on Economic Evaluation Methods — *Danny SHEATH*
- Community-centred tools for One Health operationalisation in the Horn of Africa — *Siobhan M. MOR*

SPI

SPI02 Taming the Resistant: A One Health Policy Pathway for the fight against AMR · Room 1.08 - 50 pax

Chairs: *Helen CALLABY*

- Antimicrobial resistance and political advocacy – the role of civil society — *Nicholas BROWN*
- No diagnosis, no defense; strengthening the call for diagnostics — *Helen CALLABY*
- From Aquaculture to Parliament: An Early Career Researcher's Perspective on AMR Policy — *Ava DRAKE*
- AMR in the UK parliament: replacing 20th century hubris with post-Pasteurian realism — *Natalie BENNETT*

WS **WS01 Workshop: Virtual Deployment: Simulating Rapid Response Mobile Laboratory Operations and Diagnostic Workflows Using Virtual Reality** · Room 1.10 - 50 pax

Chairs: *Ahmed ABD EL WAHED*

- Introduction of the PREPARE-TID project — *Sara SAVIC*
- Immersive VR Rotation — *Sara SAVIC*
- Debrief and Q&A — *Sara SAVIC*

WS **WS02 Workshop: One Health in Social-Ecological Systems research methods** · Room 1.06 - 45 pax

Chairs: *Jakob ZINSSTAG*

- One Health in Social-Ecological Systems research methods — *Jakob ZINSSTAG*
- Development of the One Health in Social-Ecological Systems (OHSES) method — *Jakob ZINSSTAG*
- The mathematical and economic game theoretical framework of OHSES — *Artemiy DIMOV*
- The formal inclusion of plant and ecosystem health in OHSES: case examples — *Urs SCHAFFNER*
- Moderated panel discussion on the OHSES method — *Jakob ZINSSTAG*

WS **WS03 Workshop: Building Skills for Community-Engaged One Health Research** · Room 1.07 - 45 pax

Chairs: *Elizabeth FINNIS*

- Introduction to Community-Based Research Approaches — *Elizabeth FINNIS*
- Using Participatory Mapping to Engage Communities in Identifying Environmental Risks to Human and Animal Health — *Heather MURPHY*
- Conducting Rapid Situational Analysis with Communities to Understand Systems and Key Challenges, and to Collaboratively Define Research Questions and Goals — *Silvia SARAPURA - ESCOBAR*
- Exploring Key Steps in Initiating a Conservation and Development Project Using a One Health Approach in the Context of Humanitarian and Conservation Crises — *Travis STEFFENS*

13:00 - 14:00 *Welcome Lunch and networking*

14:00 - 15:30 SCS **SCS02 Pathogens, Microbiome, & Intervention Strategies** · Auditorium I

Chairs: *Marietjie VENTER* · *Jolyn OOSTERS*

- Genomic Diversity, Evolutionary Dynamics, and Intervention Needs for Swine Influenza A virus in Europe: Insights from the European Swine Flu Network (ESFLU) and Cross Sector Pathogen Surveillance — *Gwenaëlle DAUPHIN*
- Beyond surveillance: viral genomics to uncover local transmission and inform strategies for urban rabies elimination — *Kirstyn BRUNKER*
- Dogs as carriers of highly pathogenic Campylobacter jejuni with cross-species neuropathogenic potential — *Maria-Leonor LEMOS*
- Persistent High-Pathogenic Avian Influenza Hotspots in Vietnam — *Thuy THI HOANG*
- Peptide microarray-based epitope profiling enables pan-orthoebolavirus surveillance and differential serodiagnosis for acute Ebola virus disease versus prior exposure or vaccination — *Nischay MISHRA*
- Rabies treatment revolution: intravenous immunotherapy to combat a global zoonosis — *Guilherme DIAS DE MELO*
- NECROBIOME – Microbiome of the Cinereous Vulture to Support Integrated Ecosystem Management in Baixo Alentejo — *Diana V. JORGE*

SPI **SPI03 Governance, Policy & Legal Frameworks** · Auditorium II

Chairs: *Natalia CEDIEL* · *Tasmin ALEXANDER*

- From Data Silos to Shared Governance: Developing Policy and Legal Frameworks for Wildlife Data Integration in Pandemic Early Warning — *Tracey MCNAMARA*
- Between Policy and Practice: A Qualitative Assessment of National One Health Governance Structures and Legal Framework Gaps Across Sub-Saharan African Countries — *Yusuff AZEEZ*
- Strengthening Global Wildlife Health for better One Health – The WOAH Global Wildlife Health Collaborating Centre Network (WOAH-WildNet) — *Sascha KNAUF*

- Strengthening One Health Governance in Eastern and Southern African: Structures, Systems, Strategies, and Outcomes from multi-sectoral engagement — *Simon ANGOMBE*
- One Health Systems Readiness Assessment in Croatia, Ghana and Nigeria to support Evidence-informed Policy Making — *Anna S FAHRION*
- Water-Related Exposure and Systemic Constraints in Schistosoma mekongi Endemic Region: A One Health Perspective — *Xiao-Xi ZHANG*

SPI **SPI04 From International Instruments to On-the-Ground Implementation: Wildlife Health, Surveillance, and One Health Risk Reduction** · Room 1.08 - 50 pax

Chairs: *Manon MISPIRATCEGUY* · *Mathieu PRUVOT* · *Francette DUSAN* · *Sarah OLSON*

- Wildlife Health for Pandemic Prevention, Livelihoods and Food Security — *Lina AWADA*
- From Global to Local: Integrated Approaches to Reducing Health Risks from Wildlife Trade and Use — *Chadia WANNOUS*
- Risk Pathways and Governance in Wildmeat Value Chains — *Ekta PATEL*
- Legal and Illegal Wildlife Trade and Health in the Andes–Amazon Region — *Paulo COLCHAO CLAUX*
- Wildlife, Health, and Rural Livelihoods in Lao PDR — *Watthana THEPPANGNA*
- Co-Developing One Health Approaches with Alaska Native Communities — *Michelle JOHANNSEN*
- Q&A and discussion — *Manon MISPIRATCEGUY*
- Integrating Wildlife Health Surveillance into National One Health Frameworks — *Lesa THOMPSON*
- A Community of Practice-Developed Theory of Change for Strengthening WHS Systems — *Jonathan SLEEMAN*
- WildHealthNet Cambodia: a national wildlife health surveillance network in action — *Lucy KEATTS*
- Civil Society Contributions to National Wildlife Health Surveillance Systems: Example from Peru — *Paulo COLCHAO CLAUX*
- Participatory Wildlife Surveillance with Hunters in the Congo — *Eeva KUISMA*
- An Australian National Wildlife Surveillance Network for One Health — *Tiggy GRILLO*
- Q&A and discussion — *Sarah OLSON*

SPI **SPI16 Financing One Health: Sourcing Funding, Structuring Investments, and Involving Private Sector Partners** · Room 1.05 - 45 pax

Chairs: *Junxia SONG* · *Shiyong WANG*

- Financing One Health: Sourcing Funding, Structuring Investments, and Involving Private Sector Partners — *Shiyong WANG*

WS **WS05 Workshop: Empowering Youth for Antimicrobial Resistance Action: Capacity Building and Community Engagement Approaches within a One Health Framework** · Room 1.06 - 45 pax

Chairs: *Anna LIAKOPOULOU* · *Matilde ROCHA*

- Setting the Scene: Beyond Awareness: Meaningful Youth Engagement in AMR Implementation — *Anna LIAKOPOULOU*
- Recorded contribution: From Youth-Led Action to NAP Implementation: Practical Lessons from Nigeria — *Damilola ADESUYI*
- Recorded Contribution, Xavier Canavilhas: Using One Health Data for Action: Lessons from Veterinary Surveillance and Cross-Professional Collaboration — *Anna LIAKOPOULOU*
- Interactive Training Segment: Designing a Practical Youth-Inclusive AMR Action — *Anna LIAKOPOULOU*

WS **WS07 Workshop: Simulating One Health in Action: A Card Game for Transdisciplinary Zoonotic Outbreak Response, Policy Decision-Making, and Systems-Level Collaboration** · Room 1.10 - 50 pax

Chairs: *Jessica SCHWIND* · *Jill JOHNS*

15:30 - 16:00 *Refreshment break*

16:00 - 17:30 SCS **SCS03 Food Systems, Agriculture & Plant Health** · Auditorium I

Chairs: *Junxia SONG* · *Carlos DAS NEVES*

- Genomic Ecological Microbial Source Tracking for Oceans, Nature, and the Environment (GEMSTONE): a One Health Fecal Source Tracking Approach to Support Communities and Industry — *Michael LEE*
- Establishing a Continental Roadmap for Food Safety and Health Security: Development and Validation of the Africa CDC Food Safety Strategic Framework (2026–2030) — *Yahya KANDEH*

- Promoting Health and Resilience of agricultural social-ecological systems in LMI countries: three strategies and proofs of concepts — *Michel DE GARINE-WICHATITSKY*
- Impact of an Integrated Livestock Management Intervention to Prevent the dry-Season Peak of Child Acute Malnutrition in Pastoral and Agro-Pastoral Communities in Chad: Evidence from a Cluster Randomized Controlled Trial — *Gwenaelle LUC*
- The global epidemiology of botulism outbreaks from open-source intelligence, 2017–2024 — *Damian Alexander HONEYMAN*
- Mapping Foodborne Streptococcus suis Risk across the Pork Value Chain in Nan Province, Thailand, 2025-2027: A One Health Approach to Food Systems and Cultural Practices with Joint Risk Assessment Tools — *Pitiphon PROMDUANGSI*

SPI

SPI05 One Health Implementation & Financing · Auditorium II

Chairs: *Jonathan RUSHTON* · *Maria Jose LOPEZ JARA*

- Working across boundaries: development of the Nuts a maht ('we are one') | One Health framework for the Province of British Columbia, Canada. — *Erin FRASER*
- Water security, food security and health in pastoral systems in northern Kenya; Fuzzy Cognitive Mapping to understand opportunities and barriers for One Health programs — *Sirimon THOMAS*
- Upstream by Design: Continuous Network Stewardship as a Model for Resilient One Health Implementation in Low- and Middle-Income Countries — *Mary GUTTIERI*
- One Health in AMR: Findings from evaluation of UK Fleming Fund programme — *Syed ABBAS*
- Mapping the funders of One Health research — *Hideo ISHII-ADAJAR*
- The Wealth Paradox: Survival Analysis of Behavioral Sustainability in Taenia solium Preventive Practices, Tanzania. — *Antony NYERERE*

SCS

SCS04 REVEAL: Rodent Ecology and Viral Emergence: Anthropogenic Links. Understanding rodent-borne viruses in a changing world by quantifying viral dynamics to predict and prevent spillover risk · Room 1.05 - 45 pax

Chairs: *Barbara HAN* · *James HASSELL*

- Introduction and overview of the subject — *Barbara HAN*
- Quantifying Zoonotic Risk at the Viral Community Level — *Gladys ATIM*
- Investigating Environmental Determinants of Transmission — *Rodolfo CERIANI*
- Linking Rodent Behaviour to Viral Dynamics — *Fanohinjanaharinirina RASOAMALALA*
- Understanding Integrated Risk to Rodent-borne Disease — *Emilia JOHNSON*
- Panel discussion and closing remarks — *Barbara HAN*

SCS

SCS06 Moving Upstream: Exposome-Informed One Health · Room 1.08 - 50 pax

Chairs: *Amélie DESVARS-LARRIVE* · *Francette DUSAN*

- From Social Determinants to Ecological Foundations of Health — *Chris WALZER*
- Health Determinants, Interventions and Prevention Through Community Lenses — *Salome BUKACHI*
- Operationalizing Upstream Prevention: Systems Thinking for Exposome-Informed One Health — *John AMUASI*
- Ecological Change and the Pathogen Exposome: How Biodiversity Loss Shapes Emerging Health Risks — *Serge MORAND*
- Understanding Upstream Determinants through Two-Eyed Seeing — *Susan KUTZ*
- The Soil Exposome: How Soil Health Shapes Food, Ecosystems, and Human Well-being — *Kaushik MAJUMDAR*
- Governance and Systems Change: Embedding Ecosystem and Wildlife Health in One Health Decision-Making — *Katie WOOLASTON*

SPI

SPI06 Strengthening One Health Governance for Antimicrobial Resistance: Latest Evidence and Case Studies · Room 1.06 - 45 pax

Chairs: *Geneviève BOILY-LAROUCHE*

- Introduction of panelists and framing of presentation and discussion — *Geneviève BOILY-LAROUCHE*
- One Health Governance and Antimicrobial Resistance (AMR): Conceptual Reflections — *Taylor HECKER*
- One Health governance of AMR in Rwanda: Lessons and Ways Forward — *Gloria IGIHOZO*
- Assessment of the integration of One Health principles: the case of antimicrobial resistance governance in Senegal — *Mouhamadou Moustapha SOW*
- AMR Implementation and One Health governance in Canada — *Raphael AGUIAR*

SPI

SPI09 Session: One Health in Higher Education and University led Networks · Room 1.07 - 45 pax

Chairs: *Michael LAIRMORE*

- One Health in Higher Education and University led Networks — *Elmobashar FARAG*
- North American One Health University Network — *Sid THAKUR*
- Una Europa One Health University Network — *Bruno GONZALEZ-ZORN*
- Southeast Asia One Health University Network — *Tongkorn MEEYAM*
- Africa One Health University Network — *Irene NAIGAGA*
- Middle East and North Africa One Health University Network — *Elmobashar FARAG*
- Latin America, Ibero and the Caribbean regional University Networks — *Christina PETTAN-BREWER*
- One Health Global Alliance — *Wondwossen GEBREYES*
- Moderated Q&A with the audience — *Michael LAIRMORE*

17:40 - 18:30

SCS

SCS07 Biosecurity, biosafety, global health security · Auditorium I

Chairs: *Lawrence MADOFF · Koketso Desiree MAZWI*

- Bat-Associated Pteropine Orthoreovirus Linked to Nipah-Like Illness Following Raw Date-Palm Sap Consumption in Bangladesh — *Ariful ISLAM*
- Bridging Biosecurity and Public Health: Operationalising One Health Field Epidemiology through the HSPA Model for Biothreat Reduction — *Stacie DUNKLE*
- Harnessing the Power of Conservation for Global Health Security — *Chris WALZER*
- Addressing Biothreats: Reinforcing the Legal and Regulatory Framework for the Implementation of the Biological Weapons Convention — *James PETTIT*

SPI

SPI07 The critical role of the private sector and civil society in One Health implementation · Auditorium II

Chairs: *Dominique CHARRON*

- Role of the Public-private partnership in the implementation of One Health vaccination strategies: Evaluation of behavioural and policy changes following the application of the EVACS modelling tool — *Claire HAUTEFEUILLE*
- Operationalising One Health through Interoperable Data Systems for Preparedness, Surveillance, and Response to Health Emergencies — *Gaspard PAIRAULT*

SCS

SCS05 Antimicrobial Resistance Data Systems and Informatics Solutions across Africa and Asia-Pacific · Room 1.08 - 50 pax

Chairs: *Jacob CLEMENTE*

- Antimicrobial Resistance Data Systems and Informatics Solutions across Africa and Asia-Pacific — *Jacob CLEMENTE*
- Welcome and introduction — *Jacob CLEMENTE*
- Overview of the Global Antimicrobial Resistance Informatics Discovery Project — *Paul JANKAUSKAS*
- Kenya's One Health Antimicrobial Surveillance System and Digitalization — *Susan MAHURO GITHII*
- The Philippines's Database Solution for Interoperable Phenotypic and Genotypic Antimicrobial Resistance Data — *June GAYETA*

SPI

SPI08 Developing One Health Competencies for Tomorrow: The FAO/WHO/WOAH Joint One Health Learning Taskforce in Action · Room 1.05 - 45 pax

Chairs: *Barbara ALESSANDRINI*

- Developing One Health Competencies for Tomorrow: The FAO/WHO/WOAH Joint One Health Learning Taskforce in Action — *Barbara ALESSANDRINI*
- Setting the scene — *Barbara ALESSANDRINI*
- Launch of the JOHLT Learning Need Assessment, Wrap up and take-home message — *Barbara ALESSANDRINI*
- JOHLT Mandate: Tripartite Vision for Competency-Based OH Learning — *Chadia WANNOUS*
- Evidence to Learning: Where are the training needs? — *Fairouz LARFAOUI*
- Platforms and Pathways: Delivering JOHLT Learning at Scale — *Taraneh SHOJAEI*
- Panel discussion and interactions with the audience — *Junxia SONG*

SPI

SPI10 Closing the gap between One Health policy commitments and ground-level action: lessons from dog-mediated rabies elimination · Room 1.07 - 45 pax

Chairs: *Nai Rui CHNG · Tasmin ALEXANDER*

- Panel Submission: Closing the gap between One Health policy commitments and ground-level action: lessons from dog-mediated rabies elimination — *Nai Rui CHNG*
- How the Persistence of Culling of Free-Roaming Dogs Highlights the Gap Between One Health Policy Commitments and Ground-Level Action — *Tasmin ALEXANDER*

- The Ingredients for Translating Good Intentions Into Action — *Eric BRUM*
- Whose Knowledge Counts? Community Expertise in One Health Rabies Elimination — *Camille BARKER*
- Oral Rabies Vaccination for Canine Rabies Elimination — *Gowri YALE*
- Lessons From Implementing One Health Rabies Control in Tanzania — *Kennedy LUSHASI*
- Structured Questions and Audience Q&A — *Nai Rui CHNG*
- Closing remarks — *Nai Rui CHNG*

18:30 - 19:30 *Welcome reception and networking*

Sat 5 Sep 2026

08:00 - 08:50 **SPS** **SPS02 Company, Organization lectures** · Auditorium I

Chairs: *John MACKENZIE*

- Integration of One Health Approaches in Tropical Medicine — *Júlio CARVALHO*
- Choosing the Appropriate Vaccine Technology for the Pathogen and Specific Animal (and Human) Health Requirements — *Gwenaëlle DAUPHIN*
- One Health Secure: Ten Years of EU Partnership for Preparedness and Resilience across regions — *Anne-Sophie LEQUARRE*

09:00 - 10:30 **PLE** **PLE02 Plenary session: One Health Governance: where does the EU stand?** · Auditorium I

Chairs: *Roser DOMENECH*

- Welcome and introduction — *Roser DOMENECH*
- From recommendations to action: what have we achieved so far? — *Carlos DAS NEVES*
- What role does research play in effective One Health policy — *Pilar AGUAR FERNÁNDEZ*
- Scientific Advice Mechanism Opinion “pulse check” — *Jakob ZINSSTAG*
- The Politicians view: Why One Health matters - now more than ever — *Sirpa PIETIKÄINEN*
- Delivery on the ground — *Ludovico SEPE*
- Moderated discussion — *Roser DOMENECH*
- Closing and takeaways — *Roser DOMENECH*

10:30 - 11:00 *Refreshment break*

11:00 - 11:40 **SPI** **SPI11 One Health in humanitarian contexts: climate change, conflict and forced migration** · Room 1.08 - 50 pax

Chairs: *Dorien BRAAM* · *Julianne MEISNER*

- Operationalizing One Health in fragile and conflict-affected settings — *Said ABUKHATTAB*
- Conducting One Health research in the face of civil conflict and extreme weather emergencies — *Amira ROESS*
- Impact of forced displacement on rabies transmission and strategies to prevent fatal outbreaks in the humanitarian setting — *Monique LÉCHENNE*
- Delivering One Health at the last mile: Animal health in contexts of conflict and forced migration — *Giorgia ANGELONI*

11:00 - 12:30 **SCS** **SCS09 Biodiversity, Wildlife & Pathogen Interfaces - session 1** · Auditorium I

Chairs: *Tiggy GRILLO* · *Clément LABARRERE*

- Metagenomic surveillance of rodents reveals the impact of deforestation and seasonality on pathogenic viral diversity and evolution — *Charles C.Y. XU*
- Habitat disturbance drives turnover in mosquito and virus communities across major tropical ecosystems — *Selina Laura GRAFF*
- A Market-Based Sentinel Surveillance for an Early Detection of Viral Outbreaks — *Paola MARTÍNEZ-DUQUE*
- Protected Areas and One Health: Insights and the MAP-ACT-CREATE for One Health toolkit for minimizing disease risks from an IUCN WCPA Task Force — *Sarah H. OLSON*
- Tackling the Biodiversity-Pandemics relationship at the roots through research policy transformation — *Serge MORAND*
- From detection to preparedness: A One Health approach to arbovirus surveillance in Canada’s changing climate — *Jumari SNYMAN*
- Global Sentinels: The Palearctic-Afrotropical Flyway as a Conduit for Antimicrobial Resistance in Wintering Little Stints (Calidris minuta) — *Catherine MBUTHIA*

SPI **SPI12 Structuring One Health cooperation among EU Agencies** · Auditorium II

Chairs: *Carlos DAS NEVES* · *Sigrid WEILAND*

- Structuring One Health cooperation among EU Agencies — *Stef BRONZWAER*
- ONE – how the Task Force begun — *Stef BRONZWAER*

- Framing the action — *Ole HEUER*
- In practice — *Gerardo SANCHEZ MARTINEZ*
- Lessons learned — *Evelin FABJAN*
- Challenges & Opportunities — *Ana Belen VIDAL GALLEGO*
- Intermezzo, Panel debate, Q&A — *Carlos DAS NEVES*

WS **WS06 Workshop: Practical AI for One Health Surveillance: A Beginner-Friendly Introduction to Zoonotic Disease Analysis** · Room 1.05 - 45 pax
Chairs: *Jessica SCHWIND* · *Jill JOHNS* · *Andrea KING*

WS **WS08 Workshop: Species distribution modelling for emerging infectious diseases** · Room 1.06 - 45 pax
Chairs: *Monika MOIR* · *Carla MAVIAN* · *Jenicca POONGAVANAN*

WS **WS09 Workshop: From Evidence to Action: How to Bridge the Gap Between Scientists and Decision-Makers to Solve Global One Health Challenges** · Room 1.10 - 50 pax
Chairs: *Lucy HARPER*

- From Evidence to Action: How to Bridge the Gap Between Scientists and Decision-Makers to Solve Global One Health Challenges — *Daisy NEALE*

11:50 - 12:30 SPI **SPI13 The Future of Global Health Cooperation: Risks, Resilience, and Reform** · Room 1.08 - 50 pax
Chairs: *Isabelle COCHE*

- Implications for norm-setting and global standards of weakening multilateral institutions: the role of WHO — *Claudia EMERSON*
- Innovation under constraint: Funding gaps, new tools and lessons learned from the malaria space — *Delphine THIZY*
- Moderated discussion — *Isabelle COCHE*

12:30 - 14:00 *Lunch break*

12:45 - 13:45 SPS **SPS07 From Response to Prevention: Financing and Partnerships for Sustainable One Health Impact - organized by Prezode and the World Bank** · Auditorium I
Chairs: *Marisa PEYRE* · *Andre CARLETTO*

SPS **SPS03 The societal value of animal disease prevention: vaccines in the real world** · Auditorium II
Chairs: *Benjamin HUNTINGTON*

14:00 - 15:30 SCS **SCS10 Antimicrobial resistance - session 1** · Auditorium I
Chairs: *Ricardo SOARES MAGALHAES* · *Ri SCARBOROUGH*

- Tracking Tuberculosis and Antimicrobial Resistance in Sub-Saharan Africa Through Wastewater-Based Surveillance: A One Health Approach — *Hlengiwe Nombuso MTETWA*
- From Supermarket Demands to Farm Decisions: Contextualising antibiotic use in Agriculture — *Laura HARDEFELDT*
- Environmental and Clinical Surveillance of Antimicrobial Resistance Along the Paraopeba River Basin Following a Mining Disaster in Brazil — *César R. MOTA FILHO*
- Revised African Union Framework for Antimicrobial Resistance Control 2026 - 2030: Strategic shift from high-level intent to practical, measurable interventions — *Nyambura MOREMI*
- Environmental Antimicrobial Resistance, Wildlife and Biodiversity in Tunisia: A One Health Approach Aligned with the Kunming-Montreal Global Biodiversity Framework — *Haifa EL HENTATI*
- Understanding the potential for the Community Dialogue Approach to tackle antimicrobial resistance: Evidence from a randomised control trial and process evaluation in rural Bangladesh. — *Jessica MITCHELL*
- Strengthening One Health surveillance in animal populations and food systems through the International FAO Antimicrobial Resistance Monitoring System (InFARM) — *Lina AWADA*

SPI **SPI14 Bridging Policy-to-Practice: Implementing the One Health Joint Plan of Action at National Level** · Auditorium II
Chairs: *Chadia WANNOUS*

- Opening and Framing of the Session — *Amina BENYAHIA*

- From Global Strategy to National Action: Introduction to the OH JPA and its Implementation Guide, including progress from regional and country initiatives — *Junxia SONG*
- Evidence and Systemic Insights: OHHLEP findings on key enablers and barriers to OH JPA implementation and recommendations for national operationalization — *Wanda MARKOTTER*
- Country Experience: Conducting a national One Health situation analysis to identify gaps and priorities — *Sanam KHUDAIBERGENOVA*
- Country Experience: Establishing and operationalizing multisectoral coordination mechanisms across sectors — *Anhui LIN*
- Country Experience: Translating priorities into a costed National One Health Action Plan — *To be confirmed*
- Interactive Panel Discussion: lessons learned from global guidance and country implementation — *Chadia WANNOUS*
- Q&A with audience — *Julian BLANC*
- Summary and Close of session — *Julian BLANC*

SPI **SPI15 From Governance Analysis to Practice: Integrating the Environmental Dimension into National One Health AMR Strategies** · Room 1.08 - 50 pax

Chairs: *Raphael AGUIAR*

- From Governance Analysis to Practice: Integrating the Environmental Dimension into National One Health AMR Strategies — *Srinivasa SRIGIRI*
- Welcome and Introduction — *Raphael AGUIAR*
- Towards the integration of the environmental dimension in AMR governance in Senegal — *Marion BORDIER*
- Institutional analysis for environmental integration in AMR strategies of Cambodia — *Srinivasa SRIGIRI*
- Interventions to mitigate the environmental spread of AMR in Tanzania — *Sunday OCHAI*
- Panel discussion and Q&A — *Srinivasa SRIGIRI*
- Closing remarks — *Raphael AGUIAR*

WS **WS11 Strengthening One Health Response by applying the 7-1-7 Framework to Timeliness Analysis: an Interactive Training** · Room 1.05 - 45 pax

Chairs: *Barbara KNUST* · *Grace GORYOKA*

WS **WS19 Workshop: A One Health Framework for Biosecurity on Islands** · Room 1.10 - 50 pax

Chairs: *Katey PELICAN* · *Jamechia HOYLE*

WS **WS22 Workshop: Networking as a Driver of One Health Operationalization: Lessons learned and beyond** · Room 1.06 - 45 pax

Chairs: *Nicolas ANTOINE-MOUSSIAUX*

- The bottom-up emergence of NEOH — *Barbara HAESLER*
- Afrique One — *Bassirou BONFOH*
- Workshop on successful networking — *Nicolas ANTOINE-MOUSSIAUX*

15:30 - 16:00 *Refreshment break*

16:00 - 17:30 SCS **SCS11 Data, Technology & Innovative Analytics** · Auditorium I

Chairs: *Ricardo MEXIA* · *Paulos LEMMA LEMOS DE JESUS LOUREIRO*

- Designing the PREZODE International Platform: A Collaborative Information System for Prevention of Zoonotic Diseases within a One Health Framework — *Paula CACERES*
- Digital Interoperability for One Health Surveillance in Guinea: Automated Information Exchange between Animal and Public Health Systems — *Lisette KOHAGNE TONGUE*
- Development and Implementation of a Nationwide Electronic Health Record-Based (EHR) Surveillance Platform for Vector-Borne, Zoonotic, and Environmentally-Transmitted Infectious Diseases: The Veterans Health Administration (VHA) as a Sentinel Network — *Julienne REYNOLDS*
- EFSA's Horizon Scanning for Plant Health: Advancing OneHealth for Enhanced Early Warning — *Sara Valentina TRAMONTINI*
- Metagenomics, Wastewater, and One Health: A Non-Invasive Pan-Pathogen Approach for Zoonotic Surveillance in LMICs — *Juliana GIL*
- Interoperable Digital Surveillance Tools for One Health Early Warning in Animal Health Systems — *Gisela GIOIA*
- TREADS: A Scalable, Interoperable One Health Security Ecosystem for Early Warning and Decision Support — *Lauren CHARLES*

SPI **SPI17 Operationalizing One Health: Translating Enablers, Dismantling Barriers and Aligning Global Policy** · Auditorium II

Chairs: *Wanda MARKOTTER* · *Carlos DAS NEVES*

- Operationalizing One Health: Translating Enablers into Practice, Dismantling Barriers and Aligning Global PolicyOperationalizing One Health: Translating Enablers into Practice, Dismantling Barriers and Aligning Global Policy — *Amira PREURE*
- Opening and Framing of the Session — *Wanda MARKOTTER*
- The Enablers and Barriers Analysis and Recommendations — *Nitish DEBNATH*
- Global Normative Instruments and One Health Governance — *Gian Luca BURCI*
- Interactive Panel Discussion and Q&A: Translating Global Policy into Action — *Wanda MARKOTTER*
- Close of session — *Amina BENYAHIA*

SCS **SCS12 Zoonotic Threats in a Changing World: Advanced Tools, Laboratory Capacity Building and Partnerships for Early Detection and Rapid Response** · Room 1.06 - 45 pax

Chairs: *Farai MUCHADEYI*

- Opening remarks — *Farai MUCHADEYI*
- Strengthening Zoonotic Disease Preparedness through ZODIAC and the VETLAB Network — *Charles Euloge LAMIEN*
- One Health in Action: Strengthening Pandemic Prevention and Preparedness at the Wildlife-Livestock-Human Interface — *Lina AWADA*
- Panel Discussion: From Innovation to Sustainable Impact: Practical examples of building Laboratory capacity for Future Pandemic Preparedness — *Marietjie VENTER*
- Country testimonial: Capacity and Regional Leadership: Advancing Genomic Surveillance and Outbreak Response for Emerging Zoonotic threat in West Africa case of Senegal — *Assane Gueye FALL*
- Country testimonial: Operationalizing One Health: Harnessing Advanced Diagnostic Platforms and Cross-Sectoral R&D for Zoonotic Threat Detection — *Ni Luh Putu Indi DHARMAYANTI*
- Country testimonial: Building Sustainable Veterinary Laboratory Capacity: Ghana's Experience in Decentralized Diagnostics and Pandemic Preparedness — *Theophilus ODOOM*

SCS **SCS18 Restoring nature, reducing risk: ecosystem-based approaches to zoonotic disease prevention** · Room 1.07 - 45 pax

Chairs: *Frauke ECKE*

- Restoring nature, reducing risk: ecosystem-based approaches to zoonotic disease prevention — *Frauke ECKE*
- The relationship between ecosystem restoration and disease risk - a global approach — *Frauke ECKE*
- Forest restoration and zoonotic disease risk in Brazil – when the context matters — *Paula RIBEIRO PRIST*
- Does ecosystem restoration reduce zoonotic risk? Integrating eDNA, acoustic monitoring and pathogen prevalence across restoration gradients to assess restoration-disease linkages — *Lucinda KIRKPATRICK*
- Co-constructing context-adapted solutions to improve biodiversity and reduce zoonotic risks: results from a participatory process implemented in three tropical biodiversity hotspots — *Julien CAPPELLE*
- Challenges of interdisciplinary work on how ecosystem degradation and restoration in tropical forests are related to pathogen discovery at the human-animal interface — *Jan Felix DREXLER*
- Round table discussion — *Frauke ECKE*

WS **WS14 Workshop: The One Health Mural: An Interactive Systems-Thinking Tool to Strengthen Multisectoral Understanding and Action on Complex Health Challenges** · Room 1.10 - 50 pax

Chairs: *Florence AYRAL* · *Alexis PEUTOT*

17:30 - 19:00 POS **POS01 Poster presentations and refreshments - session 1 - Olive Tree** · Foyer D and Pavillon 4

Sun 6 Sep 2026

08:00 - 08:50 SCS **SCS13 Biodiversity, Wildlife & Pathogen Interfaces - session 2** · Auditorium I

Chairs: *Peter DASZAK* · *Catherine MBUTHIA*

– From rats to residents: Orthohantavirus at the human–rodent–environment interface in informal urban settlements in Brazil — *Ana Maria BARRETO*
– Land-use change restructures mammal communities and reshapes zoonotic pathogen dynamics in Amazonian landscapes — *Maricruz JARAMILLO*
– Air sampling coupled with metagenomics accurately captures zoonotic virus diversity emerging from pig slaughterhouses in Cambodia — *Peter CRONIN*
– Health hazards in Peru's wildlife trade: Toward Operationalizing One Health — *Paulo COLCHAO-CLAUX*

SPS **SPS04 Partner Session organized by IDC: "Breath & Beyond: The IDC - A Model for Interdisciplinary Research Collaboration** · Auditorium II
Chairs: *Marco GOEIJENBIER · Kirsty SHORT · Tor BIERING-SØRENSEN*
– The IDC Story: Building an Interdisciplinary Model for Respiratory and Non-Communicable Disease Research — *Marco GOEIJENBIER*
– Understanding Influenza at Its Roots: Pathogenesis, Animal Models, and New Laboratory Insights — *Kirsty SHORT*
– Inside pragmatic vaccine trials: New Endpoints and Insights from the Largest Randomised Controlled Vaccine Trials — *Tor BIERING-SØRENSEN*

SCS **SCS14 One Health Surveillance in a Changing Climate: Data-Driven Solutions for Resilient Systems** · Room 1.08 - 50 pax
Chairs: *Anne WESSLING*
– One Health Surveillance in a Changing Climate: Data-Driven Solutions for Resilient Systems — *Anne WESSLING*
– Showcase: One Health Surveillance in Cameroon — *Elisabeth BETSI DIBONGUE*
– Community based approaches to One Health Surveillance — *To be confirmed*
– Panel discussion — *Elisabeth BETSI DIBONGUE*

SPI **SPI19 Bridging Biosecurity Gaps in Africa: Strengthening Links to Global Mechanisms through SIMBA, the UNSGM, and the BWC** · Room 1.07 - 45 pax
Chairs: *Karoline Laila OBERLÄNDER*
– Bridging Biosecurity Gaps in Africa: Strengthening Links to Global Mechanisms through SIMBA, the UNSGM, and the BWC — *Karoline Laila OBERLÄNDER*
– Tunisia and Biosecurity: A Strategic Bridge to Public Health Resilience — *Rym BENKHALIFA*
– The UNSGM as a Bridge to Close Biosecurity Gaps: Strengthening Awareness and Preparedness — *Stefan KLOTH*
– Strengthening the Biological Weapons Convention (BWC): A Comprehensive Approach to Bridging Biosecurity Gaps in Africa — *James PETTIT*

09:00 - 10:30 PLE **PLE03 Plenary session and keynotes** · Auditorium I
Chairs: *Linfa WANG*
– Mass Gathering, Maximum Readiness: Lessons from a Summer at the Helm of World Cup Health Security — *Rebecca KATZ*
– Well-being and well-spent: The socio-economic path to One Health — *Jonathan RUSHTON*
– One Health Sentinels: Marine Mammals, Spillover and Global Health Security — *Tracey GOLDSTEIN*
– Seizing the momentum: Why Europe needs a One Health network of networks, on behalf of OHP and EOHA — *Sascha KNAUF*

10:30 - 11:00 *Refreshment break*

11:00 - 12:30 SCS **SCS15 Preparedness, Resilience & Economic Evaluation** · Auditorium I
Chairs: *Daniel BAUSCH · Margarida ALHO*
– What surveillance misses: indigenous disease knowledge and ontologies could enable early detection of emerging diseases in remote rural areas — *Peregrine ROTHMAN-OSTROW*
– Source control or downstream prevention? A One Health cost-effectiveness analysis of rabies interventions — *Martha M LUKA*
– Strengthening Collaborative Systems to Address Local to Global One Health Challenges: Systems Mapping to Support One Health and Sustainable Development Goals Implementation — *Katey PELICAN*
– Responding to Clade Ib Mpox in Africa: Vaccine Strategy During Sustained Human Transmission — *Charles IBENEME*
– A BEACON for Novel Disease Threats: Leveraging Artificial Intelligence for Informal Event-Based Outbreak Surveillance — *Larry MADOFF*
– Community-Based Farmer Platforms Improve Livestock Vaccination Uptake, Reduce Losses, and Enhance Wellbeing: a Cluster-Randomized Trial in Ghana — *Francis Sena NUVEY*

SPI **SPI20 From Indicators to Preparedness -Strengthening Operational One Health Systems through Food, Agriculture, and Security Integration** · Auditorium II

Chairs: *Keith HAMILTON*

- From Indicators to Preparedness -Strengthening Operational One Health Systems through Food, Agriculture, and Security Integration — *Ekta PATEL*
- Case Study: African Swine fever — *Manuel DURÁN-FERRER*
- Panel discussion and Q&A — *Keith HAMILTON*
- Closing remarks — *Keith HAMILTON*

SPI **SPI21 Operationalizing One Health Prevention: Building Science–Society–Policy Interfaces from Local Action to Global Governance** · Room 1.08 - 50 pax

Chairs: *Marisa PEYRE · Chadia WANNOUS*

- Operationalizing One Health Prevention: Building Science–Society–Policy Interfaces from Local Action to Global Governance — *Marisa PEYRE*
- Welcoming remarks — *Marisa PEYRE*
- From global commitments to action: why science–society–policy dialogue is critical for pandemic prevention — *Nina JAMAL*
- Community empowerment and science–policy dialogue for prevention: lessons from Senegal — *Sadio Ba GNING*
- Institutionalizing One Health dialogue platforms: the national experience of Vietnam — *Phuong VU THI*
- Strengthening global science–policy–society interfaces in One Health governance — *Nitish DEBNATH*
- Financing prevention: the role of development banks in strengthening One Health governance — *Laure WEBER-VINTZEL*
- From local action to global governance: building bridges for prevention – role of civil society, communities and multi-stakeholder dialogue platforms (including insights from the PREZODE international study) — *Jeffry ACABA*

WS **WS15 Workshop: Bridging Disciplines – Integrating Ecological Principles into One Health Disease Research and Practice** · Room 1.06 - 45 pax

Chairs: *Jeanne FAIR · Andrew BARTLOW*

- Bridging Disciplines – Integrating Ecological Principles into One Health Disease Research and Practice — *Jeanne FAIR*

WS **WS16 Workshop: The 18-Month AMR Action Sprint: A One Health Policy Simulation** · Room 1.10 - 50 pax

Chairs: *Kayla STRONG · Geneviève BOILY-LAROUCHE*

WS **WS17 Workshop: Introducing the NEOH One Health Core Competencies: An Interactive Workshop for Strengthening Transdisciplinary Practice** · Room 1.07 - 45 pax

Chairs: *Sara SAVIC · Gabrielle LAING · Nicolas ANTOINE-MOUSSIAUX*

12:30 - 14:00 *Lunch break*

12:45 - 13:45 SPS **SPS05 Partner Session organized by ESWI: The Ongoing H5N1 Panzootic: A Continuing Threat to Animals and Humans** · Auditorium I

Chairs: *Ron FOUCHIER*

- Introduction and current status — *Ron FOUCHIER*
- Characterising small-scale and backyard poultry at the wildlife–poultry–human interface for avian influenza surveillance in the Netherlands — *Jolyn OOSTERS*
- Technical Industry Updates — *Taoufik RAWI*
- Panel discussion — *Thomas METTENLEITER*
- Closing remarks — *Ron FOUCHIER*

14:00 - 14:40 SPI **SPI22 Advancing gender transformative One Health approaches: how can we ensure equity, diversity and inclusion in policy and practices?** · Auditorium II

Chairs: *Phaedra HENLEY · Nina MILITZER*

- Advancing gender transformative One Health approaches: how can we ensure equity, diversity and inclusion in policy and practices? — *Nina MILITZER*
- Setting the scene: Enhancing health security by embedding DEI in OH — *Claudia ROBBIATI*
- Youth engagement in OH: key learnings for addressing gendered health risks — *Kuduishe KISOWILE*

- Government leadership in advancing DEI in OH systems: perspectives from Cameroon — *Elisabeth BETSI DIBONGUE*
- Integrating gender in wildmeat value chains: advancing equitable OH research and policy — *Chadia WANNOUS*

14:00 - 15:30 **SCS** **SCS16 Climate change, Environment, Ecosystems Health - session 2** · Auditorium I

Chairs: *Adriano A. BORDALO* · *Maria OLIVEIRA*

- NOAA One Health: Integrating Marine Ecosystem Drivers and Environmental Intelligence To Enhance the Health Sector — *Alice LAU*
- Rain, Rats, and Residents: Understanding Zoonotic transmission in Urban Brazilian Slums — *Hussein KHALIL*
- Seasonally Structured Bidirectional Microbiota Exchange between Humans and a Climate-Vulnerable Lake Ecosystem — *Yaovi Mahuton Gildas HOUNMANOU*
- Nature for Health: Reframing Upstream Prevention through Systems Thinking — *Rumbidzai GONDO*
- Nature-Based Solutions for Health: Applying a One Health Lens to Regenerative Agriculture — *Catherine MACHALABA*
- A multi-endosymbiont approach to monitoring sentinel species as bioindicators of tropical ecosystem health — *Klara Judita PETRZELKOVA*
- African pastoral commons, OECMs and agroecology principles for healthy savanna social-ecological systems — *Salome BUKACHI*

SCS **SCS08 One Health Approaches to Pathogen Surveillance, Intervention, and Prevention Strategies** · Room 1.08 - 50 pax

Chairs: *Cate DEWEY*

- Training community One Health teams in Rwanda to prevent zoonotic diseases — *Cate DEWEY*
- A proteomics-driven strategy to tackle antifungal resistance through a One Health lens — *Jennifer GEDDES-MCALISTER*
- Global bacterial antibiotic resistance sequencing (GLOBAR-SEQ): Supporting genomic surveillance of pathogens in low- and middle-income countries — *Lawrence GOODRIDGE*
- Preventing disease by enhancing vaccine willingness: Making vaccinations comfortable across the human lifespan — *C Meghan MCMURTRY*
- Pets, people, and pathogens: Navigating preventive medicine in a shared environment — *Kelsey SPENCE*

WS **WS13 Workshop: One Health Communication: How to introduce One Health to new audiences** · Room 1.07 - 45 pax

Chairs: *Deborah THOMSON*

WS **WS18 Workshop: Transformative One Health Training: Learning Together** · Room 1.10 - 50 pax

Chairs: *Cécile AENISHAENSLIN* · *Nicolas ANTOINE-MOUSSIAUX*

- Updated OH competencies — *Barbara HAESLER*
- Afrique One Health training program — *Bassirou BONFOH*
- Canopy - The Canadian One Health training program on emerging zoonoses — *Jane PARMLEY*
- Tipping Point - a serious game for OH training — *Thomas-Julian IRABOR*
- Indigenous and student perspectives — *Sean HILLIER*
- Moderated discussion — *Cécile AENISHAENSLIN*
- Breakout discussions — *Cécile AENISHAENSLIN*

14:50 - 15:30 **SPI** **SPI24 Inclusive One Health in Practice: Integrating Environment, Data, and Community Knowledge to Improve Health Outcomes in the Global South** · Auditorium II

Chairs: *Ylann SCHEMM*

- Inclusive One Health in Practice: Integrating Environment, Data, and Community Knowledge to Improve Health Outcomes in the Global South — *Ylann SCHEMM*
- Nutrition, Malnutrition, and Chronic Diseases in Conflict-Affected Populations: A One Health Perspective from Palestine — *Manal BADRASAWI*
- Green Chemistry for Safer and More Sustainable Health Solutions — *Reem OBAYDO*
- Water and wastewater, Pathogens, and Community Health: Environmental Pathways in One Health — *Sarmila TANDUKAR*
- Using Data to Advance Equity in Maternal and Child Health Systems — *Halima TWABI*

15:30 - 16:00 *Refreshment break*

16:00 - 16:40 SPI **SPI25 Biodiversity and Health: The science, policy, and implementation of biodiversity action as a One Health measure** · Auditorium II

Chairs: *Julian BLANC*

- Biodiversity and Health: The science, policy, and implementation of biodiversity action as a One Health measure — *Nadja MÜNSTERMANN*
- Panel discussion — *Julian BLANC*

16:00 - 17:30 SCS **SCS17 Antimicrobial resistance - session 2** · Auditorium I

Chairs: *Alice MATOS* · *Jomana MUSMAR*

- Defining 'appropriate' antimicrobial use in One Health: a global consensus survey — *Ri SCARBOROUGH*
- Genomic Surveillance Reveals One Health Transmission Pathways of MDR Escherichia coli and Klebsiella pneumoniae in Northern Spain — *Azucena MORA*
- Integrating Metagenomics and Microbiology to Characterise AMR Dissemination Across Wildlife, Livestock and Environmental Interfaces — *Hayley THOMPSON*
- Environmental Drivers of Antimicrobial Resistance in Aquaculture: A Comparative Governance Analysis of Canada and Norway — *Shauna THOMAS*
- Migratory Sentinels: The Role of Little Stints (Calidris minuta) in the Intercontinental Dissemination of blaCTX-M-15 within the Palearctic-Afrotropical Flyway — *Catherine MBUTHIA*
- Strengthening UK Antimicrobial Resistance Surveillance Through a Public–Private Partnership with Veterinary Laboratories — *Sophie SPALDING*
- Impact of reducing colistin use in livestock on colistin resistance in human and poultry in Indonesia (COINCIDE) — *Soe Yu NAING*

SPI **SPI26 Multi-Dimensional One Health Approach to Mitigating Mental Health Challenges in Africa** · Room 1.08 - 50 pax

Chairs: *Bassirou BONFOH*

- A Multi-Dimensional One Health Approach to Mitigating Mental Health Challenges in Africa — *Bassirou BONFOH*
- OH Approach to Mitigating Mental Health Challenges in Africa — *Bassirou BONFOH*
- Zoonotic-economic shock and grief-related trauma following death of family member — *Akissi Rose Delima N'GUESSAN*
- Livestock losses-induced mental threats and mitigation options — *Francis Sena NUVEY*
- Environmental and occupational exposure to chronic skin diseases and loss of hope — *Ismael Dognimin COULIBALY*
- Fear of seasonal food food shortage in the agricultural volatility context — *Bognan Valentin KONE*
- Mental health literacy and trauma-informed communication as the enabling competencies in OH workforce development — *Fatou NDOYE*

WS **WS21 Workshop: Quantifying, interpreting, visualizing and validating the climate-driven transmission suitability of mosquito-borne viruses** · Room 1.06 - 45 pax

Chairs: *José LOURENÇO* · *Monika MOIR* · *Carla MAVIAN*

WS **WS25 Workshop: Meaningful and Inclusive Engagement of People and Communities in One Health Implementation Session** · Room 1.10 - 50 pax

Chairs: *Chris DEGELING*

- Meaningful and Inclusive Engagement of People and Communities in One Health Implementation Session. — *Maxine WHITTAKER*
- Setting the scene : task and methods — *Dominique CHARRON*
- Meaningful community engagement including Indigenous Knowledge and Ways of doing? — *Salome BUKACHI*
- Gender equality and social inclusiveness including lessons from Villa de Leyva — *Natalia CEDIEL*
- Q and A: clarification only — *Chris DEGELING*
- Workshop: Facilitators: Natalia Cediel, Chris Degeling, Salome Bukachi, Domique Charron, Ekhlas Hailat , Serge Morand and Maxine Whittaker — *Chris DEGELING*
- Wrap-up — *Serge MORAND*

16:50 - 17:30 SCS **SCS19 Advanced tools and instruments for the detection and characterization of viral zoonoses in wildlife** · Auditorium II

Chairs: *Karen MOSSMAN* · *Samira MUBAREKA*

- Advanced tools and instruments for the detection and characterization of viral zoonoses in wildlife — *Samira MUBAREKA*

- Integrated One Health surveillance approach combining field sampling, molecular diagnostics, serology, genomics and ecological monitoring — *Wanda MARKOTTER*
- Advancing diagnostics, from innovations to field readiness — *Brad PICKERING*
- Role of virus-host interaction studies in human and reservoir host models — *Arinjay BANERJEE*
- From the field to the lab – assessing high consequence viral transmission in natural rodent reservoirs — *David SAFRONETZ*

17:30 - 19:00 **POS** **POS02 Poster presentations and refreshments - session 2 - Sardines** · Foyer D and Pavillon 4

Mon 7 Sep 2026

08:00 - 08:50 **SPS** **SPS08 Partner Session organized by DGAV: Breakfast talks - Turning One Health AMR Commitments into Action and Behavior Change: DGAV's Case – animal sector's perspective. Where scientific evidence meets policy and communication** · Auditorium II

09:00 - 10:20 **PLE** **PLE04 Plenary session and keynotes** · Auditorium I

Chairs: *Chadia WANNOUS*

- Understanding viral ecology can help prevent pandemics — *Peter DASZAK*
- Can there be One Health without safeguarding Human, Animal and environmental rights — *Daniel BAUSCH*
- Unifying the Front: A One Health Approach to AMR Policy and National Security — *Jomana MUSMAR*
- A lightning history and future perspective on diagnostics and discovery — *Walter Ian LIPKIN*
- Cooperation & Collaboration for a One Health future — *Lawrence MADOFF*

10:20 - 10:30 **PLE** **PLE06 The 10th World One Health Congress: reveal!** · Auditorium I

Chairs: *John MACKENZIE* · *Catarina LAVRADOR*

- Announcement of the 10th World One Health Congress — *John MACKENZIE*

10:30 - 11:00 *Refreshment break*

11:00 - 12:30 **SCS** **SCS20 Antimicrobial resistance - session 3** · Auditorium I

Chairs: *ANA DOMINGOS* · *Haifa EL HENTATI*

- Rapid Antibiotic Susceptibility Testing Directly from Urine: A One Health Perspective — *Mariana SOUSA-PINHEIRO*
- Beyond Policy to Practice: A political economy analysis of integrating gender and equity in the policy framework and governance of national Antimicrobial Resistance responses in Bangladesh — *Syeda Tahmina AHMED*
- Integrating Digital Monitoring and Biological Interventions to Reduce Antimicrobial Use and Greenhouse Gas Emissions in Vietnamese Aquaculture: A One Health Field Trial — *Chaokun HONG*
- eAMR CONNECT: An AI-Driven One Health Platform for Data Integration and Decision Support in Ethiopia — *Workeabeba TAYE*
- One Health molecular surveillance of methicillin and vancomycin resistance genes in Gram-positive cocci from companion animals in Southern Brazil — *Paulo FRANCA*
- Integrating environmental data into an integrated assessment model for antimicrobial resistance (iAM.AMR) — *Manuel PEREZ MALDONADO*

SCS **SCS21 From Data to Decisions: Digital Advancements, Genomics, Antimicrobial Resistance (AMR), and Climate at the Frontlines of One Health** · Auditorium II

Chairs: *Janet ROBINSON* · *Yasser SANAD*

- From Data to Decisions: Digital Advancements, Genomics, Antimicrobial Resistance (AMR), and Climate at the Frontlines of One Health — *Yasser SANAD*
- Opening remarks — *Yasser SANAD*
- Use of climate signals for vector and pathogen prediction and its implications for antimicrobial stewardship — *Thi Hoa NGO*
- AI-enabled integration and analysis of human, animal and wastewater AMR data for public health action — *Sid THAKUR*
- Leveraging AI and pathogen genomics to understand speciation, mutation, and predict AMR — *Yasser SANAD*
- Panel Discussion — *Yasser SANAD*

SPI **SPI18 Building the Investment Case for One Health: Evidence and Return on Investment from Country Implementation** · Room 1.05 - 45 pax

- Building the Investment Case for One Health: Evidence and Return on Investment from Country Implementation — *Danny SHEATH*
- Opening context and background — *Chadia WANNOUS*
- Community of Practice — *Danny SHEATH*
- Economic evaluation framework and ROI tool — *Barbara HAESLER*
- First Q&A and panel discussion — *Amira PREURE*
- Learning and replicability - Nigeria — *Clement MESEKO*
- Second Q&A and panel discussion — *Laure WEBER-VINTZEL*

SPI **SPI27 One Health perspectives from Arctic Canada** · Room 1.08 - 50 pax

Chairs: *Susan KUTZ*

- Braiding of Knowledge: Building Relationships between Community and Research — *Amanda DUMOND*
- Wildlife Health: A Foundation for One Health Action in the Canadian Arctic — *Naima JUTHA*
- Community-led public health & food sovereignty research in the Qikiqtani region — *Amy CAUGHEY*
- Panel discussion and Q&A — *Susan KUTZ*

WS **WS23 Workshop: Applying the Global One Health Index to AMR: Hands-on Local Performance Assessment for Decision-Making** · Room 1.06 - 45 pax

Chairs: *Xiao-Xi ZHANG*

- Opening & Workshop Overview — *Xiao-Xi ZHANG*
- AMR: Global Challenge & One Health Framework — *Yongzhang ZHU*
- AMR Laboratory & Surveillance Systems — *Chunlei SHI*
- Country / Institutional Snapshots — *Johanna LINDAHL*
- Demonstration: How GOHI-AMR Assessment Works — *Xiao-Xi ZHANG*
- Plenary Discussion: Applying Tools to Local Contexts — *Xiao-Xi ZHANG*
- Wrap-up & Key Takeaways — *Xiao-Xi ZHANG*

WS **WS24 From Complexity to Action: Systems Thinking for One Health Implementation (An Interactive Workshop)** · Room 1.10 - 50 pax

Chairs: *Elizabeth MUMFORD*

- Complexity, systems thinking, and systems methods useful for One Health (Core concepts in plenary) — *Elizabeth MUMFORD*
- Using systems tools to illuminate complex health scenarios (Interactive work in break-out groups) — *Elizabeth MUMFORD*
- Ask us anything (Open discussion and Q&A) — *Elizabeth MUMFORD*

12:30 - 14:00 *Lunch break*

14:00 - 15:30 SCS **SCS22 Late Breakers: novel and outstanding discoveries** · Auditorium I

Chairs: *Catarina LAVRADOR*

- Spillover of H5 influenza viruses to vampire bats at the marine-terrestrial interface — *I-Ting TU*
- Advancing One Health Solutions to Antimicrobial Resistance: Outcomes from Canada's Genomics Research and Development Initiative — *Rahat ZAHEER*
- One Health distribution of clinically relevant antimicrobial-resistant bacteria across humans, animals and the environment in rural Côte d'Ivoire: First results from a One Health cohort — *Alexandra BAHR*
- A wide diversity of viruses detected in African mammals involved in the wild meat supply chain — *Mare GERAERTS*
- A functionally extinct SARS-CoV-2 lineage persists and evolves in white-tailed deer, independently generating Omicron-defining mutations with human spillback potential — *Suresh KUCHIPUDI*
- From Evidence to Action: A 30-Year Synthesis of CGIAR One Health Implementation Models for Scaling in Low- and Middle-Income Countries — *Hung NGUYEN VIET*
- From Salmonella Strathcona outbreak traceback investigations to environmental surveillance of agricultural water: integrating epidemiology, genomics and passive sampling — *Laura BORTOLAMI*

SCS **SCS23 Late Breakers: novel and outstanding discoveries** · Auditorium II

Chairs: *Thomas METTENLEITER*

– Reemergence of New World Screwworm at the Wildlife–Livestock-Human Interface: Implications for Biodiversity, Wildlife Health Surveillance, and One Health — *Lucy KEATTS*
– Clues from persistent morbillivirus infections in dolphins for the molecular pathogenesis of SSPE in humans — *Melvin DANIEL ROJI*
– Restoring healthy landscapes to prevent zoonotic and vector-borne diseases: building on evidence to inform restoration policy and practice — *Maria Jose LOPEZ JARA*
– From livestock loss to cultural distress and ecosystem degradation: a gender responsive One Health assessment of an extreme winter disaster (dzud) in Mongolia's Eastern Steppe — *Julie GARNIER*
– Compound heat-drought events as datable early-warning signals for arbovirus outbreaks: causal evidence from Northeast Brazi — *Mattheus RODRIGUES DA SILVA*
– Genomic surveillance reveals zoonotic, foodborne, and WHO priority pathogens along the African–European bushmeat trade supply chain — *Daniel PIRES*
– One Health Implementation in the ECOWAS Region (2023 to 2025): Strong Institutional Commitment, Fragmented Operationalization — *Samanta DJALO*

15:40 - 16:40 **PLE**

PLE05 Plenary closing and keynotes · Auditorium I

Chairs: *John MACKENZIE · Ab OSTERHAUS · Jomana MUSMAR · Dominique CHARRON*

– Award ceremony: Best Oral and Best Poster presentation - One Health Outlook — *Ab OSTERHAUS*
– One Health Day & One Health Day Awards — *Cheryl STROUD*
– One Health Day Award winners — *Shivam SRIVASTAVA*
– Closing of the congress — *Ab OSTERHAUS*

Oral Abstracts

Climate change, Environment, Ecosystems Health - session 1

SCS01 · 11:30-13:00 · Auditorium I

Climate-driven Expansion of Vibrio vulnificus: Global Genomics Reveals Environmentally Persistent Pathogenic Lineages

Yaovi Mahuton Gildas HOUNMANOU (1), Jens Andre HAMMERL (2), **Anders DALSGAARD** (1)

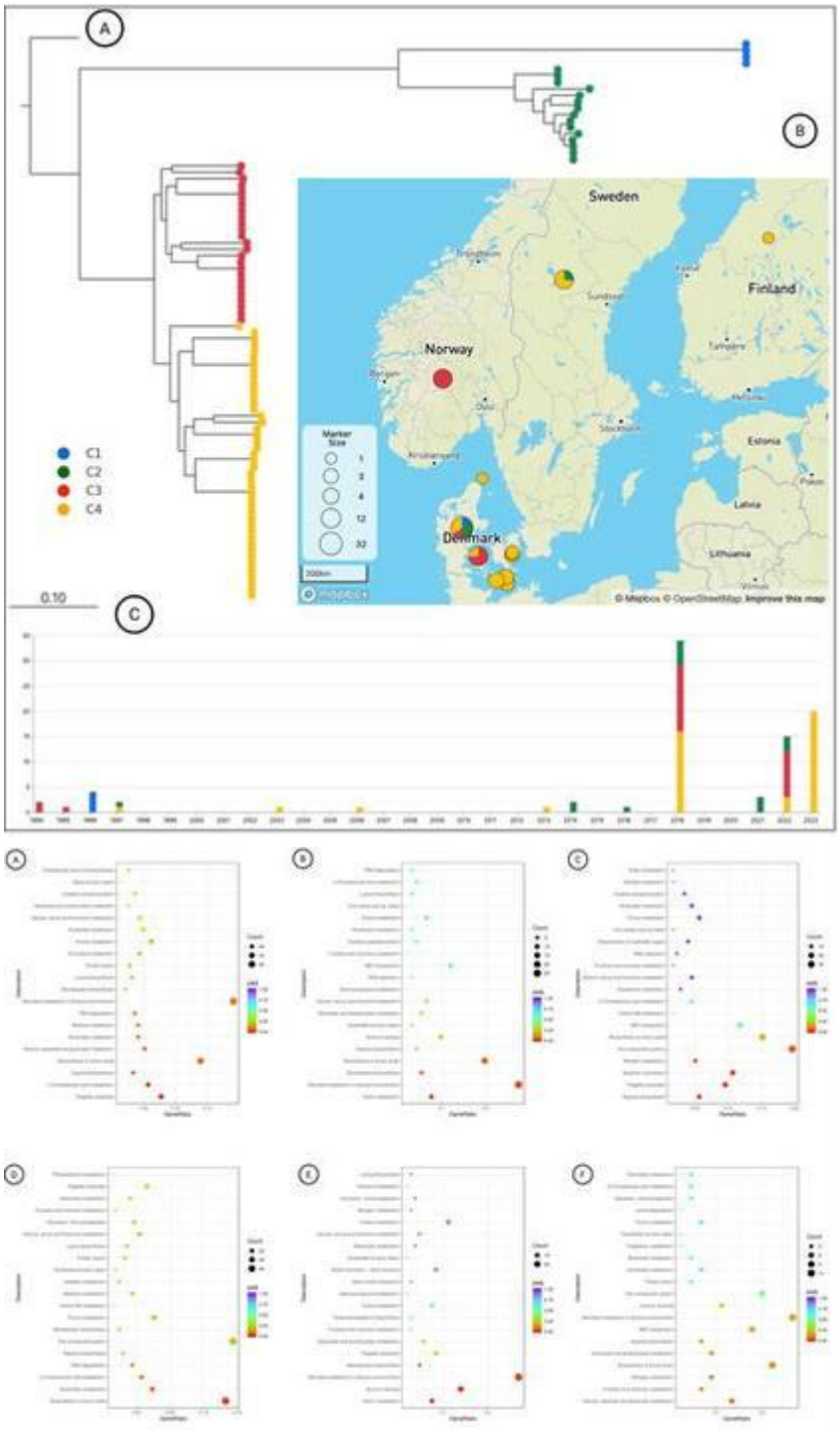
1: University of Copenhagen, Denmark; 2: German Federal Institute for Risk Assessment, Berlin, Germany

Background: *Vibrio vulnificus* is among the most lethal marine bacterial pathogens, with case-fatality rates exceeding 20–50% in septicemia. Severe infections typically occur when wounds are exposed to contaminated seawater, particularly among elderly or immunocompromised individuals, during recreational or occupational coastal activities. Clinical progression may be rapid and require extensive surgical intervention. Rising sea-surface temperatures and salinity changes have coincided with increasing infections in temperate coastal regions, including Northern Europe. However, the genomic diversity, environmental persistence, and climate-adaptive mechanisms underlying the expansion of pathogenic *V. vulnificus* lineages remain incompletely understood.

Methods: Three complementary datasets were integrated to investigate ecological and genomic determinants of *V. vulnificus* expansion. First, 117 genomes from Denmark and the Nordic region (1994–2023), including both clinical and environmental isolates, were analysed using comparative genomics. Second, a global dataset comprising 2,364 genomes, including 100 newly sequenced isolates from Germany and Denmark, was examined using phylogenomics, pangenome analysis, gene enrichment statistics, and machine-learning classification of accessory genome features. Third, RNA-seq transcriptomic profiling was performed on Baltic Sea isolates exposed to climate-relevant gradients of temperature (10–25 °C) and salinity (0.2–1.0% NaCl).

Results: Phylogenomic analysis of Nordic isolates showed no strict separation between environmental and clinical lineages. Environmental isolates carried complete virulence repertoires, including RTX toxins, capsule biosynthesis systems, and iron acquisition mechanisms, and were frequently closely related (≤40 SNPs) to clinical isolates across countries and multiple years, indicating persistent environmental reservoirs of pathogenic lineages. Analysis of the global collection revealed microevolutionary differentiation within a pangenome comprising 42,556 genes, including 3,069 core and 39,487 accessory genes. Accessory genome-based phylogenetic reconstruction identified two major genomic clusters differentiated by approximately 400 genes. Gene enrichment analysis identified 312 annotated genes significantly associated with isolation source, including 158 enriched among clinical isolates and 154 among environmental isolates, although many accessory genes encoded hypothetical proteins. Machine-learning classification further identified accessory genome features predictive of clinical origin, including genes involved in virulence regulation, stress tolerance, and antimicrobial resistance. Transcriptomic analyses demonstrated that warm, low-salinity conditions strongly induced motility, chemotaxis, metabolic activity, and virulence-associated pathways, whereas colder, higher-salinity conditions activated stress-response mechanisms. Salinity emerged as the dominant driver of transcriptional variation.

Conclusions: These findings indicate that *V. vulnificus* consists of globally distributed, environmentally persistent, and fully virulent lineages whose ecological fitness is enhanced under climate-driven warming and freshening of coastal waters. As warming coastal environments intersect with ageing and increasingly exposed populations, the risk of severe wound infections and septicemia may rise. Integrated genomic and environmental surveillance, together with targeted prevention strategies and improved clinical awareness, will therefore be essential to anticipate infection risk and strengthen climate-resilient coastal health systems.



Flooding the frontlines: Consequences of summer inundation on the ecology of mosquito-borne diseases

Reina SIKKEMA (1), Jordy VAN DER BEEK (2), Tijmen HARTUNG (1), Maarten BOONEKAMP (4), Sille PELSER (5), Kiki STRENG (1), Erley LIZARAZO FORERO (1), Stephan DE ROODE (4), Henk VAN DER JEUGD (6), Gregorius SIPS (5), Thom BOGAARD (4), Pier SIEBESMA (4), Marion KOOPMANS (1), Maarten SCHRAMA (3)

1: ErasmusMC, Netherlands, The; 2: Naturalis, Netherlands, The; 3: Leiden University, Netherlands, The; 4: TU Delft, Netherlands, The; 5: GGD Rotterdam-Rijnmond, Netherlands, The; 6: NIOO-KNAW, Netherlands, The

Introduction

Large scale adaptation strategies are being developed to enhance climate resilience in delta areas globally, but the potential health risks of this strategies are not always considered. Water buffering in the Dutch delta of Rotterdam is one of the adaptation strategies that is promoted abundantly. Inundations (flooding) of large natural water buffer areas likely affect local human and animal population dynamics, including vectors, which may ultimately change risks of vector-borne disease outbreaks, particularly in summer. This is specifically relevant in densely populated areas.

This study aims to assess the effects of a temporary summer inundation on the risk of mosquito borne virus outbreaks, using the Eendragtspolder near Rotterdam as a field lab.

Methods

In August 2025, 2,5ha of wetland was flooded using temporary water barriers. Sampling and observations took place before, during and after the inundation as well as in August 2024. Data collection included meteorological data (weather, water temperature profiles), mosquito and larval counts, bird counts and sampling (serum, swabs), water and aquatic macrofauna sampling, small mammal trapping and sampling, dead animal collection, camera trapping of large mammals, human visitor counts with additional questionnaires and the inclusion of citizen science data (Mosquito Alert App). Samples are tested using targeted (PCR, serology) and untargeted (metagenomics) approaches for viruses as well as eDNA techniques for host DNA including aquatic micro and macrofauna.

Preliminary results

Usutu virus was detected right before and during inundation in mosquitoes and wild birds. WNV was also detected. A major increase in larval and mosquito counts was observed over the duration of the inundation. Large numbers of resting mosquitoes were trapped in the surrounding vegetation throughout the experiment. A very low, but increasing number of mosquito predators was found in the water buffer. After inundation, an increase was observed in the number of carrion crows, Canadian geese, Eurasian magpies and common snipes in the area, compared to the control plot. On average 1200 human visitors visit the area daily, of whom over 200 have filled out the questionnaire. The inundation affected local temperature.

Conclusion

Temporary inundation likely causes significant fluctuations in population composition and movements of mosquitoes, birds, and their predators, which may increase the risk of mosquito-borne disease outbreaks, such as West Nile Virus.

Analysis of the 2025 Chikungunya Outbreak in Foshan, China, from a One Health Perspective

Yuan ZHANG (1,2), Daniel G. BAUSCH (1,3)

1: Geneva Graduate Institute, Switzerland; 2: National Research Institute for Health and Family Planning, Beijing, China; 3: Centre for Infectious Disease Emergency Response (CIDER), National University of Singapore, Singapore

Background: Chikungunya virus (CHIKV), transmitted primarily by *Aedes* mosquitoes, has re-emerged as a growing global health threat amid climate change, globalization, and expanding vector habitats. In 2025, multiple regions across Latin America, Europe and Asia reported renewed transmission. China experienced an unprecedented surge of CHIKV transmission in Foshan, Guangdong Province, with a total of 25,337 reported cases, the largest CHIKV outbreak on record in China.

Methods: As an illustrative case study, we examined the underlying causes of the outbreak in Foshan employing a One Health analytical framework combining epidemiological reports, climate data, policy documents, and published literature. We paid particular attention to the interconnected roles of climate change, vector ecology, human mobility, and public health governance.

Results: Our analysis identified several interconnected drivers of the 2025 CHIKV Foshan outbreak, with environmental factors being paramount (Figure 1). Within about a week after initial introduction of CHIKV into Foshan from travelers returning from Sri Lanka, a precipitous increase in cases was noted, sometimes reaching over 3,000 per week. Transmission was likely facilitated by the considerable rains noted in the region at the time, leading to increased *Aedes* populations. After a number of disease control measures were implemented, including enhanced case surveillance, community engagement to eliminated oviposition and larvae breeding sites, insecticide spraying, and public education, transmission

began to wane after about six weeks, despite continued precipitation. Control measures included innovative interventions piloted to improve operational efficiency and reduce environmental impact, such as drone-assisted insecticide application and biological control using larvivorous species. Despite these positive results, renewed heavy rain starting approximately a month later was associated with a second large peak in cases lasting for a few months, with local and regional spread facilitated by holiday travel associated with China's National Day. After this peak, precipitation significantly decreased, with accompanying waning of cases over the next two months.

Conclusions: The convergence of climate change, globalization, human mobility facilitating pathogen introduction, and rapid urbanization facilitating vector breeding and human-vector contact resulted in a large outbreak in Foshan. Paradoxically, environmental management improvements in Foshan in recent years may have unintentionally created cleaner breeding habitats favorable to *Aedes albopictus* than the previously more common *Culex* species. While CHIKV is not new, the conditions enabling its spread are intensifying around the world. Rising global temperature and precipitation anomalies (Figure 2) are expanding the geographic range and seasonal activity of *Aedes* in many regions which, together with demographic and societal transitions, will likely create conditions favorable to CHIKV transmission in many major population centers, as observed in Foshan. Effective prevention and control require moving beyond reactive, disease-specific responses toward integrated, preventive, and equitable One Health strategies.

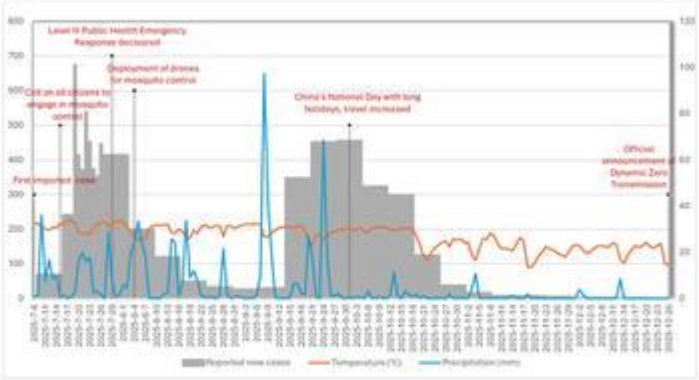


Figure 1. Reported Chikungunya Cases, Weather Trends, and Key Public Health Interventions in Guangdong, China, 8 July-26 December 2025

Data Source: Chikungunya case data are from the Guangdong CDC (https://nidcp.gd.gov.cn/yedcdzdt/dtkx/ypxx/index.html); Meteorological data of Foshan are from WeatherAPI.com. Case data were reported daily in the early stage of the outbreak and later changed to weekly reports; for visualization, the weekly data were averaged.

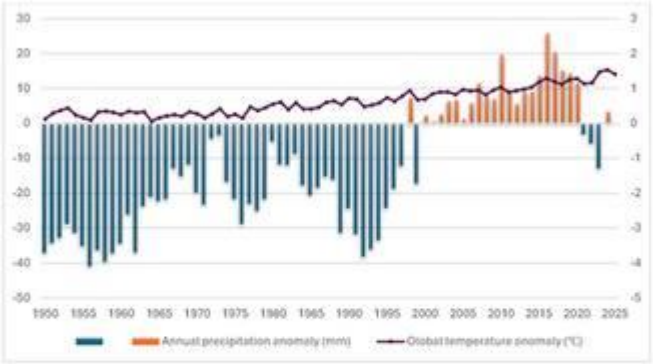


Figure 2. Global temperature anomalies and annual precipitation anomaly, 1950-2025

Data Source: Global temperature anomaly data are from Met Office Hadley Centre-HadCRUT5 (2026). Precipitation anomaly data contain modified Copernicus Climate Change Service information (2025). Both are processed by Our World in Data (ourworldindata.org). Annual temperature anomaly is the difference in average land-sea surface temperature compared to the 1861-1890 mean, in degrees Celsius. Precipitation anomalies show the difference in a specific year's total precipitation from the 1991-2020 average, measured in millimeters. Precipitation anomaly data for 2025 have not yet been released.

Climate Change and expanding sandfly activity in Sicily over ten years of surveillance within a One Health Framework

Eugenia OLIVERI, **Maria Liliana DI PASQUALE**, Francesco LA RUSSA, Marzio COMETA, Roberto HAMEL, Sara VILLARI, Fabrizio VITALE, Francesca DI GAUDIO

istituto zooprofilattico sperimentale della sicilia, Italy

Sandflies are the main vectors of *Leishmania*, the etiological agent of human and animal leishmaniasis, a zoonotic disease of major public health and veterinary importance in the Mediterranean basin. The biological cycle of sandflies, as with many other arthropod vectors, is closely linked to climatic and environmental conditions that influence their development, survival, and seasonal activity. In Italy, field observations and laboratory studies indicate that the average duration of the sandfly life cycle ranges from approximately 45 days to two months. Traditionally, their activity has been recorded between May and October; however, recent evidence suggests significant changes in their seasonal dynamics. In Sicily, an island located at the centre of the Mediterranean basin and characterized by high biodiversity and heterogeneous landscapes, environmental conditions create favourable habitats for the development and spread of numerous vector species and their associated pathogens. In recent years, the detection of adult sandflies and their trophic activity during the winter months has raised concerns about a possible extension of their active period, likely linked to climate change and the remarkable adaptive capacity of these arthropods.

This study presents the results of long-term entomological monitoring conducted in Sicily between 2010 and 2020. Sampling activities were originally implemented within the regional surveillance plan for Bluetongue disease. Black light traps were activated from dusk to dawn and positioned near livestock resting areas. The monitored sites were distributed throughout the Sicilian territory at altitudes ranging from 10 to 940 meters above sea level. These environments shared common ecological characteristics, including the presence of livestock farms and habitats composed of spontaneous vegetation alternating with anthropogenic woodlands, conditions that provide suitable microhabitats for the development of immature sandfly stages.

Although the monitoring plan was primarily aimed at bluetongue vectors, the collected data indirectly revealed the widespread presence and abundance of sandflies across the investigated areas. Remarkably, sandflies were detected in trap collections during all months of the year. Over the study period, the number of captured specimens increased significantly, with a clear prevalence in inland areas compared with coastal sites. The presence of sandflies during winter months suggests a shift in their seasonal dynamics and highlights the potential influence of climate change on vector ecology. These findings emphasize the importance of strengthening entomological surveillance programs targeting sandflies, particularly in areas associated with the presence of major *Leishmania* reservoir hosts. Improved monitoring will contribute to a better understanding of the circulation and transmission dynamics of leishmaniasis in the region. Such models will be essential for implementing targeted prevention and control strategies. In line with a One Health approach, collaboration between human, veterinary, and environmental health sectors is crucial to mitigate the increasing risk of vector-borne zoonoses in the context of climate change.

When extreme heat fuels infection: Machine Learning Evidence from Hospital Admissions in Portugal (2000–2018)

Maria Miguel OLIVEIRA (1,2,3), Ana Margarida ALHO (4,5,6), Ana Patrícia OLIVEIRA (7,8), Paulo NOGUEIRA (1,2,3)

1: Faculty of Medicine - University of Lisbon, Portugal; 2: Institute for Environmental Health, Associate Laboratory TERRA, Faculty of Medicine - University of Lisbon, Portugal; 3: Biomathematics' Laboratory, Faculty of Medicine, University of Lisbon; 4: NOVA National School of Public Health, Public Health Research Center, Comprehensive Health Research Center, CHRC, NOVA University Lisbon, Lisbon, Portugal; 5: Public Health Unit USP Francisco George, ULS Santa Maria, Lisbon, Portugal; 6: Global Health and Tropical Medicine, GHTM, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisbon, Portugal; 7: CoLAB + ÂTLANTIC, IPL-ESTM, Rua do Conhecimento nº4, 2520-614 Peniche, Portugal.; 8: Centro de Estudos Geográficos, IGOT—Instituto de Geografia e Ordenamento do Território, University of Lisbon, Lisbon, Portugal

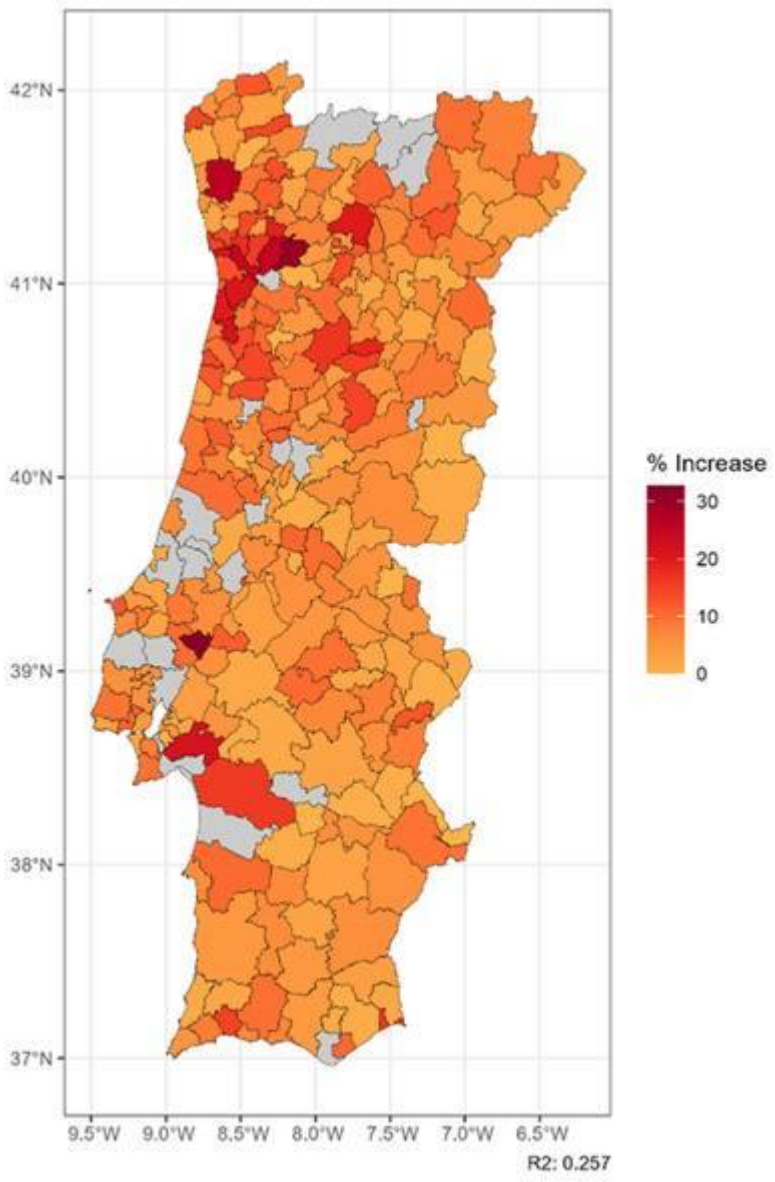
Background:

Climate change is changing the transmission dynamics of infectious agents and host susceptibility. While the direct effects of heat on cardiovascular and respiratory health are well documented, the link between thermal stress and infectious disease morbidity remains less well characterized. Rising temperatures can promote vector abundance, water- and food-borne pathogen proliferation, and reduce human immune responses. This study aims to quantify the impact of extreme heat events on daily hospital admissions for infectious and parasitic diseases in mainland Portugal.

Methods: We conducted a retrospective ecological observational study spanning 19 extended summer seasons (May–September, 2000–2018) across all 278 municipalities in mainland Portugal. We analysed daily counts of hospital admissions due to infectious and parasitic diseases and linked them with high-resolution meteorological observations. Heat exposure was characterised using the GATO-IV index, a location-specific indicator designed to reflect local thermal adaptation, by using an observations-base geospatial dataset of daily air temperatures (E-OBS dataset), while adopting a 1950 - 1999 climatological baseline period for percentile-based threshold definition (percentile 97.5). Associations between heat exposure and hospital admissions were estimated using GPBoost, which integrates gradient-boosted tree models with mixed-effects regression, enabling flexible non-linear effect estimation while explicitly modelling spatial structure through municipality-level random slopes.

Results: In validation analyses, the GPBoost model produced an R^2 of 0.26, with a root mean squared error of 0.43 and a mean absolute error of 0.21. Extreme heat increased hospital admissions for infectious and parasitic diseases by approximately 6.5% across Portugal. Despite widespread increases in risk following extreme heat exposure, the effect was highly heterogeneous, with local clusters such as the Northwestern region (Minho) showing increases exceeding 30%.

Conclusions: This study fills an important evidence gap by highlighting a previously under-documented link between extreme heat and infectious disease morbidity. Although extreme heat is a significant risk factor, it is an insufficient predictor of infectious disease burden on its own. The modest explanatory power suggests that other drivers, including environmental, ecological, and social determinants, play a strong role in shaping risk. These findings highlight the need for an integrated One Health approach that supports integrated climate–health surveillance systems and regionally tailored early-warning and response strategies to effectively protect vulnerable populations.



One Health and the Climate Agenda in Brazil: Integrating the Triple Planetary Crisis into Health Governance, Equity, and Strategic Response toward COP30

David SOEIRO-BARBOSA (1), Filipe CARVALHO DE PAULA (2), Liliane CARNEIRO (1), Claudia PIMPÃO (1), Lívia CASSEB (3), Christina PETTAN-BREWER (1)

1: Brazilian Association of One Health - ABRASUNI, Brazil; 2: Medical School of Barbacena, Brazil; 3: Evandro Chagas Institute, Ministry of Health, Brazil

Background: The triple planetary crisis (climate change, biodiversity loss, and pollution), intensifies health inequities and reshapes the conditions that drive zoonotic emergence, food insecurity, displacement, and environmental degradation. In Brazil, these dynamics are aggravated by deforestation, predatory land use, urban expansion, socio-territorial inequalities, and recurrent extreme events such as floods and droughts. Within this context, One Health offers an integrative framework to connect human, animal, plant, and ecosystem health and to support more coherent public policy responses. This study examines how Brazilian One Health debates can inform the climate and health agenda toward COP30, with particular attention to The Belém health action plan for the adaptation of the health sector to climate change to broader challenges of governance, equity, preparedness, and resilience. Methods: This study reflects ABRASUNI's strategic advocacy and direct participation in reinforcing the One Health agenda within the Belém Health Action Plan, in alignment with the National One Health Plan, during

COP30 and the Peoples' Summit. ABRASUNI has also invested in advancing these discussions in connection with the National Climate Adaptation Plan (AdaptaSUS), promoting knowledge exchange and integrating policy documents, institutional contributions, and advocacy outcomes. The analysis examines how One Health principles can address socio-environmental determinants of health, extreme climate events, zoonotic emergencies, antimicrobial resistance, biodiversity loss, and governance gaps. By applying a socioecological lens, the study demonstrates how transdisciplinary One Health advocacy can be translated into concrete policy mechanisms and territorial action. Results: Brazilian debates highlight that the triple planetary crisis produces layered and uneven health impacts, disproportionately affecting vulnerable territories and populations, including Indigenous peoples, riverine communities, peripheral urban populations, and those exposed to cycles of droughts and floods. The findings suggest that One Health can strengthen the Brazilian climate and health agenda in at least four ways: (1) by improving intersectoral governance and equity-oriented policy design; (2) by reinforcing surveillance, preparedness, and response capacities within the Brazilian Unified Health System (SUS), especially in urban-rural-forest interfaces; (3) by supporting risk management and resilience in the face of extreme events and post-disaster reconstruction; and (4) by valuing territorial knowledge, social participation, and nature-based approaches in adaptation strategies. Brazilian experiences also underscore how pollution, ecosystem disruption, and climate variability interact to alter vector ecology, water security, mental health, and infectious disease risks. Conclusions: The climate agenda in Brazil requires integrated and justice-oriented responses that move beyond fragmented institutional approaches. One Health provides a strategic pathway to connect climate adaptation, health protection, environmental governance, and social equity, particularly in the lead-up to COP30 Belém. By linking preparedness, risk governance, territorial vulnerability, and participatory policymaking, Brazilian debates offer relevant insights for building resilient socioecological systems and more effective responses to the health impacts of the triple planetary crisis.

Knowledge, Education & Communities

SPI01 · 11:30-13:00 · Auditorium II

Insights from the Collaborative One Health Research Initiative on Epidemics Across Africa and Latin America

Natacha LECOURS (1), **Stéphanie MALTAIS** (2)

1: International Development Research Centre, Canada; 2: Université de Montréal, Canada

Background

Community engagement is increasingly recognized as essential to effective One Health implementation, ensuring that interventions are grounded in local realities, culturally relevant, and socially inclusive. However, evidence on how communities shape One Health strategies - particularly in implementation research - remains limited. Since 2021, the International Development Research Centre (IDRC) has supported the Collaborative One Health Research Initiative on Epidemics (COHRIE), composed of four implementation research projects across nine countries in sub-Saharan-Saharan Africa and Latin America. These projects aim to strengthen epidemic prevention, preparedness, and response through interdisciplinary, multisectoral approaches. This abstract synthesizes learnings from COHRIE on the role of communities in shaping research and operational outcomes.

Methods

Insights were drawn from COHRIE, encompassing implementation research in Colombia, Ecuador, Peru, Guinea, Democratic Republic of Congo, Sierra Leone, Liberia, Nigeria, and Uganda. The synthesis integrates methodologies used across the projects, including participatory action research, community consultations, qualitative interviews, gender and social equity assessments, and community-led surveillance approaches. Data sources included project reports, case studies, thematic analyses, and other outputs related to COHRIE. Methods of analysis involved cross-project workshops and comparative assessments.

Results

Across projects, community engagement emerged as critical to identifying context-specific health risks, informing intervention design, and strengthening capacities for implementation of One Health systems. Communities contributed local ecological knowledge, guided the prioritization of health threats, and co-implemented surveillance and prevention strategies. Gender responsive research approaches highlighted distinct roles of women and marginalized groups in detecting and managing zoonotic and environmental health risks. Engagement with Indigenous communities demonstrated how traditional ecological knowledge enriched data interpretation and shaped culturally grounded interventions. Projects incorporating digital innovations, such as mobile reporting tools for disease surveillance, showed improved local participation and data quality. Overall, cross-cohort evidence indicated that community involvement enhanced intervention relevance, improved trust and participation, and contributed to more equitable One Health outcomes.

Conclusions

The COHRIE experience demonstrates that community engagement is not peripheral but foundational to effective One Health implementation research. Integrating community perspectives strengthens health system resilience, improves the feasibility and sustainability of interventions, and advances gender and social equity. These findings offer practical insights for researchers, policymakers, and practitioners seeking to operationalize inclusive One Health approaches across diverse settings.

Proposed Format & Presentation Titles

Format: Project presentations with introduction and closing by IDRC representative

Presentation titles:

A One Health Curriculum Self-Assessment Checklist for Evaluating Competency Integration in Higher Education

Katie NOLAN (1,2), Niamh MCLOUGHLIN (1,3), Tony HOLOHAN (1,3), **Gerald BARRY** (1,2)

1: University College Dublin One Health Centre, University College Dublin (UCD), Dublin, Ireland; 2: Veterinary Sciences Centre, School of Veterinary Medicine, University College Dublin (UCD), Belfield, Dublin 4, Ireland; 3: School of Public Health, Physiotherapy and Sports Science, University College Dublin (UCD), Belfield, Dublin 4, Ireland

Background: Universities have traditionally produced graduates trained within disciplinary silos, which restricts their capacity to integrate perspectives across sectors and address complex health challenges. The One Health approach prioritises interdisciplinarity and acknowledges that effective solutions require consideration of human, animal, and environmental systems in a collective manner. As a result, universities play a critical role in preparing graduates to translate One Health principles into practice. Despite this, many institutions lack systematic mechanisms for assessing the extent to which these principles are embedded in existing curricula. Although competency frameworks identify essential domains such as cross-disciplinary collaboration, systems thinking, and applied problem-solving, few tools are available to evaluate curriculum-level integration. To address this gap, the University College Dublin (UCD) One Health Centre, a World Health Organisation Collaborating Centre for One Health, has developed a One Health Curriculum Self-Assessment Checklist.

Methods: The development of the UCD One Health Curriculum Self-Assessment Checklist is rooted in a comprehensive review of literature on One Health education and guided by broader pedagogical principles. The checklist draws significant influence from the updated core competencies identified by Laing et al. (2023) and the global university network framework proposed by Lane et al. (2025). These sources highlight interdisciplinary collaboration, systems thinking, communication, and applied problem-solving as essential competencies for an effective One Health education. Drawing on these foundational principles, six key domains were established as shown in (Figure 1). Assessment employed a four-level rubric (Not Evident, Emerging, Developing, Established) to reflect the degree to which One Health competencies were incorporated into curriculum content, learning activities, and assessment strategies across programmes. A star-rating scale to indicate the extent to which One Health competencies were integrated into the curriculum is then produced (Figure 2).

Results: The checklist was pilot tested across undergraduate veterinary curricula at three universities. Programmes were assessed using the domain scoring checklist to evaluate the level of One Health integration. Based on the resulting scores (see example in figure 3) and in consultation with faculty representatives, tailored feedback and recommendations were provided to support bespoke curriculum development and strengthen One Health workforce development.

Conclusions: The One Health Curriculum Self-Assessment Checklist offers a structured, adaptable approach to evaluating the integration of One Health principles into higher education curricula. Pilot implementation across three veterinary universities demonstrated its feasibility and value as a reflective tool for curriculum development. Future efforts will focus on wider dissemination and application of the checklist across institutions and disciplines to support more systematic integration of One Health competencies in health professional education.

Domain	Description
Theoretical Components	Core One Health concepts across human, animal, and environmental health
Interdisciplinary Skills	Collaboration, communication, and teamwork across multiple disciplines
Systems Thinking	Understanding interconnected systems affecting health outcomes
Problem-Based Learning	Applied interdisciplinary problem-solving using real-world health challenges
Assessment Strategies	Evaluation methods measuring interdisciplinary One Health competencies
Institutional Support	Leadership, policies, and resources supporting One Health curriculum integration

Figure 1. The six domains of the UCD One Health Self-Assessment Checklist

Star Rating	Points	Description
★★★★★	15-18	Excellent Integration
★★★★☆	12-15	Strong Integration
★★★☆☆	9-12	Moderate Integration
★★☆☆☆	6-9	Emerging Integration
★☆☆☆☆	3-6	Limited Integration
☆☆☆☆☆	0-3	Not evident

Figure 2. An example of the scoring system used to convert domain-specific checklist data into a star-based visual presentation, creating salient feedback.

Area Evaluated	Star Rating
Theoretical Components	★★★☆☆
Interdisciplinary Skills	★☆☆☆☆
Systems Thinking	★★☆☆☆
Problem Based Learning	★★★☆☆
Assessment Strategies	★★☆☆☆
Institutional Support	★★★★★

Figure 3. An example of the visual presentation of results that is produced following self-assessment of a curriculum.

Development and Implementation of the Field Training for the Wildlife and Environment Sector Professionals – the Compliment to FETP and FETPV

Scott NEWMAN (1), David CASTELLAN (1), Heather ENGLEKING (2), **Jonathan SLEEMAN** (3)

1: Food and Agriculture Organisation of the United Nations, United States of America; 2: Institute for Infectious Animal Diseases (IIAD), Texas A & M; 3: College of Veterinary Medicine, University of Minnesota

BackgroundThe One Health approach has historically emphasized zoonotic diseases, antimicrobial resistance, and food safety, engaging primarily the public health and veterinary sectors. However, major gaps persist in integrating the environment, wildlife, biodiversity, and natural resource management sectors—despite their essential role in preventing ecological degradation, reducing spillover risk, and strengthening upstream pandemic prevention. To address these gaps, FAO and partners developed the Field Training Program for Wildlife, Environment, Biodiversity and Ecosystems (FTP WEBE) to complement existing in-service programs for health (FETP) and veterinary (FETPV) professionals. The program supports the Quadripartite Joint Plan of Action for One Health by equipping environmental sector professionals with the competencies needed to operate as equal partners in One Health systems.

MethodsFTP WEBE is an interoperable, in-service training program combining 25% classroom instruction with 75% applied field training. Development of the program included the creation and piloting of the Environment Sector Country Mapping and Needs Assessment Tool, which analyzes institutional structures, workforce competencies, and capacities in biodiversity, ecosystems, wildlife, and One Health domains. The program also includes a comprehensive competency framework with 107 integrated competencies, some of which have been incorporated into the Quadripartite One Health competency framework—and a suite of training modules developed by an international consortium.

ResultsCountry assessments identified extensive fragmentation and capacity gaps within environment and wildlife sectors, alongside substantial opportunities for strengthened cross-sector collaboration. FTP WEBE has enabled the development of structured competency frameworks, prerequisite training modules, and country-specific needs assessments. Importantly, implementation has now begun in Indonesia, India, Thailand, Sri Lanka, Laos PDR, and Pakistan, with additional countries expressing strong interest in joining the program. This expansion reflects growing regional demand and recognition of the vital role of environmental professionals in advancing One Health. Early program outcomes include increased awareness of environment–health linkages, greater understanding of prevention-focused interventions, and stronger mechanisms for integrating environmental priorities into national One Health governance and policy development.

ConclusionsFTP WEBE fills a critical global gap in One Health capacity development by empowering environmental, biodiversity, and wildlife professionals to contribute meaningfully to health security and ecosystem resilience. Through its emphasis on prevention, ecosystem stewardship, and multisector collaboration, the program strengthens countries' ability to address the underlying drivers of disease emergence and environmental degradation. Continued investment in module development, regional coordination, and national program rollout will be essential to expand and scale the initiative across Asia and beyond.

Community One Health Units: A gender responsive One Health approach to zoonotic diseases control in Burkina Faso

Abdoul Kader ILBOUDO (1,2), Alexis KAFANDO (2), Marine HUBERT (3,9), Assèta KAGAMBÈGA (2,4), Madi SAVADOGO (1,10), Maude GILBERT-VANASSE (5), Franck BICABA (2), Jane PARMLEY (6), Michèle BOUCHARD (5,8), Abel BICABA (2), Hélène CARABIN (3,5,8,9), Zékiba TARNAGDA (2,7)

1: Centre national de recherche scientifique et technologique, Institut de recherche en sciences de la santé, Unité des maladies épidémiques, maladies émergentes et zoonoses, Burkina Faso; 2: Société d'études et de recherche en santé publique, Projet Elles luttent contre les zoonoses, Burkina Faso; 3: Faculté de médecine vétérinaire, Université de Montréal, Saint-Hyacinthe, Québec, Canada; 4: Université Joseph Ki-Zerbo, Ouagadougou, Burkina Faso; 5: UdeM International, Université de Montréal, Québec, Canada; 6: Ontario Veterinary College, University of Guelph, Ontario, Canada; 7: Association One Health Burkina Faso; 8: École de Santé Publique, Université de Montréal, Montréal, Canada; 9: Groupe de recherche en épidémiologie des zoonoses et santé publique (GREZOSP), Université de Montréal, Saint-Hyacinthe, Québec, Canada; 10: Direction de la santé animale, Direction générale des services vétérinaires, Ministère de l'Agriculture, de l'eau, des Ressources animales et halieutiques, Ouagadougou, Burkina Faso

Background: Zoonotic diseases are a One Health concern in resource-limited settings, yet they often remain under-detected and under-reported by routine surveillance systems. Community engagement and cross-sectoral collaboration are central to strengthening early detection and prevention. This study describes the implementation of a community-based One Health Unit approach in Burkina Faso to enhance prevention and reporting of zoonotic diseases.

Methods: This work was implemented within the ELUZO project ("Elles luttent contre les zoonoses"), a community-driven, gender-responsive One Health initiative. Community One Health Units were established in five communes through a participatory design process involving local authorities and community stakeholders. Each unit brought together representatives from government technical services (agriculture, animal health, human health, environment, and gender), community-based human health and animal health workers, smallholder farmers and rural women leaders. Members of the Units were trained using standardised modules and picture-based tools developed by the ELUZO project team covering community-based zoonotic disease surveillance, detection and reporting of unusual health events, hygiene, gender and women's empowerment. These members subsequently conducted cascade trainings to community health workers and women leaders. A community-managed electronic data collection platform was developed and deployed to document unusual health events, including suspected zoonoses.

Results: A total of 25 government staff from the different sectors were trained, who in turn trained 24 community health workers and 300 rural women leaders. Between November 2025 and February 2026, local communities and the One Health Units reported and investigated 16 suspected rabies cases. In addition, animal health services, in collaboration with communities, reported and seized 95 suspected animal organs from various slaughterhouses in the study areas. One field follow-up training for communities was also conducted by the technical team of the One Health Units. One joint field visit was

conducted to provide on-site support for community-level management of these events. No community event-based surveillance alert was detected during this period.

Conclusion: The pilot One Health Unit demonstrated the ability of local communities to actively contribute to zoonotic disease prevention and community-based surveillance. The explicit focus on rural women as key actors in zoonotic disease surveillance and control highlighted the added value of gender-responsive, community-based approaches for strengthening One Health systems in resource-limited settings.

Grounding Ethics in Climate Change and Health Research: A collaborative study triangulating perspectives of the communities, researchers and ethical committees

Joris MICHIELSEN (1), Katerina CEBALLOS (1), Kochupurackal Ulahannan SABU (2), Ana Lucia MARTINEZ ABARCA (3), **Soledad COLOMBE** (1)

1: Institute of Tropical Medicine, Belgium; 2: Independent consultant, India; 3: Independent consultant, Belgium

Background

As effects of climate change intensify, ethical considerations become critical for populations disproportionately affected by climate-induced health hazards. While EcoHealth, One Health, and Planetary Health frameworks emphasize stakeholder co-creation, existing ethical guidelines remain theoretical and top-down, rarely consulting affected communities. Persistent challenges include risk communication without actionable adaptation options, power asymmetries in research agenda-setting, tensions between global scientific priorities and community-identified needs, and the difficulty of navigating differences in risk perception and lived experience across knowledge systems. This two-phase study triangulates perspectives of communities, researchers, and ethics committees to develop grounded ethical recommendations for climate-health research.

Methods

We gathered community perspectives through interviews and focus groups discussions (FGD) with Indigenous populations in India (16 interviews, 2 FGD) and coastal communities in the Philippines (16 interviews, 8 FGD), exploring experiences of ethical processes and practices. In total, 91 community members participated across both sites, including farmers, fisherfolk, community health workers, youth, and Indigenous Adivasi community members and activists. This informed the development of vignettes and corresponding statements for an online 2-rounds Delphi study comprising 20 scenario-based statements spanning intergenerational justice, procedural flexibility, fair compensation, epistemic justice, and community co-creation. Each statement was rated on dual 5-point Likert scales assessing both ethical agreement and practical feasibility; consensus was defined a priori as ≥75% agreement with researchers and ethics committee members (52 respondents round 1; 23 round 2).

Results

A central tension emerged between institutional ethics emphasizing individual procedural consent and extractive knowledge production versus communities' expectations of collective governance and relational accountability. Communities stressed reciprocity as foundational: willingness to participate and share data depends on researchers sharing their expertise, disseminating actionable findings, responding to community needs, and building long-term trust. Reciprocity was further described as requiring research materials in local dialects, respecting the traditional decision-making processes, and engaging community co-researchers. Delphi respondents emphasized balancing long-term climate objectives with participants' immediate rights, safety, and dignity. Strong consensus emerged on anticipating climate-related burdens, prioritizing participant well-being even when requiring protocol deviations, enabling context-appropriate compensation for contributed labor, and valuing Indigenous and experiential knowledge alongside scientific data. Though consensus was strong, feasibility was often questioned, and institutional rigidity was identified as a main barrier to grounded ethical practice.

Conclusion

Findings highlight the necessity for ethical frameworks explicitly addressing climate-specific vulnerabilities, reformed funding structures enabling ethical practices currently deemed aspirational, and methodological pluralism integrating quantitative and qualitative approaches with Indigenous knowledge

systems as standard practice. Bridging the principle-to-practice gap requires collective action. Funders must resource ethical commitments beyond token budgets, ethics committees must develop climate-specific review capacity, and institutions must support the community participation from proposal development untill validation.

Evaluating the Value of One Health: Results from the Quadripartite Online Course on Economic Evaluation Methods

Maria DE LA PUENTE AREVALO (1), **Danny SHEATH** (1), Charlotte RENDINA (1), Sian WESTCOMBE (1), Katrin TAYLOR (1), Alessandra ALVITI (1), Lina AWADA (1), Chadia WANNOUS (2), Sinaia NETANYAHU (3), Marisa PEYRE (4), Yoeri BOOIJINK (4), Mauro DE ROSA (2), Katie WOOLASTON (5), Laure WEBER VINTZEL (6), Amira PREURE (7), Barbara HAESLER (1), Madhur DHINGRA (1), Zelalem TADESSE (1), Junxia SONG (1)

1: Food and Agriculture Organization of the United Nations, Rome, Italy; 2: One Health Department, World Organisation for Animal Health (WOAH), Paris, France.; 3: Prevention and Health Promotion Division, European Centre for Environment and Health, World Health Organisation (WHO), Regional Office for Europe, Bonn, Germany.; 4: CIRAD, UMR ASTRE, F-34398 Montpellier, France.; 5: United Nations Environment Programme (UNEP), Nairobi, Kenya.; 6: The World Bank, Washington DC, USA.; 7: World Health Organisation (WHO), Geneva, Switzerland

Background

Despite growing recognition of the One Health (OH) approach, investment remains limited, partly because robust evidence on its economic returns is scarce. Demonstrating the return on investment of OH is increasingly gaining priority at both national and global levels. In January 2026, the Quadripartite (FAO, UNEP, WHO, WOAH) launched the online course "*Evaluating the Value of One Health", hosted by* the FAO Virtual Learning Centers. Developed jointly, and also in collaboration with CIRAD and the World Bank, this is the first Quadripartite-led training dedicated to economic evaluation methods applied to OH — a topic largely absent from existing capacity development programmes.

Methods

The course combined self-study modules, step-by-step calculation exercises, live webinars, and facilitated discussion forums. It covered OH fundamentals and key economic evaluation methods, including cost-effectiveness, cost–benefit, and cost–utility analysis addressing the health, agriculture and environmental sectors. The course was offered to the members of the Quadripartite Community of Practice on the Return of Investment for One Health and One Health investment planning. It was delivered in a tutored format, during a five-week period. Pre- and post-course surveys assessed participant profiles, self-rated competencies across five learning objectives (scale 1–5), and satisfaction. Competency data were analyzed descriptively; open-ended responses reviewed thematically.

Results

A total of 191 participants were enrolled in the course; 122 accessed the training (64% of those enrolled) and 76 completed it (62% of those who accessed). Pre-course surveys were completed by 106 respondents from 46 countries across all world regions (Africa 37%, Europe 23%, Asia and Middle East 16%, Americas 9%, Oceania 6%). Most participants worked in universities or research centres (36%), government institutions (26%), or international organisations (14%). The majority (85.6%) had no prior One Health economic evaluation training. Post-course surveys were completed by 70 participants.

Self-rated competencies improved across all five learning objectives. The largest gain was in identifying and comparing OH evaluation methods: 69.8% of pre-course respondents rated themselves at the two lowest competency levels, versus 0% post-course, and 37.1% rated themselves highly competent post-course. The ability to plan and conduct an OH economic assessment rose from a pre-course mean of 2.31 to 3.80 post-course. Confidence to apply learning averaged 4.16/5. Overall satisfaction was high (mean 4.64/5), with trainer satisfaction at 4.74/5 and job relevance at 4.46/5. As suggestions to improve future editions of the course, participants requested more opportunities to practice through additional exercises and case studies.

Conclusions

This course addressed a critical and largely unmet need: building OH economic evaluation capacity among diverse multisectoral professionals worldwide. Strong competency gains, high satisfaction, and

broad geographic reach support its scaling. Integrating economic thinking into OH capacity development is essential to translate OH principles into sustained political and financial commitments.

Community-centred tools for One Health operationalisation in the Horn of Africa

Farah I. MUMIN (1,2,3), **Siobhan M. MOR** (1,2)

1: University Of Liverpool; 2: international Livestock Research Institute; 3: Red Sea University

Background: Pastoral and agro-pastoral communities in the Horn of Africa face intersecting risks from zoonotic diseases, antimicrobial resistance, and foodborne hazards. Despite this burden, they are routinely excluded from One Health planning and programming. Operationalizing One Health at the community level requires tools that are validated, accessible in low-literacy settings, and capable of generating policy-relevant evidence.

Methods:A programme of research was conducted across Ethiopia, Kenya, and Somalia to develop, validate, and apply three community-centred One Health tools: an instrument to measure community knowledge, attitudes, and practices (OH-KAP); a participatory health education intervention (Community Conversations, CC); and a community-led zoonoses prioritisation tool combining Participatory Epidemiology with Multicriteria Decision Analysis (CZP). Tools were developed iteratively with communities and tested with over 1,100 pastoral and agro-pastoral participants across the region.

Results: All three tools demonstrated feasibility, validity, and utility in low-literacy field settings. The OH-KAP instrument provided a psychometrically robust measure of One Health knowledge, attitudes, and practices suitable for pastoral communities. CC sessions, evaluated using OH-KAP, produced significant improvements across all three domains. The CZP tool enabled communities to independently rank zoonotic disease priorities, with strong agreement within and across groups, and produced rankings that diverged meaningfully from Somalia's national prioritisation framework, reflecting livelihood concerns absent from expert-led processes.

Conclusions: Pastoral communities are capable and willing participants in One Health measurement, education, and priority-setting. This toolkit provides practical, validated means to include community voices in One Health programming and policy. Divergence between community and national priorities highlights the risks of expert-led frameworks that exclude those most affected. These tools are ready for scale-up and adaptation across similar low-resource, high-burden settings.

Pathogens, Microbiome, & Intervention Strategies

SCS02 · 14:00-15:30 · Auditorium I

Genomic Diversity, Evolutionary Dynamics, and Intervention Needs for Swine Influenza A virus in Europe: Insights from the European Swine Flu Network (ESFLU) and Cross Sector Pathogen Surveillance

Gwenaëlle DAUPHIN (1), Katarzyna PODGORSKA (12), Gautier RICHARD (7), Sasan FEREIDOUNI (9), Annika GRAAF RAU (4), Pia RYT-HANSEN (5), Tijs TOBIAS (6), Alex BYRNE (2), Helen EVERETT (3), Enrique MATEU (8), Dimitris PAPADOPOULOS (10), Dinko NOVOSEL (11), Lorena FRANCO (13), Marie SJOLUND (14), Lars LARSEN (5)

1: Ceva Santé Animale (FR); 2: The Francis Crick Institute Limited (UK); 3: Animal Plant and Health Agency (UK); 4: Helmholtz Institute for One Health (D); 5: University of Copenhagen - Faculty of Health and Medical Sciences (DK); 6: Utrecht University (NL); 7: Agence Nationale de la Securité Sanitaire de l'Alimentation de l'Environnement et du Travail (FR); 8: Universitat Autònoma de Barcelona (SP); 9: University of Veterinary Medicine Vienna (AT); 10: Aristotle University of Thessaloniki (GR); 11: Croatian Veterinary Institute (HR); 12: National Veterinary Research Institute (Poland); 13: University of Murcia (SP); 14: National Veterinary Institute (SE)

Swine influenza A virus (swIAV) is widespread and persistent across Europe and the virus rapidly evolves in pig populations. These dynamics complicate detection, risk assessment, and intervention strategies. High prevalence, low swine vaccine coverage, and fragmented surveillance systems contribute to the under-recognition of strains with zoonotic potential. The European Swine Flu Network (ESFLU; funded by the COST Association, 2022–2026) was established to address these scientific and operational gaps.

ESFLU activities were developed across four working groups on pathogen identification and characterization, genomic and surveillance data integration, herd-level management and intervention practices, and communication strategies. 180 active members from 32 countries have joined this open network (a few members from a public health institution).

ESFLU has compiled five pan-European swIAV sequence datasets, ran a survey on the current pig surveillance systems, sponsored 14 scientific missions and 4 laboratory/surveillance training schools, and held six thematic workshops addressing biosecurity, surveillance, pig vaccine efficacy, economic and anthropologic dimensions of swine flu, and zoonotic risk. The zoonotic-risk consultation included participation from international national animal and public health institutes/agencies, reference laboratories, pharmaceutical industry and pig-sector representatives. ESFLU genomic results are shared with the global animal flu network (OFFLU) and key sequences shared with WHO.

The ESFLU surveillance survey confirmed the insufficient and heterogeneous SwIAV surveillance in pigs across Europe. Swine flu is not categorised in the EU Animal Health Law, leading to insufficient detection of SwIAV. SwIAV surveillance in humans exposed to infected pigs and timely detection of spill-over events could also be improved.

Genomic analyses conducted by ESFLU (over 900 strains from 20 European countries) have confirmed a complex landscape of co-circulating subtypes and genotypes (70 identified), including emerging reassortants from viral segments of human and swine origin, and various countries. They have also revealed retro-zoonotic events of human seasonal influenza viruses into pig populations.

ESFLU's support has strengthened laboratory readiness by training 60 specialists in animal-health laboratory testing, sequencing, bioinformatics and surveillance, and by generating harmonized SOPs to improve pathogen-characterization workflows.

Stakeholder consultations identified the need for expanded genomic sequencing of both pig and exposed human populations, interoperable data pipelines, and improved approaches to detect variant viruses with public health relevance.

ESFLU findings have highlighted major gaps in early detection and strain monitoring; the identification of human-to-swine IAV infections have stressed the need for integrated human and swine influenza surveillance. ESFLU approach demonstrated that a networked, cross-sector approach can enhance monitoring of viral diversity, strengthen laboratory capacity, and guide evidence-based mitigation strategies. Improving sequencing capacity, adopting harmonized virus characterization protocols, and promoting real-time data sharing across animal and human health sectors within a One Health framework are essential to reduce the emergence and spread of novel swIAV variants with zoonotic potential.

Beyond surveillance: viral genomics to uncover local transmission and inform strategies for urban rabies elimination

Kirstyn BRUNKER (1,2), Alejandra DAVILA-BARCLAY (1,3), Elvis W. DIAZ (3), Sandeep KASARAGOD (1,2), Rowan DURRANT (4), Edith ZEGARRA (5), Ynes MONROY (5), Ricardo CASTILLO-NEYRA (3,6,7)

1: School of Biodiversity, One Health & Veterinary Medicine, University of Glasgow, Glasgow, UK; 2: MRC-University of Glasgow Centre for Virus Research, University of Glasgow, Glasgow, UK; 3: One Health Unit, School of Public Health and Administration, Universidad Peruana Cayetano Heredia, Lima, Peru; 4: Department of Biology, McMaster University, Hamilton, Canada; 5: Laboratorio de Referencia Regional de la Gerencia Regional de Salud de Arequipa, Arequipa, Peru; 6: Department of Biostatistics, Epidemiology & Informatics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, USA; 7: Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, USA

Background: The global goal of "Zero by 30" for dog-mediated human rabies requires shifting from reactive control to precision elimination. However, "cryptic" transmission and transboundary host and viral movements often undermine traditional surveillance in complex urban ecosystems. Such is the case of persistent pockets of urban canine rabies in Latin America despite ongoing control efforts. While genomic epidemiology offers unparalleled resolution, its integration into routine One Health surveillance remains underutilized globally. Here, we present a decade-long genomic reconstruction of an urban rabies epidemic with insights for control that may provide a model for high-burden low-resource regions.Methods: We generated the largest whole-genome sequence (WGS) collection for canine rabies (RABV) in Latin America (n=167) from rabies-positive brain samples in Southern Peru. By integrating genomic, epidemiological, and spatio-temporal data into modern continuous and discrete phylogeographic models, we assessed viral diffusion dynamics across Arequipa city, a major urban center in Peru, over 10 years. We also employed a novel analytical model to estimate total outbreak size using solely sequence data to reconstruct the true epidemic trajectory, despite gaps in case detection.Results: Phylogenetic ancestral reconstruction revealed a "silent" viral circulation period of two years before official detection of the first case in 2015. We identified several transboundary incursions from neighboring regions and Bolivia. Our phylogeographic models quantified the impact of urban topography, identifying the Chili River, which divides the city, as a major transmission determinant. Crucially, we distinguished between "source" districts that maintain viral persistence and "sink" districts, where effective vaccination may have driven certain lineages to extinction. The outbreak-size model estimated that the number of reported cases represents a very small fraction (5%) of the actual number of cases occurring in the city.Conclusions: City-level genomic analysis can uncover cryptic transmission even in areas previously declared dog rabies-free, supporting early-warning systems. It can also aid in identifying high-risk "source" populations for targeted resource allocation, assist in evaluating the effectiveness of control strategies, and gauge the true size of an epidemic within closed urban systems in the presence of significant under-reporting. This framework supports actionable "One Health Intelligence" offering a reproducible strategy for rabies-endemic countries to transition from persistent outbreaks toward validated regional elimination.

Dogs as carriers of highly pathogenic Campylobacter jejuni with cross-species neuropathogenic potential

Maria-Leonor LEMOS (1,2,3), Alexandra NUNES (4,5), Koen BOSSERS (3), Paulo MARTINS DA COSTA (2), Astrid HEIKEMA (3), Mónica OLEASTRO (1)

1: National Reference Laboratory for Gastrointestinal Infections, Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge, Lisbon, Portugal; 2: Laboratory of Microbiology and Food Technology, Institute of Biomedical Sciences Abel Salazar, University of Porto, Porto, Portugal; 3: Leiden Centre for Applied Bioscience, University of Applied Sciences Leiden, Leiden, The Netherlands; 4: Genomics and Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge, Lisbon, Portugal; 5: Veterinary and Animal Research Centre (CECAV), Faculty of Veterinary Medicine, Lusófona University, Lisbon University Centre, Lisbon, Portugal

The One Health approach provides an important framework for understanding zoonotic pathogens. Campylobacteriosis is the most frequently reported zoonosis in the European Union and is primarily associated with poultry consumption. However, other potential reservoirs, including companion animals,

remain poorly explored despite the close contact between dogs and humans and previous reports of zoonotic transmission.

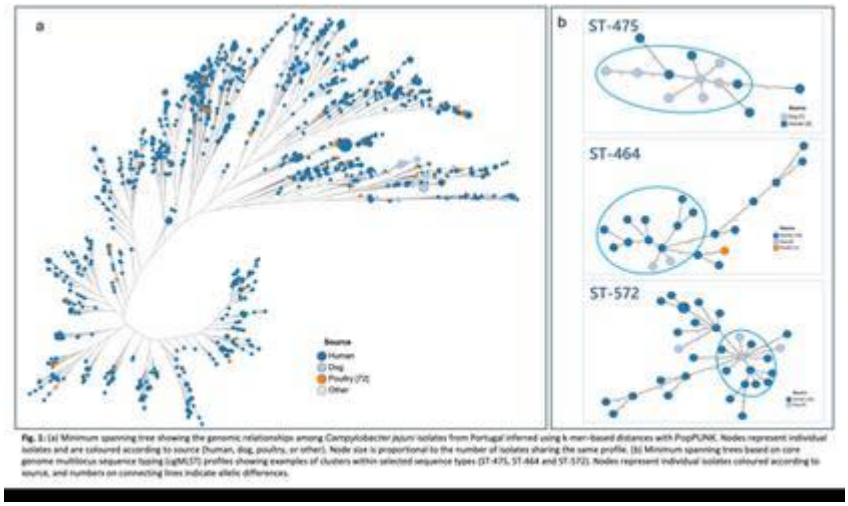
Between 2023 and 2024, a total of 650 rectal swabs were collected from dogs in veterinary clinics, shelters, and hunting packs across Portugal. *Campylobacter* spp. were detected in 30% of samples, with a prevalence of 12% for *Campylobacter jejuni*. Eighty-six isolates were subjected to whole-genome sequencing (WGS) and compared with contemporaneous Portuguese (PT) human isolates (n = 1105) and other animal/food isolates (n = 90), including poultry (n = 72).

In silico MLST identified 25 sequence types (STs) among dog isolates, grouped into 16 clonal complexes. Notably, 88% (22/25) of STs detected in dogs were also present among human isolates, whereas only 48% (12/25) overlapped with poultry isolates. Phylogenetic analysis further revealed several clusters containing both dog and human isolates separated by ≤10 allelic differences, while poultry isolates generally formed distinct clusters (Fig.1).

Given the established association between specific *C. jejuni* types and the immune-mediated neuropathy Guillain–Barré syndrome (GBS), genomic markers linked to neuropathogenic potential were investigated. Genes involved in lipooligosaccharide (LOS) sialylation, a key factor in molecular mimicry and GBS pathogenesis, were detected in 83% (71/86) of dog isolates, compared with 47% (34/72) of poultry isolates. Capsular genotyping further revealed a notable prevalence of genotypes strongly associated with GBS among dogs: 43% of the isolates classified as HS19 (9/21) and 53% of the classified as HS41 (9/17) originated from dogs, whereas poultry carried only three HS19 isolates (14%; 3/21) and none belonging to HS41.

These findings are particularly relevant given the similarities between GBS in humans and acute polyradiculoneuritis (APN) in dogs. While associations between *Campylobacter* infection and APN have previously been suggested, the presence of anti-LOS antibodies in affected dogs had not previously been confirmed. Serological analyses showed that sera from PT dogs diagnosed with APN reacted with *C. jejuni* LOS, suggesting that infection with neuropathogenic strains may act as a trigger for this condition.

Overall, these results demonstrate that dogs can harbour highly pathogenic *C. jejuni* strains, including lineages carrying neuropathogenic markers commonly associated with severe human disease. These findings highlight the importance of integrating companion animals into *Campylobacter* surveillance within a One Health framework to improve our understanding of transmission pathways and support more effective disease prevention strategies.



Persistent High-Pathogenic Avian Influenza Hotspots in Vietnam

Thuy THI HOANG (1), Renata DE LARA MUYLAERT (1), Carsten THURE KIRKEBY (2), Michael PATRICK WARD (1)

1: Sydney School of Veterinary Science, Faculty of Science, The University of Sydney; 2: Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen

Background Highly pathogenic avian influenza (HPAI) continues to threaten poultry production, wildlife biodiversity, and public health globally. Vietnam has experienced recurrent HPAI outbreaks since 2003

and remains a key hotspot in Southeast Asia. Understanding persistent spatial patterns of outbreaks is essential for designing targeted surveillance and risk-based control strategies to minimise health risks.

Methods We analysed HPAI outbreak records (2006-2022) from WAHIS (World Organisation for Animal Health) and EMPRES-i (Food and Agriculture Organisation). Poultry population data were obtained from the General Statistics Office of Vietnam (annual, provincial level). Spatiotemporal clustering was assessed (SaTScan v10.1) under two complementary approaches: a space-time permutation model to identify recurrent outbreak activity and a discrete Poisson model incorporating poultry population data to detect population-adjusted risk clusters. Multiple spatial (10-100 km) and temporal (30-90 days) window configurations were evaluated. Clusters detected repeatedly across 50% parameter settings were considered robust. Scanning outputs were further processed and analysed (R v4.5.1).

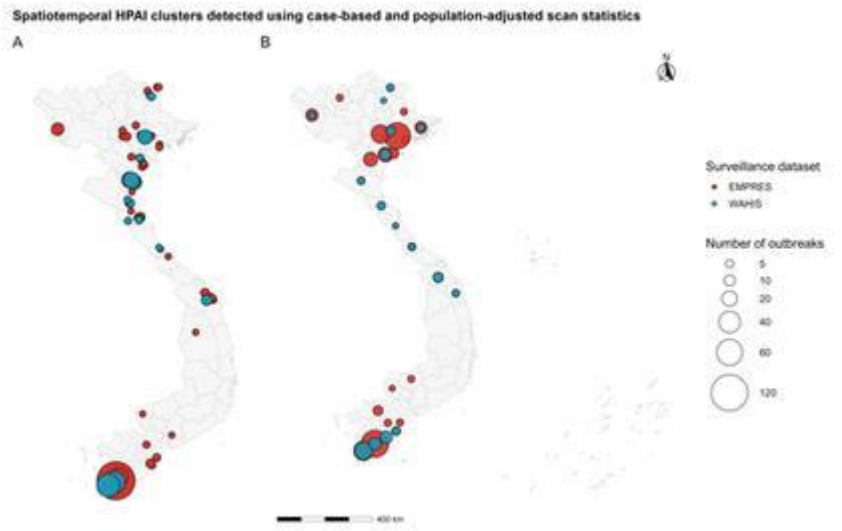
Results Both models identified obvious spatial concentrations of HPAI outbreaks in northern and southern Vietnam. The space-time permutation model highlighted recurrent outbreak activity in the Red River Delta and Mekong Delta regions, indicating repeated outbreaks in major poultry production areas. The population-adjusted model identified robust high-risk clusters in the same regions, suggesting outbreak occurrence substantially higher than expected relative to poultry population size.

Population-adjusted analysis also detected additional clusters in parts of northwestern Vietnam, a largely remote region, suggesting potential localised transmission signals not evident in case-based clustering alone. In contrast, few clusters were detected in the Central Highlands and the south-central coastal region using either model, indicating marked geographic heterogeneity in outbreak detection.

Several clusters represented substantial outbreak burdens: up to 132 outbreaks were detected within individual cluster windows. Smaller clusters were also observed along the central Vietnamese corridor, suggesting episodic transmission outside the primary hotspot regions.

Across both models, EMPRES and WAHIS showed broadly consistent spatial patterns, although generally more clusters were detected from EMPRES, reflecting its higher reporting volume. Areas identified by in both datasets and analytical approaches represent robust hotspot signals; discrepancies highlight the influence of reporting coverage and surveillance structure on cluster detection.

Conclusions Consistent identification of hotspot regions confirms that the Red River Delta and Mekong Delta function as persistent HPAI transmission systems within Vietnam's poultry sector. The population-adjusted model revealed additional clusters in northwestern Vietnam that might reflect emerging or previously under-detected risk. Differences in cluster detection between EMPRES and WAHIS demonstrate how surveillance structure and reporting intensity shape the spatial signals observed in outbreak data. These findings highlight the importance of integrating multiple surveillance data sources and analytical approaches to support risk-based surveillance strategies, prioritising established hotspot regions while strengthening detection capacity elsewhere.



Peptide microarray-based epitope profiling enables pan-orthoebolavirus surveillance and differential serodiagnosis for acute Ebola virus disease versus prior exposure or vaccination

Sunil Kumar DUBEY (1), Andrea MARZI (2), Ian CROZIER (3), Richard T. DAVEY JR (4), Irina Maljkovic BERRY (5), Zirui ZHOU (1), Riddhi THAKKAR (1), Shreyas JOSHI (1), Dean FOLLMANN (6), Olivier Tshiani MBAYA (3), H. Clifford LANE (4), W. Ian LIPKIN (1,7), Lisa E. HENSLEY (8), **Nischay MISHRA** (1,7)

1: Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, NY, USA; 2: Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Hamilton, MT, USA; 3: Clinical Monitoring Research Program Directorate, Frederick National Laboratory for Cancer Research, Frederick, MD, USA; 4: Laboratory of immunoregulation, National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Bethesda, MD, USA; 5: Integrated Research Facility at Fort Detrick (IRF-Frederick), National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Frederick, MD, USA; 6: Biostatistics Research Branch, Division of Clinical Research, National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, Bethesda, MD, USA; 7: Epidemiology, Columbia University Irving Medical Center, United States of America; 8: National Bio and Agro-Defense Facility (NBAF), United States Department of Agriculture (USDA), Manhattan, KS, USA

Background: Orthoebolaviruses pose a major global health threat due to recurrent outbreaks, high case-fatality rates, zoonotic spillover, and viral recrudescence in survivors. Serological surveillance and diagnosis are confounded by extensive antibody cross-reactivity among orthoebolaviruses and the widespread deployment of rVSV-based ebolavirus vaccines, limiting the ability of current assays to distinguish vaccine-induced from infection-derived immunity and to resolve acute Ebola virus disease (EVD) from subclinical infection. High-resolution, epitope-based serology provides an agnostic strategy to define conserved and infection-specific antibody signatures, enabling *pan*-orthoebolavirus surveillance and differential serodiagnosis.

Methods: Proteome-wide epitope-mapping was performed using a high-density peptide-microarray comprising ~391,000 overlapping 12-mer-peptides spanning the *Filoviridae* proteomes, vaccine antigens, and controls . We analyzed plasma from rVSV-Ebola-virus-glycoprotein (rVSV-EBOV-GPMakona)- and rVSV-Marburg-virus-GP (rVSV-MARV-GPAngola)- vaccinated non-human primates (NHPs) challenged with EBOV-Makona, rVSV-EBOV-GPKikwit human vaccinees, EVD-survivors, and acute-EVD patients **(Figure.1)**. Immunoreactive epitopes were identified using predictive classification models and validated with biotinylated-peptide ELISA panels.

Results: We identified EBOV *Glycoprotein1,2 (GP1,2)* specific immunoreactive epitopes and rVSV vector-focused epitopes after vaccination in NHPs and human vaccinees **(Figure.2**). After vaccination and EBOV-Makona challenge in NHPs, proteome-wide, multi-antigen antibodies were identified against immunoreactive epitopes including EBOV-*GP1,2*,*nucleoprotein (NP), VP35* and *VP40*. In all cohorts, *GP1,2* epitopes were consistent and located across sites critical for viral entry and antibody neutralization, including the glycan cap, mucin-like domain, heptad repeat region 2, and membrane-proximal external region. MLD region epitopes are prone to antigenic drift and immune evasion, and harbored additional mutations in recent EBOV/DRC/2025 outbreak. Antibody responses to immunogenic peptides were age-dependent and increased following booster dose in human vaccinees (**Figure.2)**. Based on the sensitivity and specificity of selected immunogenic regions, we developed a multi-antigen focused 8-plex peptide-ELISA assay (four in *GP1,2*: GP1, GP2, GP3, and GP4; one each in *NP*: NP-1, *VP40*: VP40-1 , *VP35*: VP35-1; and rVSV matrix protein: VSV5) that enabled a *pan*-orthoebolavirus surveillance and differential serodiagnosis assay **(Figure.3)**. Multi-antigen 8-plex peptide-ELISA has utility as a rapid differential serodiagnostics assay and achieved 100% sensitivity and specificity in differential diagnosing for acute infection, EVD survivors, vaccinated individuals, distinguishing infection from vaccination, and vaccinated individuals with prior infection (**Figure.3**). All eight peptides map to surface-exposed regions and are readily accessible to antibody binding. Two *GP1,2*epitopes (GP1 in glycan cap and GP4 in MPER region) are in the most conserved regions among all orthoebolaviruses, suggesting their utility as *pan*-orthoebolavirusdetection targets for emerging ebolaviruses, prior zoonotic exposures and spillovers, animal reservoirs, and detecting asymptomatic infections.

Conclusion: Agnostic serology overcomes key limitations of current *GP1,2*-based orthoebolavirus serological assays to enable discrimination between vaccine-induced and natural immunity. Our multi-antigen based serological tools are critical in outbreak preparedness, decentralized rapid-screening, and enhance One Health surveillance to guide spillover risk assessment in endemic and resource-limited settings.

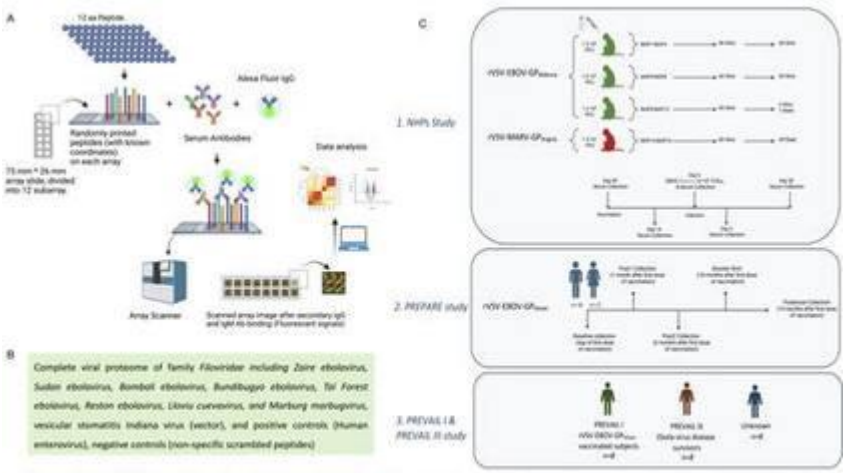


Figure 1 (a) Workflow of B-cell epitope mapping using high-density peptide microarray experiment and analysis (b) Peptide array design elements (c) Experimental plan for three study groups employed in the study

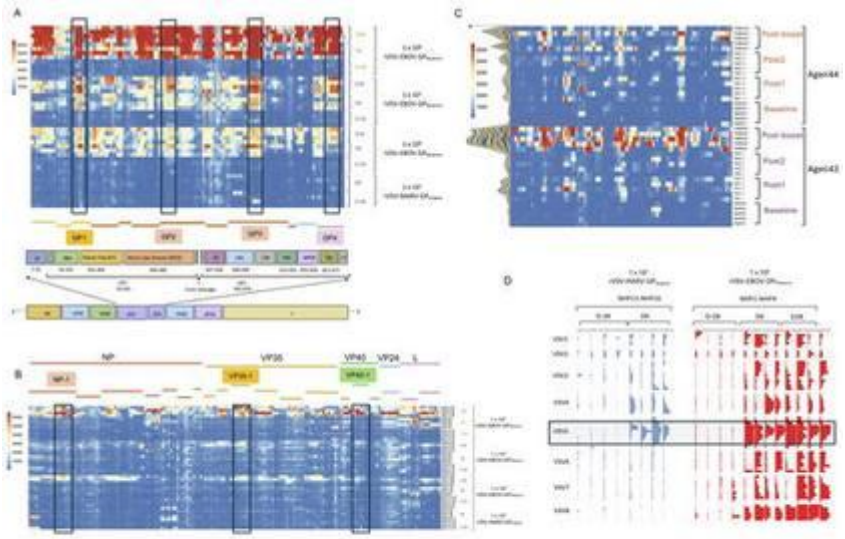
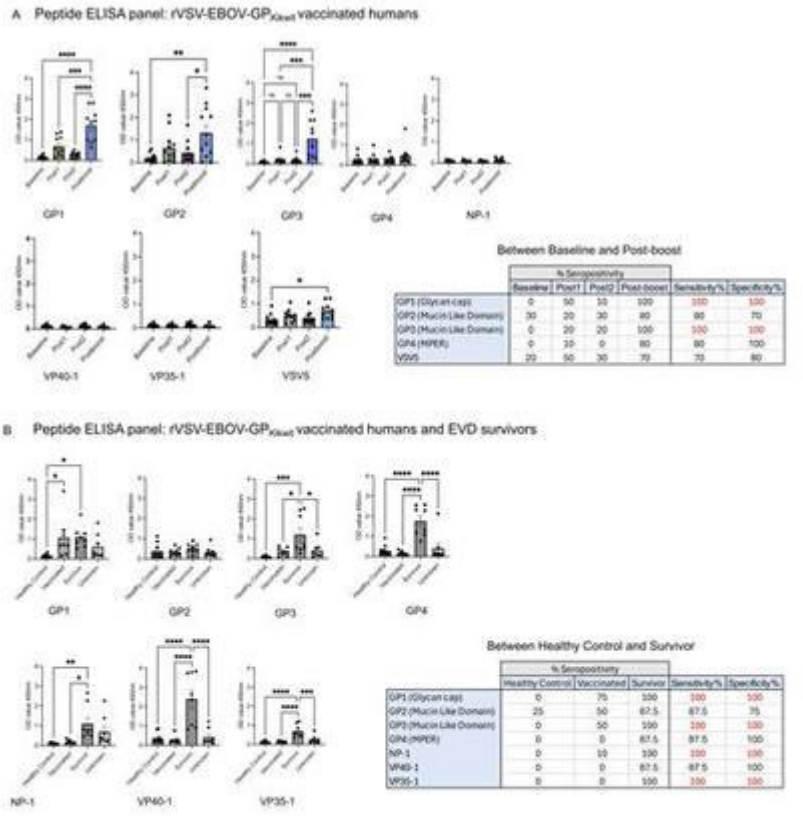


Figure 2 (a) Identified immunoreactive epitopes in Glycoprotein$_{1,2}$ in non-human primates after vaccination with rVSV-EBOV-GP$_{Makona}$ (dose dependent) and rVSV-MARV-GP$_{Angola}$ (Controls), and challenge with EBOV-Makona (b) Other EBOV proteins' immunoreactive epitopes in NHPs after challenge with EBOV-Makona (c) Age dependent immunoreactivity of GP$_{1,2}$ epitopes in human vaccinees [rVSV-EBOV-GP$_{Kikwit}$] (d) Identified immunoreactive epitopes of rVSV vector backbone in NHPs.



Peptide (Domain)	Baseline	Post1	Post2	Post-boost	Sensitivity%	Specificity%
GP1 (Glycan cap)	0	50	10	100	100	100
GP2 (Mucin Like Domain)	30	20	30	80	80	70
GP3 (Mucin Like Domain)	0	20	20	100	100	100
GP4 (MPER)	0	10	0	80	80	100
VSV5	20	50	30	70	70	80

Peptide (Domain)	Healthy Control	Vaccinated	Survivor	Sensitivity%	Specificity%
GP1 (Glycan cap)	0	75	100	100	100
GP2 (Mucin Like Domain)	25	50	87.5	87.5	75
GP3 (Mucin Like Domain)	0	50	100	100	100
GP4 (MPER)	0	0	87.5	87.5	100
NP-1	0	10	100	100	100
VP40-1	0	0	87.5	87.5	100
VP35-1	0	0	100	100	100

Peptide (Domain)	Acute Infection	EVD Survivor	Vaccination + Acute Infection	Vaccination only
GP1 (Glycan cap)	☑	☑	☑	☑
GP2 (Mucin Like Domain)	☑	☐	☑	☑
GP3 (Mucin Like Domain)	☑	☑	☑	☑
GP4 (MPER)	☐	☑	☑	☑
NP-1	☑	☑	☑	☐
VP40-1	☑	☑	☑	☐
VP35-1	☑	☑	☑	☐
VSV5	☐	☐	☑	☑

Figure 3 Indirect peptide ELISA of plasma (a) from rVSV-EBOV-GP$_{Kikwit}$ vaccinated human subjects from PREPARE study and % sensitivity, % specificity of peptides between baseline and post-boost (b) and from PREVAIL I (rVSV-EBOV-GP$_{Kikwit}$ vaccinated human subjects), PREVAIL III (EVD survivors), and unknown blind samples along with healthy controls from PREPARE study % sensitivity, % specificity of peptides between healthy control and survivors. (c) Peptide panel for differential identification between acute infection, EVD survivor, Vaccination + acute infection, and vaccination only. *This project was supported by the USDA (NACA-58-3022-2-02), and in part by the Intramural Research Program of the NIAID (NIH), and part NCI (NIH) (Contract No. 75N91019D00024).*

Rabies treatment revolution: intravenous immunotherapy to combat a global zoonosis

Seonhee KIM (1), Anthony COLEON (1), Florence LARROUS (1,2), Lauriane KERGOAT (1,2), Said MOUGARI (1,2), Julien LANNOY (1,2), Marta TIAGO (1,3), David HARDY (4), Etienne KORNOBIS (5,6), Felix A. REY (7), Fabio BENIGNI (8), Davide CORTI (8), Hervé BOURHY (1,2), **Guilherme DIAS DE MELO** (1,2)

1: Institut Pasteur, Université Paris Cité, Lyssavirus Epidemiology and Neuropathology Unit, F-75015 Paris, France; 2: Institut Pasteur, WHO Collaborating Centre for Reference and Research on Rabies, European Union Public Health Reference Laboratories for Emerging, Rodent-borne and Zoonotic Viral pathogens (EURL-PH-ERZV); 3: Universidade de Lisboa, Faculdade de Medicina Veterinária, 1300-477 Lisboa, Portugal; 4: Institut Pasteur, Université Paris Cité, Histopathology Core Facility, F-75015 Paris, France; 5: Institut Pasteur, Université Paris Cité, Bioinformatics and Biostatistics Hub, F-75015 Paris, France; 6: Institut Pasteur, Université Paris Cité, Plate-forme Technologique Biomics, F-75015 Paris, France; 7: Institut Pasteur, Université Paris Cité, Structural Virology Unit, F-75015 Paris, France; 8: Humabs BioMed SA, a subsidiary of Vir Biotechnology, 6500 Bellinzona, Switzerland

Rabies is a complex disease that has defied efforts to develop an effective treatment. Although it can be successfully prevented through vector control or pre- or post-exposure prophylaxis, no therapeutic options exist for symptomatic rabies, and the disease is still responsible for about 59 000 human deaths each year. Following our successful attempts to use the human monoclonal antibodies RVC20 and RVC58 for intracerebroventricular treatment of rabies, we report here on the effects of these mAbs when

administered intravenously to symptomatic rabid mice. Only a small proportion of mAbs was detected to cross the blood-brain barrier, yet this limited amount sufficiently cleared the viral infection and was enough to cure the infected animals. Remarkably, these mAbs were more effective at preventing rabies-related death when used individually rather than when used as a cocktail. RVC58 achieved an 80% survival rate, likely due to its distinct binding topography, potent viral neutralization, and enhanced FcγR engagement in the presence of virions. The significance of this work is that the use of a single mAb could substantially lower the costs and improve treatment accessibility in under-resourced settings, potentially contributing to improved equity of global health. These findings establish intravenous mAb therapy as a promising therapeutic approach for symptomatic rabies and provide a foundation for clinical development of an accessible treatment option.

NECROBIOME – Microbiome of the Cinereous Vulture to Support Integrated Ecosystem Management in Baixo Alentejo

Diana V. JORGE (1,2,4), Maria P. COUTO (3,1), Raquel XAVIER (2,4), Pedro ROCHA (5), Milene MATOS (1), Fernando TAVARES (2), José TAVARES (1)

1: Vulture Conservation Foundation, Switzerland; 2: Department of Biology, Faculty of Sciences - University of Porto, Portugal; 3: Department of Preventive Veterinary Medicine, College of Veterinary Medicine and College of Public Health - The Ohio State University, USA; 4: CIBIO-InBIO - Research Centre in Biodiversity and Genetic Resources, Portugal; 5: Herdade da Contenda E.M., Portugal

Background: The agro-silvo-pastoral system of Baixo Alentejo is a critical One Health interface where wildlife, livestock, and human livelihoods converge. Within this landscape, the Cinereous vulture (*Aegypius monachus*) underpins environmental health and ecosystem sustainability. Through carcass consumption, it modulates pathogen spread, nutrient cycling, and biological waste elimination. As obligate scavengers, their disease-avoidance adaptations - e.g., specialized oral and gastrointestinal microbiomes -position them as sentinels for public health biosurveillance.

In Portugal, the species is classified as *Endangered*, facing multi-level threats, such as food scarcity, low-quality feeding resources, habitat degradation and restrictive biological-waste management policies. Weakened vulture populations and shortage of trained One Health actors in Baixo Alentejo, particularly in the rural areas where traditional agricultural systems are increasingly undermined, compound public health vulnerabilities.

NECROBIOME is an applied research project designed to (a) promote the conservation of the Cinereous vulture and the long-term sustainability of associated ecosystems, and (b) implement an operational One Health strategy at the wildlife-livestock-human interface and at the community capacity-building training.

Methods: Led by a consortium comprising the Vulture Conservation Foundation, Herdade da Contenda E.M., and the Faculty of Sciences (University of Porto), the project uses licensed supplementary feeding stations (CAAN/APAAN) as its model-territory, anchored in Portugal's Plan for the Conservation of Scavenger Birds (PACAN) milestones.

NECROBIOME is structured around two interdependent axes:

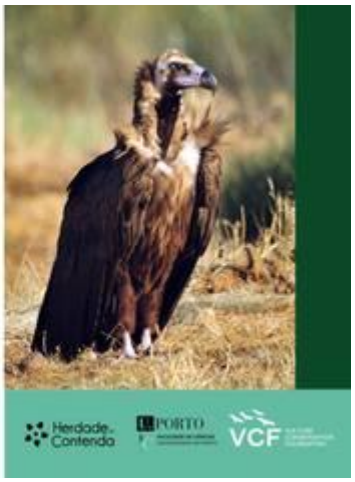
Axis-1 (Scientific Reference & Innovation) applies metagenomic profiling (metabarcoding of bacterial and fungal communities and whole-genome sequencing) to four matrices: wild vulture oral and cloacal swabs, feeding-site soils, and ungulate carcasses. Cross-matrix comparative analyses reconstruct microbial flux at the oral–fecal route, to infer trophic interactions, and metabolization dynamics of pathogens and virulence factors. Virulence and AMR-targeted determinants will inform detection protocols for reporting zoonotic pathogens.

Axis-2 (Model-Territory & Community) implements a WOAH framework: competency-based Community Animal Health Workers (CAHWs) training programme, co-designed with local stakeholders. Training modules will be iteratively shaped by risk profiles emerging from Axis-1, contributing to targeted training of the rural public health workforce.

Results: To date, DNA has been extracted from 98 vulture samples, and genomic amplification is underway. Taxonomic and functional outputs are expected by June 2026, providing the first systematic microbiome and mycobiome characterization of wild Cinereous vultures in Portugal and enabling a

preliminary assessment of pathogen modulation capacity and contaminant flux. In parallel, the first CAHW capacity-building cohort is scheduled for June 2026.

Conclusion: By establishing an interdependent framework that integrates wildlife-livestock-human dynamics with structured community capacity-building, NECROBIOME operationalizes the cCinereous vulture as a bio-surveillance sentinel, within a One Health strategy anchored in PACAN. The project directly addresses the absence of evidence-based tools to monitor pathogen modulation and metabolization across the trophic chain; and advances a scalable model for public health preparedness and local ecosystem and livelihoods resilience.



Governance, Policy & Legal Frameworks

SPI03 · 14:00-15:30 · Auditorium II

From Data Silos to Shared Governance: Developing Policy and Legal Frameworks for Wildlife Data Integration in Pandemic Early Warning

Tracey MCNAMARA (1), Louise GRESHAM (2), Lauren CHARLES (3)

1: Western University of Health Sciences College of Veterinary Medicine, United States of America; 2: PAX sapiens, United States of America; 3: Pacific Northwest National Laboratory, United States of America

Background: A significant proportion of emerging infectious diseases are of zoonotic origin, with wildlife serving as reservoirs for novel pathogens. The profound weaknesses in health surveillance of free-ranging wildlife around the world represents a critical gap for early warning. However, global surveillance of free-ranging wildlife remains limited. A World Organisation for Animal Health (WOAH) survey of 103 countries found that more than half reported having some wildlife disease surveillance data, but much of it is in paper form and spreadsheets limiting sustainability and timely signal detection. Many countries expressed the need for guidance and support to build national information systems capable of detecting and responding to emerging wildlife health events. We report on a governance and policy-oriented process that resulted in data sharing across previously siloed federal/state government wildlife agencies, academia, and the private sector in the USA and Canada, with continued engagement with European Union agencies. In bridging the gap between advanced data practice that previously had been unavailable to the wildlife community, this process opened the door to collaboration. It influenced governance frameworks and policy aimed at global harmonization of wildlife databases for early detection of emerging health threats.

Methods: Two international conferences—the Global Wildlife Data Sharing Conferences (GWDSC)—were convened in 2024 and 2025 with support from PAX sapiens. The first GWDSC was hosted at Pacific Northwest National Laboratory (PNNL) in Richland, Washington, USA, convening representatives from 9 government agencies, 11 academic institutions, 11 non-governmental organizations, and 8 countries. Notably, private-sector wildlife ecologists and wildlife rehabilitators—holders of previously underutilized data—participated for the first time.

The second GWDSC, held in Spain, engaged 40 international experts from 16 countries. Both conferences employed facilitated sessions to identify barriers to data sharing, evaluate existing governance structures, and co-develop frameworks for biosurveillance, signal detection, and early warning.

Results: Conference participants negotiated memorandums of understanding and co-developed a set of core values and principles—including data integrity, privacy protection, sovereignty respect, equitable access, and ethical use—to govern cross-sectoral data exchange. Standardized templates for secure, tiered data sharing were created to preserve data ownership while enabling aggregation for early-warning analytics. Subsequent policy changes facilitated interagency data exchange and formalized the PNNL– US Geological Survey's National Wildlife Health Center (NWHC) partnership, contributing to the establishment of the National Wildlife Disease Database (NWDD).

Conclusions: The GWDSC process demonstrates that multi-sectoral stakeholders with distinct institutional mandates can converge on shared governance principles and operationalize tiered, secure data-sharing mechanisms. This approach offers a replicable model for other regions seeking to integrate fragmented wildlife health data into coordinated surveillance systems that strengthen early warning and pandemic preparedness within a One Health framework.

Between Policy and Practice: A Qualitative Assessment of National One Health Governance Structures and Legal Framework Gaps Across Sub-Saharan African Countries

Yusuff AZEEZ (1,2,3), Oyindamola OGUNSEYE (4)

1: ACES AFRICA, Nigeria; 2: University of Ibadan; 3: Iconic Open University; 4: University of Ilorin

Background: The One Health Joint Plan of Action calls for integrated, legally anchored governance systems coordinating human, animal, and environmental health sectors at national level. Yet in sub-

Saharan Africa, One Health governance remains largely informal — characterized by ad hoc inter-ministerial coordination, weak legal mandates, and policy frameworks that exist on paper but lack implementation infrastructure. This study examined national One Health governance architectures across sub-Saharan African countries, identifying legal gaps, coordination failures, and equity dimensions undermining effective implementation.

Methods: A qualitative multi-country study was conducted across eight sub-Saharan African countries selected through purposive sampling to represent variation in income level, epidemic history, and One Health policy maturity. Key informants were identified through government ministry directories, WHO and FAO country office rosters, and professional networks, with initial contact made via formal email invitation. A total of 64 key informant interviews were conducted via video conferencing with senior officials from ministries of health, agriculture, environment, and finance, alongside WHO, FAO, and WOAH country office representatives. Six focus group discussions were facilitated remotely with frontline One Health implementers. National policy documents, legal texts, and inter-ministerial coordination agreements underwent systematic document review. Thematic analysis employed NVivo, grounded in WHO Joint External Evaluation criteria and Ostrom's institutional analysis framework. Ethical approval was obtained and all participants provided informed consent.

Results: Across all eight countries, One Health coordination mechanisms existed primarily as donor-funded technical working groups without statutory legal backing, rendering them vulnerable to funding discontinuity. Only two of eight countries had enacted legislation explicitly mandating inter-sectoral One Health coordination. Ministries of finance were absent from governance structures in seven countries, systematically excluding domestic financing from policy design. Key informants consistently identified jurisdictional ambiguity between human and animal health ministries as the primary operational barrier, with zoonotic outbreaks frequently triggering inter-ministerial disputes over mandate and resource control. Frontline implementers reported operating without clear legal authority, limiting enforcement of One Health protocols. Communities in rural and border areas remained structurally excluded from policy processes despite bearing the highest zoonotic disease burden.

Conclusions: One Health governance in sub-Saharan Africa is architecturally fragile, resting on informal coordination mechanisms lacking legal permanence, domestic financing integration, and community participation structures. Achieving OH Joint Plan of Action ambitions requires legally anchored national frameworks, statutory mandates for inter-sectoral coordination, and deliberate inclusion of finance ministries and affected communities in governance design. Regional harmonization drawing on the Africa CDC Statute and AU Model Law on biosafety represents an underutilized pathway toward sustainable governance reform.

Strengthening Global Wildlife Health for better One Health – The WOAH Global Wildlife Health Collaborating Centre Network (WOAH-WildNet)

Casey BARTON BEHRAVESH (1), Kelly BATEMAN (2), Charlotte BERG (3), Jemma BERGFELD (4), Mathieu BOURGAREL (5), Cristina CASALONE (6), Claire CAYOL (7), Erin DAVIS (8), Alexandre FEDIAEVSKY (7), Charlene FERNANDEZ (9), Antonio FERNANDEZ (10), Merid GETAHUN (11), Federica GIORDA (6), Keith HAMILTON (7), David T. S. HAYMAN (12), Damien JOLY (13), **Sascha KNAUF** (14,22), Christa KÜHN (14), Jean-Claude MANUGUERRA (15), Daniel MASIGA (11), Anita MICHEL (16), Paolo MULATTI (17), Misheck MULUMBA (18), Annah NJUI (11), Sarah OLSON (19), Richard PALEY (2), B. Dharmaveer SHETTY (7), Eva SIERRA (10), David Poumo TCHOUASSI (11), Steve UNWIN (8), Jandouwe VILLINGER (11), Christian WALZER (19), Youming WANG (20), Frank WONG (4), Anna WONG (9), Gongxun ZHONG (21)

1: Centers for Disease Control and Prevention, United States of America; 2: Centre for Environment, Fisheries and Aquaculture Sciences, United Kingdom; 3: SLU-SCAW Swedish Centre for Animal Welfare, Sweden; 4: Australian Centre for Disease Preparedness, Australia; 5: Centre international en recherche agronomique pour le développement, France; 6: Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, Italy; 7: World Organisation for Animal Health, France; 8: Wildlife Health Australia, Australia; 9: National Parks Board Singapore, Centre for Wildlife Forensics, Singapore; 10: Institute for Animal Health and Food Safety, University of Las Palmas de Gran Canaria, Spain; 11: International Centre of Insect Physiology and Ecology, Kenya; 12: Massey University, Molecular Epidemiology and Public Health Laboratory, School of Veterinary Sciences, New Zealand; 13: Canadian Wildlife Health Cooperative, Canada; 14: Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Germany; 15: Institut Pasteur, France; 16: University of Pretoria, South Africa; 17: Istituto Zooprofilattico Sperimentale delle Venezie, Italy; 18: International Animal Health Consultant, Zambia; 19: Wildlife Conservation Society, USA; 20: China Animal Health and Epidemiology Center, China; 21: Harbin Veterinary Research Institute, China; 22: Faculty of Veterinary Medicine, Justus Liebig University, Giessen, Germany

Wildlife health is foundational to ecosystem integrity, biodiversity conservation, and global health security. Yet, despite its importance to the One Health paradigm, wildlife health initiatives have historically operated in fragmented institutional and geographic silos, limiting the capacity to address transboundary disease threats, biodiversity loss, and environmental change.

The World Organisation for Animal Health (WOAH) established the Global Wildlife Health Collaborating Centre Network (WOAH-WildNet) in 2023 to contribute to structuring this landscape and increase fruitful connectivity. Built on WOAH's mandate authority and aligned with the WOAH Wildlife Health Framework and future strategy, the network connects 22 Collaborating Centres across the world into a coordinated, standards-aligned, systems-based platform.

WOAH-WildNet contributes to operationalising One Health by advancing the "Four Cs": Communication, Coordination, Collaboration, and Capacity Strengthening. It links scientific excellence and innovation (diagnostics, epidemiology, pathology, genomics, surveillance, wildlife forensic and non-invasive methodologies) with institutional mechanisms (international standards for animal health, training and capacity building, and data harmonisation for 183 WOAH Members). This enables a shift from reactive, outbreak-driven responses to proactive, preventive, and globally harmonised wildlife health governance. The network contributes to global gap analyses, supports evidence-based decision-making for Members, and strengthens protocols. It advocates for evidence-based wildlife management and the importance of wildlife for the health of humans, animals and ecosystems. Several field and lab projects based on collaborations between network members are on the way. Outputs of the network are a SOP for wildlife outbreak investigations with in-country piloting and updated standards. By embedding wildlife health into international standards and strengthening cross-border technical coordination, WOAH-WildNet enhances the prevention, preparedness and response to disease outbreaks with the aim to reduce zoonotic spillover risks and to improve ecosystem resilience. The network supports a structural shift in global wildlife health governance—moving from isolated, national, and reactive approaches toward a more coordinated, preventive, and systemically resilient global framework that supports the Quadripartite's commitment to One Health.

Strengthening One Health Governance in Eastern and Southern African: Structures, Systems, Strategies, and Outcomes from multi-sectoral engagement

Simon ANGOMBE (1), Flora PULE-MEULENBERG (2), Salome BUKACHI (3), Lucinda DE ARAUJO (4), Gabriel M. SHIRIMA (5), Theodore KNIGHT-JONES (6), Shauna RICHARDS (6), Buke YUSSUF (6), Alex CARON (7), Margaret KAREMBU (8), Edna MACHARIA (8), Geofrey NGURE (8), Brooker SIMON (6), Gift MATOPE (9)

1: University of Namibia; 2: Botswana University of Agriculture and Natural Resources; 3: University of Nairobi; 4: Universidade Eduardo Mondlane; 5: Nelson Mandela - African Institution of Science and Technology; 6: ILRI; 7: CIRAD; 8: ISAAA; 9: University of Zimbabwe

Background

One Health (OH) governance across many African countries has historically faced gaps including weak institutional anchoring, inadequate multisectoral coordination, limited integration of environmental health, and inconsistent implementation and financing of OH strategies (Bukachi et al., 2024). These challenges are extensively documented across the Capacitating One Health in Eastern and Southern Africa (COHESA) 12-country case study series, which highlights systemic weaknesses such as unclear mandates, inconsistent policy implementation, and insufficient resourcing of OH platforms (Richards, 20241; Richards et al., 20242, Angombe et al., 2024). The COHESA project sought to address these gaps by strengthening coordination structures, strategic planning processes, and mechanisms for cross sectoral engagement.

Methods

COHESA applied a three-pillar governance approach: (1) *institutionalization* through technical support to strengthen, establish, or formalize national OH coordination mechanisms and secretariats; (2) *policy and planning* through co-creation, review, and endorsement of OH strategic plans integrating environment and ecosystem health; and (3) *engagement and capacity strengthening* through stakeholder mapping, policy dialogues, parliamentarian engagement, and science–media café activities. Through a programme-level flexible theory of change and a country-level demand-driven activity prioritization, stakeholder mapping.

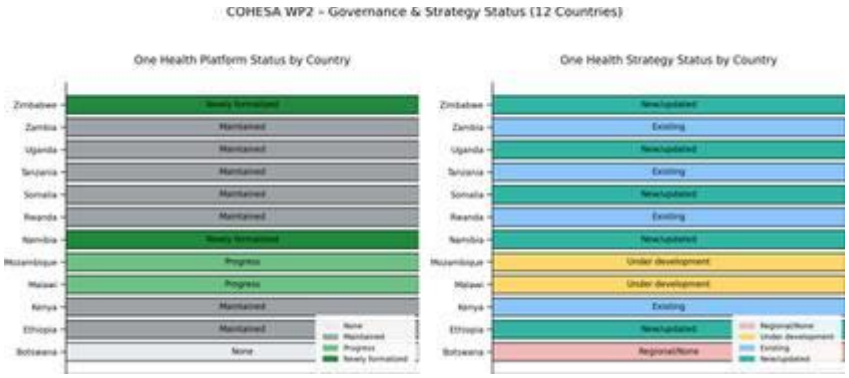
Results

Across the twelve countries, progress varied depending on baseline status (Figure 1). Nine countries formalized or renewed their OH coordination mechanisms during COHESA implementation, including Namibia and Zimbabwe, while Somalia revitalized its National OH Technical Working Group to strengthen multisectoral collaboration. Malawi advanced a multisectoral MoU, while Mozambique strengthened its national OH Secretariat (De Araújo et al., 2024). Countries with pre-existing platforms, Ethiopia, Rwanda, Kenya, Tanzania, Uganda, and Zambia, further operationalized their system through targeted facilitation, aligning with trends across the COHESA case series (ILRI, 2025; Richards et al., 2024). Strategic planning progressed through validated or updated OH strategies, while stakeholder-mapping, parliamentary engagement, and media initiatives enhanced political traction.

These governance improvements delivered measurable outcomes. Domestic financing increased, with recurrent allocations for OH secretariats in Mozambique, Rwanda, and Uganda. Multisectoral rapid assessments for zoonotic alerts in Kenya and Tanzania demonstrated faster coordination. Updated OH strategies integrating environmental and ecosystem health were completed in Namibia, Zimbabwe, and Ethiopia. Political visibility grew through parliamentary briefings across five countries, while stakeholder engagement expanded to over 800 participants.

Conclusions

The COHESA experience shows that strengthening OH governance requires not only platform establishment but also clear mandates, political anchoring, predictable financing, and operational mechanisms enabling coordinated action. The project delivered tangible gains across 12 countries, including formalization of coordination structures, increased domestic financing, and improved multisectoral response capacities. Sustained investment in legal frameworks, financing mechanisms, and monitoring systems is essential to consolidate these gains and ensure long-term OH governance resilience across the region.



One Health Systems Readiness Assessment in Croatia, Ghana and Nigeria to support Evidence-informed Policy Making

Racha FADLALLAH (2), Fadi EL-JARDALI (2), Francis Sena NUVEY (1), Davi ROMAO (3), Tanja KUCHENMULLER (3), Nadine DARWICHE (2), **Anna S FAHRION** (1)

1: Friedrich Loeffler Institut FLI, Germany; 2: Knowledge to Policy Center, American University of Beirut, Lebanon; 3: World Health Organization, Switzerland

Background: Global commitments to integrated governance for managing cross-sectoral health threats continue to grow, yet many countries struggle to operationalize the One Health (OH) approach. Fragmented institutional mandates, weak coordination mechanisms, and limited policy coherence frequently hinder the translation of OH principles into national governance systems. Within the Evidence-Informed Policy Approaches for One Health (OH-EVI) project, supported by the Global Health Protection Programme (GHPP), this study assessed national readiness for OH implementation, and identified governance, policy, and institutional gaps affecting evidence-informed decision-making.

Methods: Within the frame of the project, an assessment tool for One Health readiness was developed and piloted in Croatia, Ghana, and Nigeria between September 2024 and February 2025. The "Knowledge to Policy One Health Systems Readiness Assessment Tool" followed a four-step protocol comprising: (i) desk review of national legal and policy frameworks with stakeholder mapping; (ii) multisectoral deliberative workshops; (iii) consensus-based scoring across five components (policy and institutional frameworks, OH data and trends, policy analysis for OH principles, evidence-informed policymaking structures, and stakeholder analysis); and (iv) consolidation through SWOT analysis and priority setting. Indicators were scored using structured consensus and harmonized into three reporting levels (available, partial, absent).

Results: Across all three countries, foundational elements for OH implementation exist but remain unevenly institutionalized. None had a dedicated national OH policy or a dedicated national budget for cross-sectoral collaborative (OH) activities. Nigeria had a national OH strategic plan and coordinating unit but faced challenges in inter-ministerial coordination and subnational integration. Ghana had an active multisectoral technical working group and a draft One Health policy, though legal mandates and data integration remained limited. Croatia showed strong surveillance infrastructure and regulations align with European Union frameworks, particularly in food safety and antimicrobial resistance, but lacked a formal OH strategy/policy or coordinating platform. Common cross-country gaps included absent dedicated budget lines, fragmented data-sharing systems across human, animal and environment health sectors, weak institutionalized knowledge translation mechanisms, limited community engagement, and weak system-wide monitoring and evaluation.

Conclusions: Persistent governance and policy barriers continue to constrain institutionalization of One Health across diverse national contexts. Strengthening OH implementation requires formal policy frameworks, sustainable domestic financing, interoperable data-sharing systems, and institutionalized platforms for multisectoral coordination and evidence-informed policymaking. The K2P Systems Readiness Assessment Tool provides a practical governance-oriented framework for diagnosing system gaps and linking national OH assessments to policy dialogue and strategic priority setting, thereby supporting implementation of global One Health governance initiatives.

Water-Related Exposure and Systemic Constraints in Schistosoma mekongi Endemic Region: A One Health Perspective

Meng-Hua YU (1,2), Jian HE (1,2,3), Peter STEINMANN (5), Rita REYBURN (6), Kazim SANIKULLAH (7), Thipphavanh CHANTHAPASEUTH (6), Virak KHIEU (8), Peter ODERMATTE (4,5), Somphou SAYASONE (9), Kun YIN (1,2), Guo-Hong LI (1,2), Su-Ying GUO (10), Wang-Ping DENG (10), Chao LV (10), Li-Juan ZHANG (10), Jing XU (10), Xiao-Nong ZHOU (1,2,10), **Xiao-Xi ZHANG** (1,2)

1: School of Global Health, Chinese Center for Tropical Diseases Research, Shanghai Jiao Tong University School of Medicine, Shanghai, People's Republic of China; 2: School of Public Health, Shanghai Jiao Tong University School of Medicine, Shanghai, People's Republic of China; 3: Jiangsu Institute of Parasitic Diseases, Key Laboratory on Technology for Parasitic Disease Prevention and Control, Ministry of Health, Jiangsu Provincial Key Laboratory on the Molecular Biology of Parasites, Wuxi, Jiangsu, China; 4: Swiss Tropical and Public Health Institute, Allschwil, Switzerland; 5: University of Basel, Basel, Switzerland;

6: Integrated Communicable Disease Unit, World Health Organization, Lao PDR Country Office, Vientiane, Lao PDR; 7: World Health Organization, Western Pacific Regional Office (WPRO), Manila, Philippines; 8: National Center for Parasitology, Entomology and Malaria Control, Ministry of Health, Phnom Penh, Kingdom of Cambodia; 9: Lao Tropical and Public Health Institute, Vientianne, Lao People's Democratic Republic; 10: National Institute of Parasitic Diseases at Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research), NHC Key Laboratory of Parasite and Vector Biology, WHO Collaborating Centre for Tropical Diseases, Shanghai, People's Republic of China

Background:

Despite sustained mass drug administration (MDA) and sanitation campaigns reducing the burden of *Schistosoma mekongi* in the Lao People's Democratic Republic (Lao PDR) and Cambodia, transmission persists along the Mekong River. Progress toward elimination is increasingly hindered by systemic constraints at the intersection of human behavior, environmental exposure, and cross-sectoral governance. This qualitative study examines these constraints from a One Health perspective, focusing on how governance structures and policy implementation shape transmission dynamics in the Mekong Basin.

Methods:

Semi-structured interviews and focus group discussions were conducted with 17 stakeholders, including community members, health workers, implementation partners, and policymakers in schistosomiasis-endemic districts of Lao PDR and Cambodia (September 2025-February 2026). The study was guided by the Social Ecological Model (SEM) and the One Health Governance Model (OHGM), which informed stakeholder-specific interview guides and structured the analysis across individual, community, institutional, and policy levels. Data were analyzed using grounded theory, with independent back-to-back coding to ensure rigor and thematic saturation.

Results:

Stakeholders reported high MDA coverage (mentioned by 76.5% of participants) and near-universal household latrine adoption as key achievements contributing to reduced infection burden. However, routine contact with Mekong River water persists due to livelihood activities (e.g., fishing, farming), domestic practices (e.g., washing, bathing), and limited access to safe water. System-level constraints include reliance on symptom-based diagnosis at village level and reduced sensitivity of Kato-Katz in low-intensity settings. While national policies endorse the One Health approach, cross-sectoral collaboration and data sharing remain limited in practice. Moreover, the ecological and epidemiological interdependence of Mekong Basin countries underscores the need for transnational coordination, yet such mechanisms are not yet operationalized.

Conclusions:

Current control strategies, while effective in reducing morbidity, do not sufficiently address the environmental drivers of transmission. Elimination will require integrating water-safety improvements with strengthened diagnostics and operationalized One Health governance across sectors and borders. In the Lower Mekong Basin, where disease dynamics transcend national boundaries, sustainable elimination depends on coordinated stewardship and policy alignment. This study underscores the need for incremental, context-adapted interventions alongside long-term investments in safe water infrastructure and cross-border collaboration.

Food Systems, Agriculture & Plant Health

SCS03 · 16:00-17:30 · Auditorium I

Genomic Ecological Microbial Source Tracking for Oceans, Nature, and the Environment (GEMSTONE): a One Health Fecal Source Tracking Approach to Support Communities and Industry

Michael LEE (1), James KWAN (2), Angie NICOLAS (1), Natalie PRYSTAJECKY (2,3,4)

1: Environmental Health Services, British Columbia Centre for Disease Control, Canada; 2: University of British Columbia Centre for Disease Control, British Columbia Centre for Disease Control, Canada; 3: Public Health Laboratory, British Columbia Centre for Disease Control, Canada; 4: Pathology and Laboratory Medicine, University of British Columbia, Canada

Background: Fecal contamination of coastal waters negatively impacts the health of ecosystems, animals, and humans and is a common One Health issue worldwide. For example, fecal contamination increases nutrient levels associated with harmful algae blooms, they can introduce human and animal pathogens into the environment, and can alter ecosystem function affecting wildlife and human food sources such as shellfish. However, managing fecal contamination is complex because fecal sources include humans, pets, agricultural animals and fertilizer, and wildlife, highlighting the need for integrated One Health surveillance across human, animal, and environmental reservoirs. In this study, we assessed the utility of Microbial Source Tracking (MST) tools to identify the source of contamination in three shellfish harvesting areas in British Columbia (BC), Canada. Our objectives were to (1) validate the use of specific MST markers, (2) develop targeted knowledge translation materials, and (3) transfer MST technology to local community and industry partners. Unlike many other MST projects, our goal was to build local capacity to employ these methods for One Health surveillance and autonomous investigation of contamination sources. **Methods**: To validate and transfer these tools to sector partners, the BC Centre Disease Control (BCCDC) carried out this project in close collaboration with a local Indigenous community and an association representing the local shellfish industry. Together, we collected water samples biweekly for one year in our three study sites and used quantitative Polymerase Chain Reaction (qPCR) to detect host-specific fecal microbes to identify whether feces were from humans or other animals. To examine trends and drivers, we compared these MST data to long-term fecal coliform data collected in the same sites by a federal monitoring program and environmental datasets including land-use, precipitation, and streamflow. **Results**: Preliminary results indicated high marker specificity, but moderate sensitivity. There was ongoing fecal contamination in each of our three sites, but intermittent contamination from humans, pets, gulls, and ruminants. There was a low correlation between multiple general fecal indicators and species targets. Regression analyses are ongoing to establish contamination trends and relationships with environmental variables. We have developed a package of knowledge translation materials to facilitate transfer of the technology to our sectors partners. This package includes hands-on workshops, a high-level MST brochure, step-by-step laboratory standard operating procedures, primer-probe recipes, a shorter job-aid, and validation report. **Conclusions**: MST is one tool that can help build the foundation for managing fecal contamination, but is unlikely to serve as a solitary solution. Instead, managing fecal contamination requires integration of multiple fecal indicator datasets, environmental data, and close collaboration with local partners to ensure long-term buy-in and coordinated One Heath response.

Establishing a Continental Roadmap for Food Safety and Health Security: Development and Validation of the Africa CDC Food Safety Strategic Framework (2026–2030)

Yahya KANDEH (1), Chinenye EMELIFE (1), Wilnold MBINDYO (2), Yewande ALIMI (1), Merawi ARAGAW (1)

1: Africa Centres for Disease Control and Prevention, Zambia; 2: Eureka Idea Co.

Background

The development of the Africa CDC Food Safety Strategic Framework (2026-2030) was a structured, consultative, and technically rigorous process, designed to ensure continental ownership, policy alignment, and operational relevance. Recognizing that Foodborne diseases (FBD) impose a significant public health and economic burden across Africa, necessitating a unified, multi-sectoral response. The core objectives were to: support the development of a framework aligned with continental priorities;

assess the current status of food safety systems and FBD surveillance across African Union (AU) Member States (MS); and identify priority gaps and emerging needs. Furthermore, the process aimed to define strategic areas where Africa CDC can provide technical and programmatic support to Member States, ensuring that national food safety strategies are harmonized with regional and continental frameworks to guarantee long-term coherence and sustainability.

Methods

The process launched in April 2025 with the inaugural virtual meeting of the Africa CDC Food Safety Expert Technical Working Group (TWG), comprising experts from AU Member States, research institutions, and independent food safety specialists. This group mapped continental partners and priority intervention areas for FBD surveillance and One Health coordination. Following the establishment of formal Terms of Reference, a drafting workshop was held in June 2025. This iterative process incorporated situational analyses and expert inputs across governance, surveillance, laboratory systems, and risk management. A final validation workshop in September 2025 brought together MS and AU agencies, technical and development partners to refine strategic objectives and integrate case studies from national foodborne outbreak experiences.

Results

The process culminated in the successful development and validation of the Africa CDC Food Safety Strategic Framework (2026–2030). The validated framework serves as a formal instrument for Africa CDC to provide structured support to Member States. It establishes a consensus-based approach to strengthening foodborne disease surveillance and provides a clear mechanism for harmonizing national food safety implementations with continental health security goals.

Conclusions

The development of the Africa CDC Food Safety Strategic Framework (2026-2030) reflects a collaborative, evidence-informed process that prioritizes inclusive stakeholder engagement. By providing a unified continental roadmap, the Framework establishes the necessary governance to strengthen food safety systems, facilitate multi-sectoral coordination, and ultimately reduce the burden of foodborne diseases across the African continent.

Keywords: Food Safety, Strategic Framework, Foodborne Diseases.

Summary of Abstract

The Africa CDC Food Safety Strategic Framework (2026–2030) provides a technically rigorous, continentally owned roadmap for AU Member States. It transforms fragmented food safety systems into a unified, evidence-based ecosystem, ensuring that investments in surveillance and laboratory capacity are aligned to reduce the continental burden of foodborne diseases.

Promoting Health and Resilience of agricultural social-ecological systems in LMI countries: three strategies and proofs of concepts

Michel DE GARINE-WICHATITSKY (1), Muriel FIGUIE (2), Aurélie BINOT (4), Julien CAPPELLE (1), Antoine BARREAUX (5), Alexandre CARON (3)

1: ASTRE, CIRAD, INRAE, Montferrier-sur-Lez, France; 2: MOISA, CIRAD, Montpellier, France; 3: ASTRE, CIRAD, ILRI, Nairobi, Kenya; 4: MHS-Sud, Montpellier, France; 5: INTERTRYP, CIRAD, ICIPE, Nairobi, Kenya

The global context of polycrisis is particularly impacting negatively on tropical agricultural social-ecological systems: climate change, pollutions, accelerated erosion of biodiversity, and multiplication of health crises (emergence of zoonoses, antimicrobial resistance, invasive species,...). These crises are interconnected, but interventions to counter them often remain sectoral. Agricultural activities have a major direct impact on food systems and living conditions of farmers and consumers of agricultural products, particularly in developing tropical or subtropical countries, due to high socio-economic dependency on agriculture, often deficient public health infrastructures, and high vulnerabilities to climate change; pollutions and biodiversity erosion.

Two complementary approaches have been developed and implemented over the past decades in order: i) to improve the sustainability of agri-food systems and agroecosystems (i.e. Agroecology); and ii) to

enhance the health and resilience of social-ecological systems (i.e. One Health-SES Health). Although diverse agendas and definitions have been proposed, agroecology can be unified through the principles of systems thinking, resilience, biodiversity, and production1. The approach has been further operationalized through structured domains/areas of work with farmers and various institutions2, including for example “soil health”, “pests and diseases”, and “relationships between diversity and resilience”. These topics are also particularly relevant to the One Health approach, as defined by OHHLEP in 20214 and the associated Joint Plan of Action5. The scope of One Health has been gradually broadened, from an initial focus on public health and zoonotic diseases affecting humans, domestic and wild animals, to include plants and ecosystem health. The holistic expansion of health beyond infectious diseases (of humans, animals, plants), and beyond the strict bio-physical component of ecosystems, further led to the concept of social-ecological systems health, which is also closely associated with systems thinking, transdisciplinary approaches, resilience and biodiversity5.

We analysed the interlinkages between the operational approaches, One Health and Agroecology, and the framework social-ecological systems and associated SES concepts. We propose three operational questions that promote transformative actions of agro-ecosystems, with selected illustrative examples drawing from ongoing recent projects, network initiatives or partnership arrangements:

i) “promoting the health of animals, plants and agro-ecosystems to prevent and better manage the emergence of zoonotic pathogens”; examples of the approach include the projects ARCHE6 and AfriCam7 associated with the PREZODE initiative

ii) “promoting health of agroecosystems through agroecological practices” ; examples of the approach include the project Santés-Territoires8 and the recently launched regional partnership on “Transforming Agriculture for Animal, Crop and Ecosystem Health in the East African Rift” 9

iii) “promoting the health and resilience of agroecosystems by enhancing bio-cultural diversity”, as illustrated by the project One Limpopo One Health in Mozambique10

Each topic explores different facets of the Agriculture-Biodiversity-Health nexus, articulating One Health, Agroecology and Resilience at various scales and in different LMI countries.

Table: Bibliographic references and web sites of projects cited.

Ref. Number	Bibliographical reference/Project web site
1.	Brym, Z.T. and Reeve, J.R. 2016. Agroecological principles from a bibliographic analysis of the term agroecology. In *Sustainable Agriculture Reviews*: Volume 19. pp. 203-231. Springer International Publishing
2.	Transformative Partnership Platform on Agroecological Transitions https://www.agroecologytpp.org/
3.	Adisasmito, W.K. et al. 2022. "One Health: A new definition for a sustainable and healthy future". *PLoS Pathogens*, 18(6): e1010537.
4.	FAO, UNEP, WHO, and WOAH. 2022. "One Health Joint Plan of Action (2022-2026). Working together for the health of humans, animals, plants and the environment". Rome. doi.org/10.4060/cc2289en
5	De Garine-Wichatitsky, M. et al. 2021. "Health in" and "Health of" social-ecological systems: A practical framework for the management of healthy and resilient agricultural and natural ecosystems. *Frontiers in Public Health*, 8, 616328.
6.	PREZODE Initiative PEPR https://prezode-initiative.org/en/pepr/
7.	AfriCam project. https://www.cirad.fr/dans-le-monde/cirad-dans-le-monde/projets/projet-africam
8.	Santés-Territoire project. https://www.santes-territoires.org/
9.	dP TRACE https://agriculture.uonbi.ac.ke/index.php/latest-news/launching-dp-trace-regional-partnership-transforming-agriculture-east-african-rift
10.	One Limpopo One Health https://www.peaceparkstv.com/one-limpopo-one-health/

Impact of an Integrated Livestock Management Intervention to Prevent the dry-Season Peak of Child Acute Malnutrition in Pastoral and Agro-Pastoral Communities in Chad: Evidence from a Cluster Randomized Controlled Trial

Gwenaelle LUC (1), Modibo KEITA (1), Prospere DJEKORNONDE (1), Fatima ABDELRAZAKH (2), Armelle SACHER (1), Bibata WASSONGUEMA (1), Baguinebie BAZONGO (1), Moursal AKOINA (3), Mahamat GARBA ISSA (4), Moussa ABDERAMANE (5), Cyprien BIAOU (1), Tiphaine SEYVET (1), Abdelkader ABAKAR (1), Vincent MOUTEDE (7), Camille HEYLEN (6), Matthew BENTLEY (8), Christine JOST (8), Helen YOUNG (6), Mahamat BECHIR (4), Mahamat FAYIZ ABAKAR (2), Anastasia MARSHAK (6), Clair NULL (1), Abdal Monium OSMAN (1)

1: Food and Agriculture Organization of the United Nations (FAO); 2: Institut de Recherche en Élevage pour le Développement (IRED), Ministry of Livestock, Chad; 3: Ministry of Hydraulic and Environment, Chad; 4: Direction de l'alimentation et de la nutrition appliquée, Ministry of Public Health, Chad; 5: ASRADD, Chad; 6: Feinstein International Center, Tufts University, United State; 7: University of N'Djamena, Chad; 8: United States Agency for International Development (USAID)

Background: Child acute malnutrition remains persistently above emergency thresholds in Chad's Sahelian drylands, with a predictable dry season peak linked to declining pasture and livestock productivity, reduced milk availability and heightened exposure to zoonotic infections. Humanitarian responses remain largely reactive and treatment-focused, with limited evidence on preventive strategies

that address drivers embedded in local livelihood systems. We evaluated the effectiveness and return on investment (ROI) of an integrated livestock management intervention designed to prevent the dry-season peak of child acute malnutrition in pastoral and agro-pastoral communities in Chad.

Methods: We conducted a cluster-randomised controlled trial in Kanem and Barh-El-Gazel provinces, Chad. Seventy-six villages were randomised (1:1) to intervention or control. Eligible households had at least one child aged 6–59 months and access to milking livestock during the dry season. The intervention (December 2024–June 2025) combined livestock feed supplementation to sustain milk production near households during the dry season, household-level zoonotic risk mitigation, and nutrition counselling. Primary outcomes were the prevalence of global acute malnutrition (GAM) and severe acute malnutrition (SAM) at the dry-season peak (May 2025), assessed in a prespecified random subsample of 52 clusters. All 76 clusters were assessed post-peak (July 2025). Analyses followed an intention-to-treat approach using mixed-effects models. A societal ROI analysis was conducted over six months with projections to 24 months.

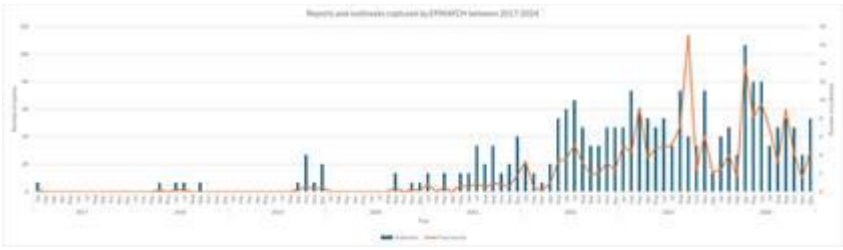
Results: At the dry-season peak, 821 children from 521 households were assessed across 52 villages. GAM prevalence was 22·2% in intervention villages versus 47·4% in controls (adjusted OR 0·29 [95% CI 0·18–0·49]; p0·001), and SAM prevalence was 4·4% versus 19·4% (adjusted OR 0·17 [0·08–0·37]; p0·001). Intervention households had higher daily milk availability (+588 mL per household; p0·001), and children consumed more milk (+102 mL per day; p=0·008). Odds of diarrhoeal disease and acute respiratory infection were substantially lower among children in intervention villages (aOR 0·21 [0·10–0·44] and 0·22 [0·11–0·46], respectively). Post-peak, women's dietary diversity increased (aOR 3·68 [1·90–7·13]), alongside reduced workload, lower household food insecurity and distress livestock sales, improved livestock condition, and a benefit–cost ratio of 5·40 at six months, rising to 16·40 at 24 months.

Conclusion: Protecting livestock productivity and sustaining children's access to milk while reducing zoonotic exposure during the pastoral lean season effectively prevents seasonal peaks of child acute malnutrition. This integrated anticipatory action and One Health livelihood-based approach offers a scalable, dignifying, high-return lifesaving preventive model for pastoral and agro-pastoral humanitarian settings.

The global epidemiology of botulism outbreaks from open-source intelligence, 2017–2024

Damian Alexander HONEYMAN (1), David James HESLOP (2), Chandini Raina MACINTYRE (1)

1: The Kirby Institute, UNSW, Sydney, Australia; 2: School of Population Health, UNSW, Sydney, Australia



Mapping Foodborne Streptococcus suis Risk across the Pork Value Chain in Nan Province, Thailand, 2025-2027: A One Health Approach to Food Systems and Cultural Practices with Joint Risk Assessment Tools

Pitiphon PROMDUANGSI (1), Sudarat DAMRONGWATANAPOKIN (1,2), Somchai PEERAPAKORN (3), Kirana NORADECHANON (4), Teerasak CHUXNAM (1), Serge MORAND (5,6), Soawapak HINJOY (1)

1: Department of Disease Control, Ministry of Public Health, Thailand; 2: Regional Public Health Laboratory Network, Thailand; 3: Department of Disease Control Foundation, Thailand; 4: Wildlife Conservation Office, Department of National Parks, Wildlife and Plant Conservation, Thailand; 5: The International Research Laboratory on Health, Disease Ecology, Environment, and Policy, Kasetsart University, Thailand; 6: Faculty of Tropical Medicine, Mahidol University, Thailand

Background:*Streptococcus suis* (*S. suis*) causes meningitis, septicemia, and hearing loss through infected pigs or contaminated pork. It was prioritized as an important zoonotic threat in Nan Province based on likelihood, severity, and cross-sector relevance during a subnational prioritization workshop. The traditional cuisine of raw spicy minced pork creates foodborne risks embedded within local food systems. This study aimed to conduct the Joint Risk Assessment (JRA) to characterize transmission pathways, identify critical food safety intervention and develop cross-sectoral action plans under the ASAMCO framework.This study represented the first JRA of *S. suis* conducted at the provincial level in Thailand, engaging stakeholders from policy leaders to frontline community representatives under a One Health framework.

Methods:A JRA was conducted with multisectoral stakeholders from public health, livestock, environment, and local governance. Five sequential steps were applied: 1) risk questions by defining population and scope with two-year timeframe; 2) risk pathway analysis mapping the node of pork food chain from production through slaughter, distribution, and consumption; 3) risk characterization scoring likelihood, consequence, and uncertainty at each node; 4) prioritization of high-risk nodes; and 5) action translation into sectoral and cross-sectoral interventions among high-risk nodes.

Results: The risk question was the probability and the effect of *S. suis* infection from pigs and pork production. Risk pathway analysis mapped 13 nodes across the pork food system. The highest transmission risks were concentrated in unregulated slaughter practices, particularly during festivals, and

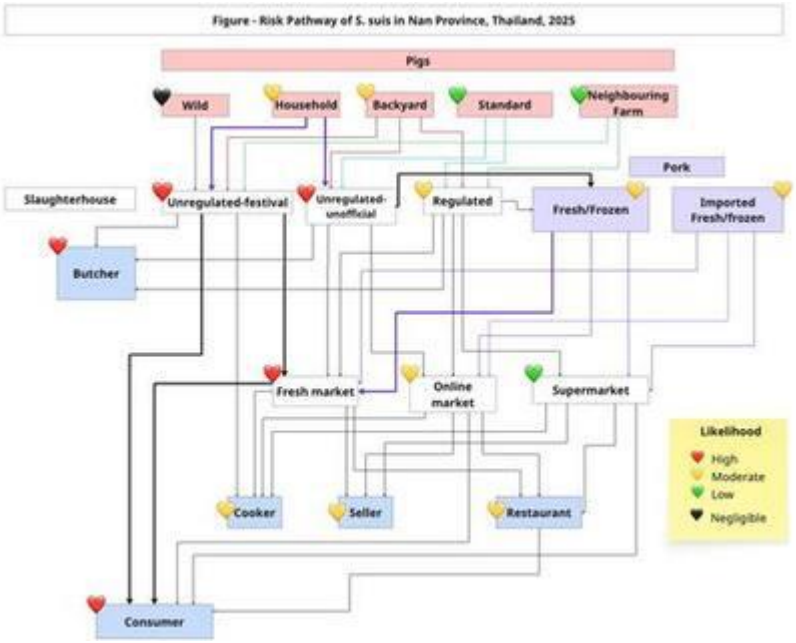
in fresh markets where hygiene gaps and cross-contamination risks were prominent. While standard farms presented "Low" likelihood, unregulated facilities were rated "High Risk" due to poor hygiene, crude techniques, and lack of inspection. Fresh markets played a central role in daily food access and therefore represented critical intervention points linking food safety with community behaviors. The highest foodborne transmission risk occurred through raw and undercooked pork consumption. Health consequences were rated "Moderate" severity due to the symptoms. The joint action plan highlighted four clear pillars for intervention; 1) Governance- “1 District–1 Slaughterhouse” standardizing the slaughter process; 2) Environmental/Market- “Disease-free cutting board and “Safe Market” certification; 3) Social/Behavioral- Leveraging “Schools, Temples, and community health Volunteers” to change raw meat consumption habits; and 4) Monitoring- *S. suis*-free district certification with annual Intra-Action Reviews (IAR).

Conclusions

This study demonstrated that *S. suis* risk in Nan Province is deeply embedded in unregulated pork production and cultural practices. The provincial JRA under a One Health approach provided a shared evidence base to identify risks and co-develop coordinated action plans across sectors and community stakeholders. This model highlighted the importance of integrating food safety promotion, health literacy, and multisector collaboration to reduce foodborne zoonotic risks and offered a scalable framework for One Health risk governance at subnational levels.

Table - Consequences Assessment Level

Category	Impact	Severity Level	Description / Rationale
Human	Morbidity (Deafness/Meningitis)	Moderate	-Not epidemic -No human-to-human transmission
Non-human	Economic and tourist	Minor	-Restaurants can't sell the raw-pork menu



One Health Implementation & Financing

SPI05 · 16:00-17:30 · Auditorium II

Working across boundaries: development of the Nuts a maht ('we are one') | One Health framework for the Province of British Columbia, Canada.

Erin FRASER (1,2), Danielle MITCHELL (3), Shannon WATERS (4), Janene ERICKSON (1), Jennifer VINES (1), Joyce AUSTIN (5), Theresa BURNS (5)

1: British Columbia Centre for Disease Control, Vancouver, BC, Canada; 2: School of Population and Public Health, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada; 3: D.A. Mitchell Consulting, BC, Canada; 4: Office of the Provincial Health Officer, British Columbia Ministry of Health, Victoria, BC, Canada; 5: British Columbia Ministry of Agriculture and Food, Abbotsford, BC, Canada

Background

Escalating climate, ecological, and socio-economic pressures across British Columbia (B.C.) are intensifying interconnected challenges across environmental, animal, and human health. Shifts in climate, habitat and biodiversity, water and air quality, the emergence of zoonotic diseases and antimicrobial resistance reflect complex drivers spanning socio-economic, cultural, political and biological realms. Addressing this complexity requires highly collaborative, cross-sectoral approaches that support sustainable, holistic, and effective action.

First Nations worldviews understand relationships among land and soil, air, water, plants, animals, and humans as sacred and foundational to well-being. The Coast Salish law Nuts a maht ("we are one") reflects this intergenerational knowledge and affirms the inseparability of all living systems. B.C. holds legal and ethical obligations to uphold Indigenous rights and laws as articulated in the Canadian Constitution (S.35), Treaties, and federal and provincial legislations related to the Declaration of the Rights of Indigenous Peoples. The Nuts a maht | One Health Framework emerged within this context - amid urgent ecological, public, and animal health pressures, and a critical need to centre Indigenous laws and knowledge systems in addressing One Health challenges in B.C.

Methods

The Framework was developed through a multi-year collaborative process involving provincial agencies working across environmental, animal, and human health sectors. Key methods included a jurisdictional scan of sub-national One Health structures and strategies, in-person gatherings, and iterative co-development processes intentionally designed to braid Indigenous and western knowledge systems. The Framework articulates guiding principles, a shared vision, high-level goals and anticipated outcomes, three interconnected collaboration streams, and eight thematic areas of focus that reflect B.C.'s unique One Health landscape.

Results

The Framework outlines guiding principles such as relationality, multi-generational thinking, centering localized knowledge, upholding inherent Indigenous rights and laws, working across boundaries, "guide not prescribe," and strengths-based shared leadership. Three high-level goals include:

The Framework identifies thematic focus areas such as shared environments, antimicrobial resistance and stewardship, emerging and re-emerging pathogens, interconnections between humans and animals, and food safety and security. Collaboration is organized into three interconnected streams: preventative and restorative; response and recovery; and long-term sustainability and stewardship.

Conclusion

The Nuts a maht | One Health Multi-Jurisdictional Framework offers a transformative pathway for re-imagining how health is understood and acted upon in B.C. It serves as both a guide and an invitation to build relationships, advance inclusive and coordinated action, and uphold Indigenous rights, knowledge, and evidence-informed practice. By centering relationality, shared responsibility, and long-term stewardship, the Framework provides a model for addressing complex health challenges that reflect the true interdependence of all living beings.

Water security, food security and health in pastoral systems in northern Kenya; Fuzzy Cognitive Mapping to understand opportunities and barriers for One Health programs

Sirimon THOMAS (1,2), Rowan JACKSON (1), Eric FEVRE (2), Lisa BODEN (1)

1: University of Edinburgh, United Kingdom; 2: International Livestock Research Institute (ILRI), Kenya

Background:

Pastoralism dominates the arid and semi-arid lands, which cover roughly 80% of Kenya's area. One Health aligns well with Pastoralism due to the interdependence of people, animals and the environment in these complex adaptive systems. The complexity of these systems is a barrier to interdisciplinary collaboration and sustainable development. Capturing the complexity of pastoral systems, including the diversity of drivers and outcomes, and their relationships, is therefore crucial to implementing an inter-disciplinary One Health and social-ecological systems approach to sustainable development in pastoral contexts. We use Fuzzy Cognitive Mapping to create weighted directed network representations of the pastoral system in Kenya to understand system behaviour, identify leverage points for intervention prioritisation, and explore stakeholder and gender differences in system conceptualisation.

Methods:

We conducted 35 Fuzzy Cognitive Mapping (FCM) key informant interviews in Gabra areas of Marsabit county, Kenya. These covered 23 primary stakeholders and 12 secondary stakeholders and 13 interviewees were women and 22 were men. No concepts were pre-defined, although a focus on food security, water and health was described during consenting. Interviewees could raise any concepts that related to food, water and health. Concepts (or nodes), connections (or edges), weights and direction of influence were recorded by the interviewer, with weights recorded between 1 (weak association) and 3 (strong association).

The resulting networks were aggregated by averaging weights of equivalent edges. This was also done separately for primary stakeholders (pastoralists), secondary stakeholders (NGO & government), men and women's networks, to create stakeholder and gender disaggregated graphs.

Results:

The aggregated system network contains 455 concepts (nodes) and 1726 edges. 'Financial security' and 'water availability' consistently rank as the strongest nodes across stakeholder and gender networks.

Primary stakeholders generally place more importance on nodes relating to basic resources (water availability, food security, grazing, health), while secondary stakeholders include more external factors among the most important nodes (government, NGO support, mobility).

Women see concepts associated with household management, such as income, schooling, malnutrition etc. as more important, while men hold livestock related concepts (grazing, rainfall, insecurity & conflict) as more important in the network.

Conclusions:

The complexity of the presented network highlights the need for systems thinking approaches to sustainable development in pastoral areas, which One Health can powerfully contribute to.

Analysis of node strength and centrality highlight the most important concepts in the overall network, which should be prioritised for interventions, including financial security and water availability.

Disaggregated networks by stakeholder and gender reveal significant differences in prioritisation of concepts. This suggests that NGO and government programming is often poorly targeted to the communities' own priorities, highlighting a need for better community-led intervention design. Gender differences in network structure emphasise the importance of gender-sensitive programming in sustainable development.

Top 5% of nodes by strength

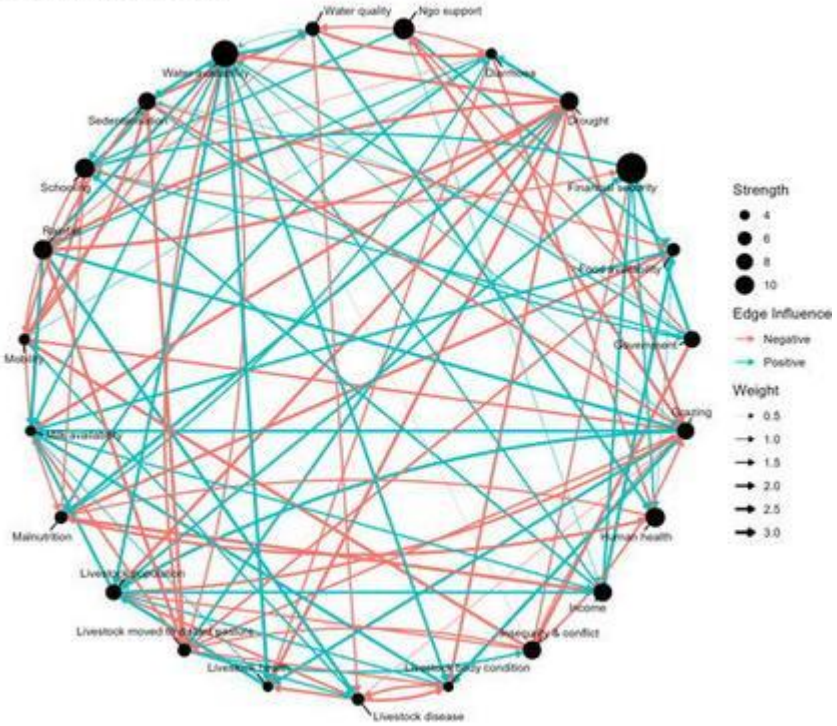


Table 1: Node metrics for aggregated and disaggregated networks.

Metric	Aggregated	Primary	Secondary	Women	Men
Mean Degree	7.59	6.78	6.23	5.62	6.86
Mean Strength	16.98	15.14	14.18	12.39	15.69
Density	0.01	0.01	0.01	0.01	0.01
Transitivity	0.13	0.15	0.12	0.11	0.14
Mean Path Length	8.56	8.60	10.08	10.05	9.28
Diameter	27.00	22.86	27.00	25.17	28.88
Mean Closeness	0.17	0.17	0.16	0.16	0.16
Mean Betweenness	0.01	0.01	0.01	0.01	0.01
Mean Eigenvector Centrality	0.08	0.08	0.12	0.09	0.09

Table 2: Top 10 nodes by strength for aggregated and disaggregated networks.

Rank	Aggregated	Primary	Secondary	Women	Men
1	financial security	water availability	financial security	financial security	water availability
2	water availability	financial security	water availability	water availability	financial security
3	NGO support	rainfall	human health	NGO support	rainfall
4	human health	livestock population	schooling	income	government
5	schooling	food availability	insecurity & conflict	human health	sedentarisation
6	income	human health	NGO support	rainfall	human health
7	drought	drought	government	schooling	insecurity & conflict
8	rainfall	NGO support	grazing	drought	grazing
9	insecurity & conflict	grazing	mobility	water quality	NGO support
10	sedentarisation	water quality	livestock health	malnutrition	schooling

Upstream by Design: Continuous Network Stewardship as a Model for Resilient One Health Implementation in Low- and Middle-Income Countries

Mary GUTTIERI, Karen SAYLORS
Labyrinth Global Health, Inc., United States of America

Background: The One Health implementation gap persists not because frameworks are lacking, but because partnerships form too late and few organizations can bridge the distance between global innovation and local adoption. Closing this gap requires intermediaries who actively steward networks spanning health ministries, national laboratories, academic institutions, and private sector innovators who possess multilingual technical capacity, and who can identify, match, fund, and sustain implementation across diverse geopolitical contexts. Labyrinth Global Health, Inc. has built its model around this continuous network stewardship function, initiating collaboration at the ideation stage and maintaining the relational infrastructure to adapt when circumstances change.

Methods: The model operates across three phases. **Pre-funding**: Labyrinth continuously monitors partner needs and emerging opportunities – engaging academic institutions, research bodies, health ministries, and private sector innovators to co-develop proposals, providing matchmaking intelligence, relational access, and field design expertise that transforms concepts into fundable initiatives. **Implementation**: consortium-based delivery using Organizational Capacity Assessments, the Mentored Experiential Learning and Training (MELT) methodology, and on-the-ground execution supported by ministry and national laboratory relationships across multiple languages. **Sustainability**: institutional planning, governance strengthening, and earned income development anchor capacity beyond project cycles. Representative partnerships illustrating this approach span university collaborators (University of California, Davis over two decades), international research institutions (Institut Pasteur du Cambodge), regional One Health networks across 15+ countries in Africa and Southeast Asia, and private sector innovators (Detect-ION).

Results: The model's full arc is illustrated by Labyrinth's collaboration with Detect-ION: matching the company's breath-diagnostic technology to malaria detection, connecting it with the Institut National de Recherche Biomédicale in the Democratic Republic of Congo based on national laboratory capacity and disease endemicity, and co-developing the proposal that secured Gates Foundation funding. When geopolitical tensions imposed restrictions, Labyrinth activated its relationship with the Laboratoire National de Santé Publique in Republic of Congo, adjusted ethics protocols, and sustained the study, demonstrating that network relationships provide implementation resilience. A Gates Foundation collaboration with Institut Pasteur du Cambodge evaluated environmental sampling for zoonotic pathogen detection in Cambodia. Labyrinth is also a named partner in the NSF Center for Pandemic Insights, a UC Davis-led initiative advancing pre-emergence pandemic science. Across the USAID One Health Workforce-Next Generation consortium in 15 countries, the model produced 30+ modules in university curricula, 12 national sustainability plans, and 1,000+ certified professionals.

Conclusions: These outcomes, including a study sustained through geopolitical disruption via rapid network activation, demonstrate that continuous network stewardship is itself a determinant of One Health implementation quality and resilience. By maintaining trusted, multilingual relationships across sectors and geographies before they are needed, Labyrinth consistently produces more co-designed, fundable, and locally-owned initiatives. This model offers a replicable framework for closing the distance between global One Health innovation and durable local impact.

One Health in AMR: Findings from evaluation of UK Fleming Fund programme

Syed ABBAS (1), Rebecca MAUDLING (2), Tim SHORTEN (2)
1: Institute of Development Studies, United Kingdom; 2: Independent consultant

Background The One Health (OH) approach has long been promoted as a means to address complex infectious disease threats, including antimicrobial resistance (AMR), zoonoses and emerging infections. When the Fleming Fund programme was launched, OH was adopted as a core principle intended to strengthen multisector governance, integrated surveillance and evidence-based policy. However, despite strong global endorsement, countries lacked practical guidance on how to operationalise OH within

diverse political, administrative and technical contexts. Over the past ten years, evolving global OH governance, alongside the implementation of Fleming Fund activities across 23 countries, has provided a unique opportunity to examine how OH partnerships emerge, function and vary across settings.

Methods This evaluation synthesises findings from three rounds of multi-country visits (2019–2022), complemented by a literature review of multisector collaborations, key informant interviews and analysis of national OH structures and practices. The evaluation approach evolved over time: Country Visit 1 focused on identifying formal OH institutional mechanisms; Visit 2 assessed trajectories and ambitions using a graded OH model; and Visit 3 explored the wider landscape of formal and informal spaces in which OH partnerships operate. We developed a framework to categorise different forms of One Health partnerships in Fleming Fund supported countries.

Results Countries began the Fleming Fund at widely differing starting points, with variation in existing cross-sector relationships and institutional capacity. Initial expectations for standardised, formalised OH structures proved unrealistic. Instead, countries exhibited diverse, context-dependent models of collaboration, ranging from highly centralised (e.g., Senegal) to socially networked and having informal components (e.g., Bhutan, Timor-Leste). Across countries, integration of surveillance data and joint epidemiological analysis - a major assumption of early OH guidance - remained difficult to achieve. Although formal committees such as AMR coordination mechanisms existed, substantial cross-sector interactions occurred informally through professional networks, personal relationships, academic collaborations and subnational exchanges that were not captured by conventional OH templates. Over time, the evaluation found little change in the structural categories of multisector partnerships but identified persistent challenges in achieving deeper collaboration or integration. Most countries remained at the stages of coordination or information-sharing rather than joint analysis or co-implementation.

Conclusions The evaluation demonstrates that OH partnerships are inherently shaped by local administrative cultures, political incentives and informal relationships. A rigid, institutional model of OH implementation is insufficient for supporting AMR-related collaboration across diverse contexts. Future AMR programmes should adopt pragmatic, flexible approaches that recognise multiple feasible forms of OH partnerships. Expanding OH beyond a narrow focus on integrated epidemiological analysis and harnessing informal networks and locally embedded actors, offers a more realistic pathway to sustainable multisector collaboration. Tailoring OH models to each country's institutional landscape will enhance the long-term viability and impact of AMR responses.

Figure 1 Approach to evaluating One Health across different country visits

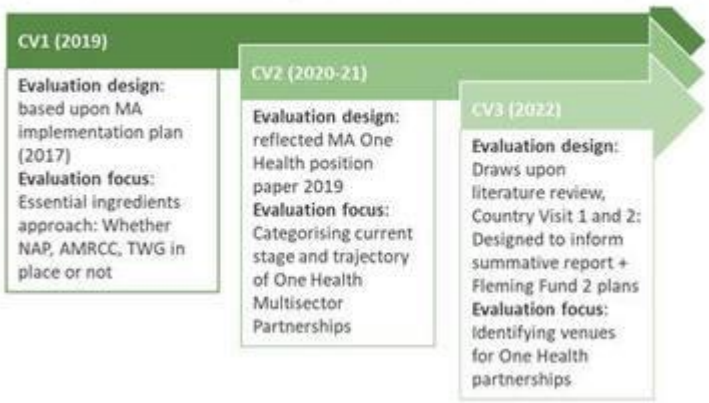


Figure 2 Distribution of Fleming fund supported countries, by functional status of One Health partnerships (2020-23)

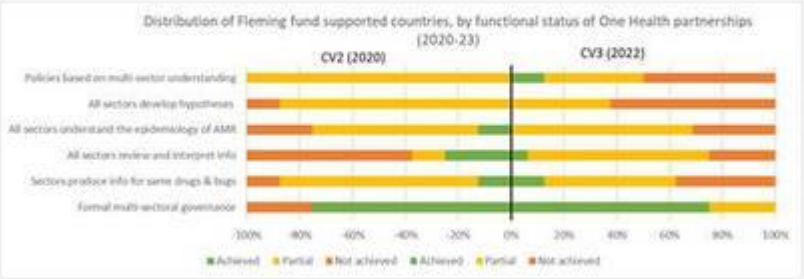
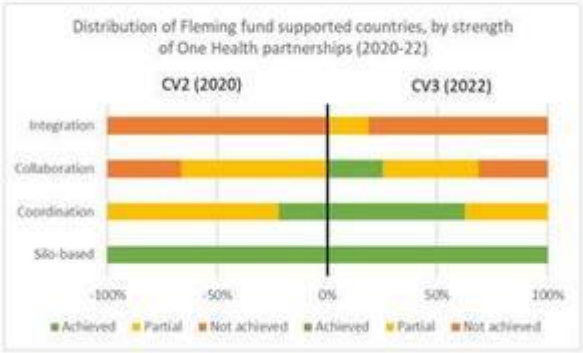


Figure 3 Distribution of Fleming fund supported countries, by strength of One Health partnerships (2020-22)



Mapping the funders of One Health research

Alvaro VALVERDE (1), Eleanor RAJ (2), Mariam KADZAMIRA (3), **Hideo ISHII-ADAJAR** (3), Martin SZOMSZOR (4), Dannie ROMNEY (5)

1: CAB International, Austria; 2: Independent researcher; 3: CAB International, Ascot, United Kingdom; 4: Electric Data Solutions LTD; 5: CAB International, Africa Centre, Kenya

Background: The concept of One Health (OH) has gained increasing prominence over the past two decades as an integrated framework for understanding and addressing the interconnections between human, animal and ecosystem health with a wide array of One Health related research outputs, scientific networks and thematic trends. However, there is a knowledge gap in terms of who funds the research, and how funding influences research agendas, scientific priorities, capacity efforts and thematic focuses. This study aimed to analyse source of funding for One Health-labelled research, to determine if funding is aligned with global strategic priorities identified in the Quadripartite One Health Joint Plan of Action (OH-JPA) or whether certain areas are systematically under-supported. To the authors knowledge, this study provides the first comprehensive mapping of the funders that support One Health-labelled research globally.

Methods: Using bibliometrics, we analyse more than 6,000 One Health-labelled peer-reviewed publications (2014–2024) and their associated funding acknowledgements. This is achieved by harmonising approximately 600+ distinct funder names, classifying funders into institutional categories, and mapping each funded publication to the six Action Tracks of the Quadripartite OH-JPA.

Results: We find that between 2014 to 2024 national research councils, public science funders and government agencies form the backbone of One Health-labelled research publications, supporting large, diverse portfolios across mainly Actions Tracks 2 5 with meaningful, though smaller, contributions to Action Tracks 1 and 6. An analysis of the patterns in the funding of One Health-labelled published

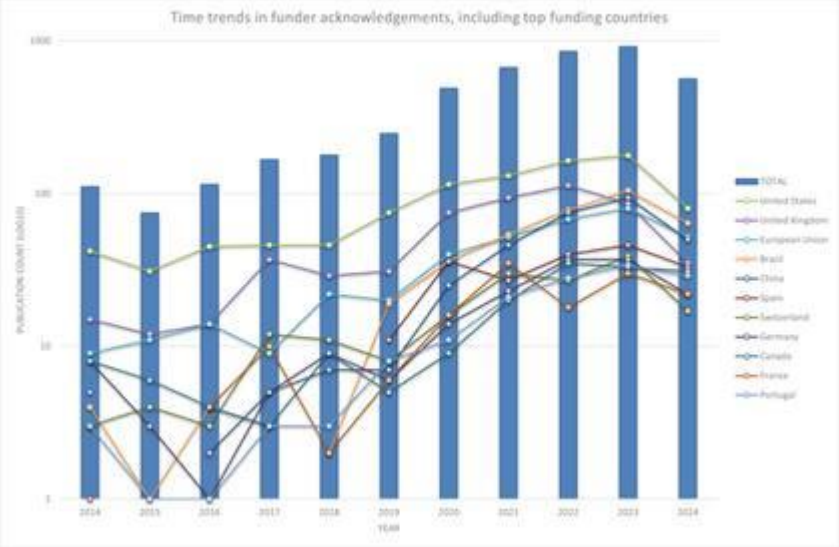
research demonstrates that the institutional and geographic landscape of One Health-labelled funding has been found to be highly uneven, with a strong concentration of the most influential funders in high income countries. Despite these funding patterns, the thematic distribution of funded One Health-labelled research is broader than expected and cuts across all Actions Tracks under the OH JPA, including research in areas that traditionally are more a priority for low-and-middle income contexts, specifically capacity strengthening and surveillance.

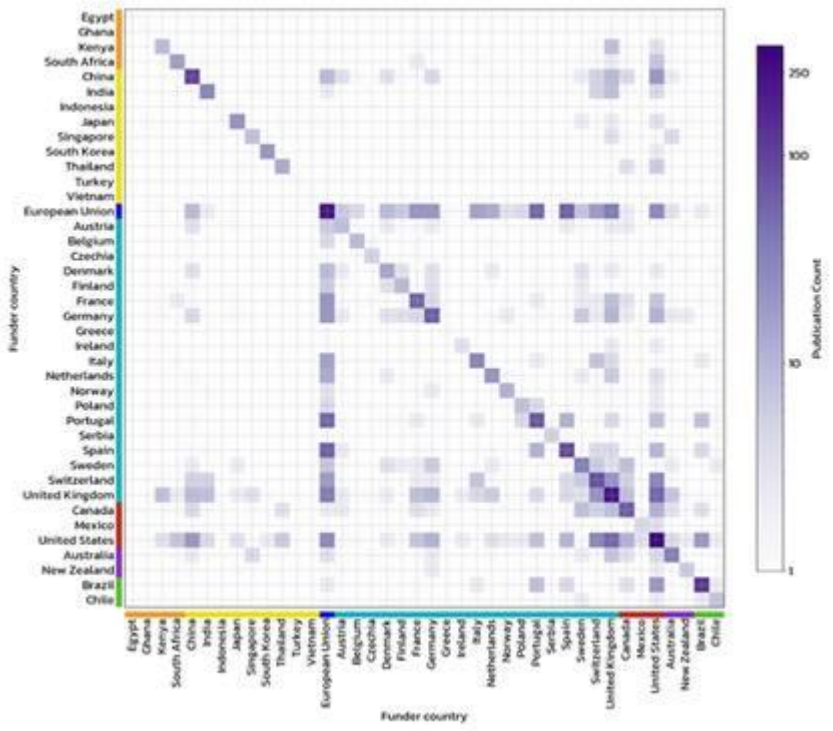
Conclusion: Our analysis reveals a more extensive, diverse and uneven One Health research funding landscape than commonly assumed, indicating that the One Health-labelled research domain is expanding, diversifying and maturing—but doing so within a global health architecture that is inequitable. To fully achieve the ambition of the OH JPA, there is a need to fully address the existing structural and power asymmetries of who funds One Health-labelled research and which themes receive sustained investment. A more equitable, coordinated and strategically balanced One Health funding landscape is therefore essential to operationalising One Health as a genuinely integrated and globally relevant approach to safeguarding health across human, animal, plant and environmental systems.

Distribution of funders by type and associated publications

Funder Type	No. funders	Publications acknowledging funder	% of all funders
Academic / university / hospital	90	313	14.24%
Government / ministry / public agency	213	2,690	**33.70%**
Multilateral / intergovernmental	19	1,607	3.01%
NGO / non-profit organisation	36	268	5.70%
National research council / public science funder	143	3,288	**22.63%**
Other / not classified[2]	2	18	0.32%
Philanthropic foundation / charity	86	1,285	13.61%
Private sector / industry	43	195	6.80%
Total	**632**		**100%**

Source: Author compilation from Dimensions data of 5,488 publication (2014-2024)





The Wealth Paradox: Survival Analysis of Behavioral Sustainability in Taenia solium Preventive Practices, Tanzania.

Antony NYERERE, Lupindu ATHUMANI, Helena NGOWI, Mkupasi ERNATUS, Fedy MLOWE, Christopher MAHONGER
sokoiniene university of agriculture, Tanzania

Background: Sustainability is often treated as a binary, cross-sectional outcome, obscuring discontinuation, relapse, and re-adoption dynamics. We reconceptualized sustainability as a time-dependent survival process and examined whether determinants of adoption differ from maintenance, highlighting equity implications.

Methods: We analyzed longitudinal data from a three-wave cluster-randomized trial (2019, 2021, 2025) of a health education intervention for *Taenia solium* prevention in 521 households in Kongwa and Songwe Districts, Tanzania. Outcomes were latrine use, pig confinement, and household water treatment. Time-to-adoption was modeled using Cox proportional hazards with shared village-level frailty. Discontinuation and re-adoption ("practice cycling") were modeled using phase-specific logistic regression. Covariates included household wealth, education, gender, by-law awareness, and cost constraints.

Results: Sustainability dynamics varied across behaviors and phases. Discontinuation was front-loaded: 58% of lapses occurred within two years, defining a critical "danger zone." Twenty-three percent of households exhibited practice cycling rather than permanent adoption. Adoption determinants (education, intervention exposure) did not prevent discontinuation. Socioeconomic gradients reversed across phases: higher-wealth households adopted pig confinement faster (aHR 2.08; 95% CI 1.38–3.14) but were 35% more likely to discontinue (aOR 1.35; 95% CI 1.03–1.77). Latrine use was stabilized by by-law enforcement (aOR 0.43; 95% CI 0.23–0.80). Water treatment coverage at endline (65%) overestimated sustained use (38%), a 27-point gap. Village-level frailty (θ = 0.24, p 0.01) indicated contextual clustering.

Conclusions: Hazard-based, phase-disaggregated modeling uncovers dynamics invisible to cross-sectional assessment: early discontinuation, practice cycling, and shifting equity gradients. The Wealth Paradox demonstrates that adoption equity does not guarantee maintenance equity. Implementation

science must focus on behavioral durability, phase-specific determinants, and contextually feasible interventions.

Biosecurity, biosafety, global health security

SCS07 · 17:40-18:30 · Auditorium I

Bat-Associated Pteropine Orthoreovirus Linked to Nipah-Like Illness Following Raw Date-Palm Sap Consumption in Bangladesh

Ariful ISLAM(1,2) James NG (3) Sharmin SULTANA (2) Ellen MURPHREE (4) Pronesh DUTTA (2) Md. Arif KHAN (2) Wenxin TIAN (3) Sunil Kumar DUBEY (3) Reed F JOHNSON (4) Jade K FORWOOD (1) W Ian LIPKIN (3,5) Lisa E HENSLEY (4) Tahmina SHIRIN (2) Nischay MISHRA (3,5)

1: Gulbali Institute, Charles Sturt University, Locked Bag 588, Wagga Wagga, NSW 2678, Australia; 2: Zoonotic Disease Research Program, Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka 1212, Bangladesh; 3: Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, USA; 4: Zoonotic and Emerging Disease Research Unit (ZEDRU), National Bio and Agro-Defense Facility (NBAF), United States Department of Agriculture (USDA), Manhattan, KS, USA; 5: Epidemiology, Mailman School of Public Health, Columbia University, New York, NY, United States.

Bridging Biosecurity and Public Health: Operationalising One Health Field Epidemiology through the HSPA Model for Biothreat Reduction

Geoffrey NAMARA, George MOMANYI, Dana AWWAD,**Stacie DUNKLE**, Catherine SMALLWOOD

World Health Organisation, Germany

Harnessing the Power of Conservation for Global Health Security

Chris WALZER, Lucy KEATTS, Diego MONTECINO, Emily DENSTEDT, Mathieu PRUVOT, Sarah OLSON

Wildlife Conservation Society, United States of America

Addressing Biothreats: Reinforcing the Legal and Regulatory Framework for the Implementation of the Biological Weapons Convention

Sylvain FANIELLE,**James PETTIT**, Remi BACOUILLARD

United Nations Office for Disarmament Affairs, Switzerland

The critical role of the private sector and civil society in One Health implementation

SPI07 · 17:40-18:30 · Auditorium II

Role of the Public-private partnership in the implementation of One Health vaccination strategies: Evaluation of behavioural and policy changes following the application of the EVACS modelling tool

Geraldine VELEZ LOZA (1), Emmanuel RAISON (2), Claudio PROIETTI (2), Marisa PEYRE (1), Gwenaelle DAUPHIN (3), **Claire HAUTEFEUILLE** (1)

1: CIRAD, UMR ASTRE, Montpellier, France; 2: CIRAD, ImpresS Team, DIMS, Montpellier, France; 3: CEVA animal health, Libourne, France

Highly pathogenic avian influenza (HPAI) represents a threat for both animal and human health. Vaccination of poultry is a complementary strategy to control virus circulation, protect animal health and reduce the risk of zoonotic transmission to humans. EVACS (Evaluation of Vaccination Strategies) is a modelling tool designed to simulate and compare vaccination strategies within animal production networks and to identify those likely to be most efficient under specific epidemiological and production contexts. Between 2013 and 2023, EVACS was applied to evaluate vaccination strategies against HPAI in poultry production networks in eight different countries. These applications were conducted through a public-private partnership (PPP) between Cirad, the research institute that developed the EVACS tool, and Ceva animal health, a global company involved in the development and production of avian influenza vaccines. The objective of our study was to identify the enablers and barriers to behavioural, institutional and policy changes following application of EVACS.

A generic theory of changes was developed based on the grey literature from the eight countries were EVACS has been applied, combined with insights from middle-range theories of change on ways to influence political change. Two inductive evaluation approaches, outcome harvesting and outcome evidencing, were used to identify and analyse the changes associated with this theory of change. The evaluation concentrated on two selected case studies: Vietnam and France. Data were collected through semi-structured interviews from key informants (8 in France and 19 in Vietnam) and findings were validated during stakeholder socialisation workshops.

The generic theory of changes identified three key types of changes required for the adoption of new vaccination strategies (Figure 1). In France, a multi-stakeholder working group involving representatives from the poultry sector and the animal health sector was established in 2022 to explore new strategies to control HPAI, including vaccination. Ceva, as member of this group, shared the EVACS modelling results, which were presented to the Ministry of Agriculture and contributed along with other scientific studies, to the adoption of the national vaccination strategy implemented in France since 2023. In Vietnam, EVACS results supported the registration of Ceva recombinant vaccine with application at hatchery level. While the strategy recommended by EVACS is not used in smallholder farms, it is currently applied by large poultry producers of poultry with long production lifespans (breeders or layers).

This evaluation highlights the importance of early and sustained engagement of relevant stakeholders to facilitate understanding, ownership and the use of scientific outputs in decision making processes. More broadly, it suggests that successful PPP for One Health interventions require partners to explicitly consider long-term pathways to change and impact, clarify their respective roles and incentives, and maintain dialog beyond the initial production of the scientific results.

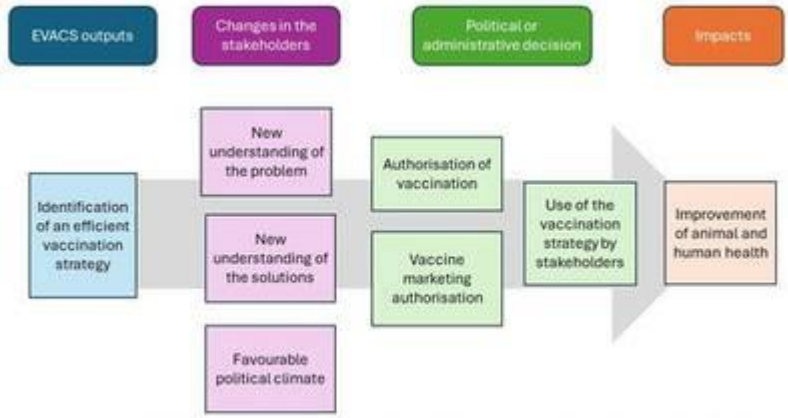


Figure 1: simplified theory of changes following the application of the EVACS tool

Operationalising One Health through Interoperable Data Systems for Preparedness, Surveillance, and Response to Health Emergencies

Gaspard PAIRAULT, Grégoire LURTON
Bluesquare, Belgium

Data integration and interoperable systems are critical for operationalising the One Health approach for preparedness, surveillance, and response to health emergencies. By connecting routine surveillance data across sectors, ministries can improve early warning systems, strengthen preparedness, and enable faster, evidence-based responses in their country.

Routine surveillance data are often integrated into health monitoring information systems for human health. However, data systems across multiple sectors remain fragmented. This delays the detection of emerging threats and limits coordinated responses during health emergencies. The interoperability of routine data systems, including HMIS as well as animal and environmental health systems, within a central One Health platform is an important approach for the preparedness, surveillance and response to health emergencies.

Beyond the challenges of data interoperability and fragmentation faced by each sector, effective coordination, data integration, and governance across One Health sectors also require engagement from all stakeholders, and partners. This talk will include short examples on initiatives for scaling interoperable One Health data systems.

Biodiversity, Wildlife & Pathogen Interfaces - session 1

SCS09 · 11:00-12:30 · Auditorium I

Metagenomic surveillance of rodents reveals the impact of deforestation and seasonality on pathogenic viral diversity and evolution

Charles C.Y. XU (1,2), Mathieu PRUVOT (2,1), Vireak HEANG (3), Vibol HUL (3), Sokha CHEA (4), Alex D. GREENWOOD (5), Sarah H. OLSON (1), Erik KARLSSON (3)

1: Wildlife Conservation Society, USA; 2: University of Calgary, Canada; 3: Institut Pasteur du Cambodge, Cambodia; 4: Wildlife Conservation Society, Cambodia; 5: Leibniz Institute for Zoo and Wildlife Research, Germany

Small mammal reservoirs are primary sources of emerging zoonotic pathogens and represent a major agricultural interface risk, yet the ecological and evolutionary impacts of land-use change on their viromes remain poorly characterized. In Southeast Asia, rapid deforestation is restructuring human-wildlife interfaces, potentially facilitating novel spillover pathways. This pilot study utilized metagenomic enrichment to characterize the viromes of three dominant rodent species (*Maxomys surifer*, *Rattus sp. R3*, and *Mus cervicolor*) across a deforestation chronotone in Cambodia during dry and rainy seasons.

Rectal swabs were collected across three zones: primary forest (undisturbed), disturbed (ongoing clearing), and cleared (recent agricultural conversion). Viral enrichment was performed using the Twist Comprehensive Viral Research Panel followed by Illumina MiSeq sequencing. Alpha and beta diversities were used to characterize differences in virome composition. Evolutionary dynamics were assessed through genome reconstruction, phylogenetic inference, and selective constraint analysis.

Preliminary results revealed virome composition did not change significantly across deforestation zones but differed by host species with higher diversity during the dry season. Genomes of high-priority pathogens were recovered, including Japanese encephalitis virus (JEV; genotype III) and porcine circovirus 2 (PCV2; genotype 2a). Discrete ancestral trait reconstruction identified cleared zones as the primary source of PCV2 dissemination into disturbed and forest zones, whereas forest zones served as the primary source of JEV transmission into disturbed and cleared zones. *Rattus* sp. R3 likely functions as a critical bridge host, driving bidirectional transmission of PCV2 with *M. cervicolor* (with downstream spillover to *M. surifer*) alongside bidirectional JEV transmission with *M. surifer* (with downstream spillover to *M. cervicolor*). Although purifying selection predominated genome-wide across both viruses ($\omega\pi$ 1), significant deviations in selective constraints were localized and gene-specific. Genome-wide $\omega\pi$ of both viruses was descriptively higher in cleared than forest zones for both viruses, but this shift was not statistically significant; however, non-synonymous diversity (πN) in the Rep and ORF3 genes of PCV2 was significantly greater in cleared zones.

These findings demonstrate diverse viral circulation across wild rodent hosts. Deforested environments may alter viral evolutionary trajectories even without significant shifts in virome composition. We hypothesize that seasonal fluctuations in host contact rates and resource availability drive viral expansion during the dry season, while repeated demographic and transmission bottlenecks in cleared zones reduces viral effective population size and locally relaxes purifying selection relative to genetic drift. This accumulation of non-synonymous variation after deforestation may increase standing genetic diversity and the potential for viral adaptation. These results highlight the utility of metagenomics for proactive surveillance and illustrate how land-use change drives viral ecology and evolution at human-wildlife interfaces.

Habitat disturbance drives turnover in mosquito and virus communities across major tropical ecosystems

Selina Laura GRAFF (1), Victor Sebastian SCHARNHORST (1), Georg Joachim EIBNER (1), James Robert OCHIENG (2), Anthony Mutebi NSUBUGA (3), Julius Julian LUTWAMA (4), Innocent Bidason RWEGO (5), Sandra JUNGLEN (1)

1: Institute of Virology, Charité – Universitätsmedizin Berlin, corporate member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, 10117 Berlin, Germany; 2: Department of Zoology, Entomology and Fisheries Sciences, College of Natural Sciences, Makerere University, Kampala, Uganda; 3: Department of Plant Sciences, Microbiology and Biotechnology, Makerere University, Kampala, Uganda; 4: Department of Arbovirology, Uganda Virus

Research Institute (UVRI), Entebbe, Uganda; 5: Department of Biosecurity, Ecosystems and Veterinary Public Health, Makerere University, Kampala, Uganda

Human-driven land-use change, such as deforestation, urbanisation, and agricultural expansion, has profound consequences for ecosystems and the emergence of infectious diseases. Pristine ecosystems harbor rich biodiversity and diverse pathogen reservoirs, but habitat disturbance reshapes host and vector communities, while the ecological mechanisms linking land-use change to pathogen dynamics remain poorly understood. Most studies focus on single vector or pathogen species within one ecosystem, limiting the identification of generalizable patterns. This study investigates how mosquito community composition responds to habitat disturbance and how these changes are reflected in virus assemblages across three major African ecosystems: lowland rainforest, montane rainforest, and savannah.

A total of 32,632 mosquitoes, representing 130 species from 13 genera, were collected in undisturbed and disturbed sites across three distinct ecosystems in Uganda and subsequently screened for virus infections using PCR-based detection assays.

Mosquito species richness was consistently higher in undisturbed habitats, but disturbance did not uniformly reduce diversity. Instead, differences in community composition were primarily driven by species turnover rather than nested species loss across ecosystems. Temperature emerged as a key driver of mosquito abundance and diversity in intact habitats, though this effect was significantly weakened in disturbed areas. In total, we detected 651 viral sequences belonging to 132 OTUs (operational taxonomic units), including 100 potential previously unknown virus species. Virus richness was higher in all undisturbed habitats, and mosquito-virus interaction networks were more complex, with greater connectivity and specialisation. In contrast, disturbed habitats exhibited simplified, homogenised interactions, and were characterised by a loss of specialist mosquito species and a shift toward generalist taxa. Across ecosystems, mosquito abundance and diversity were positively correlated with virus abundance and diversity.

These findings provide general ecological patterns linking habitat disturbance, vector community turnover, and viral community structure. By adopting a multi-vector, multi-pathogen approach and integrating ecosystem-wide comparisons, this study advances a mechanistic understanding of how habitat disturbance reshapes mosquito-virus community assembly, with implications for disease ecology, biodiversity conservation, and ecosystem functioning.

A Market-Based Sentinel Surveillance for an Early Detection of Viral Outbreaks

Paola MARTÍNEZ-DUQUE (1,2), Marco A. JIMÉNEZ-RICO (1,2), Lucio A. BACAB-CAB (3), Aarón G. CANTÓN (3,4), Rhys P.D. INWARD (5,6), Bernardo GUTIÉRREZ (5,6,7), Sumali BAJAJ (6,8), Stien VANDENDIESSCHE (9), Henry PUERTA-GUARDO (3), James ERNEST (10), Pablo MANRIQUE-SAIDE (3), Gonzalo VAZQUEZ-PROKOPEC (11), Daniel CANUL-CANUL (3), Karina Jaqueline CIAU CARRILLO (3), Guadalupe AYORA-TALAVERA (3), David ROIZ (2,12,13), Carlos MACHAÍN-WILLIAMS (14), Arturo REYES-SANDOVAL (14), Moritz U. G. KRAEMER (5,6), Miguel A. GARCÍA-KNIGHT (15,16), Gerardo SUZÁN (1,2), Marina ESCALERA-ZAMUDIO (17)

1: Facultad de Medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México, UNAM, México.; 2: International Joint Laboratory IRD/UNAM, Yucatán, México.; 3: Universidad Autónoma de Yucatán, Mérida, Yucatán, México.; 4: School of Biological Sciences, Queen's University Belfast, Belfast, Northern Ireland.; 5: Department of Biology, University of Oxford, Oxford UK.; 6: Pandemic Sciences Institute, Oxford UK.; 7: Universidad San Francisco de Quito, Quito, Ecuador.; 8: Department of Statistics, University of Oxford, Oxford UK.; 9: Ghent University Hospital, Ghent, Belgium.; 10: Burnett School of Biomedical Sciences, FL, USA.; 11: Emory University, Atlanta, USA.; 12: MIVEGEC, Univ. Montpellier, CNRS, IRD, Montpellier, France.; 13: SaBio Group, IREC (UCLM-CSIC-JCCM), Ciudad Real, Spain; 14: Instituto Politécnico Nacional (IPN), México.; 15: Instituto de Investigaciones Biomédicas, Universidad Nacional Autónoma de México, Mexico.; 16: Wellcome Sanger Institute, Hinxton, United Kingdom.; 17: Department of Genetics, Evolution & Environment, University College London, London, UK.

Background

Mexico has experienced recurrent viral epidemics of substantial intensity, including hyperendemic dengue, COVID-19, and recent reports of avian influenza A (H5N1) infections in birds, posing an ongoing risk of zoonotic transmission. From the perspective of a One Health approach, traditional food markets are ecological interfaces where humans, animal reservoirs, and vectors interact within closed environments. Thus, they represent a unique opportunity for low-cost pathogen surveillance. Under the hypothesis that markets represent sentinel sites for virus monitoring, we tested a pilot surveillance

program at the central market of Merida city, Yucatan, Mexico, considered a regional hotspot for multiple viral outbreaks.

Methods

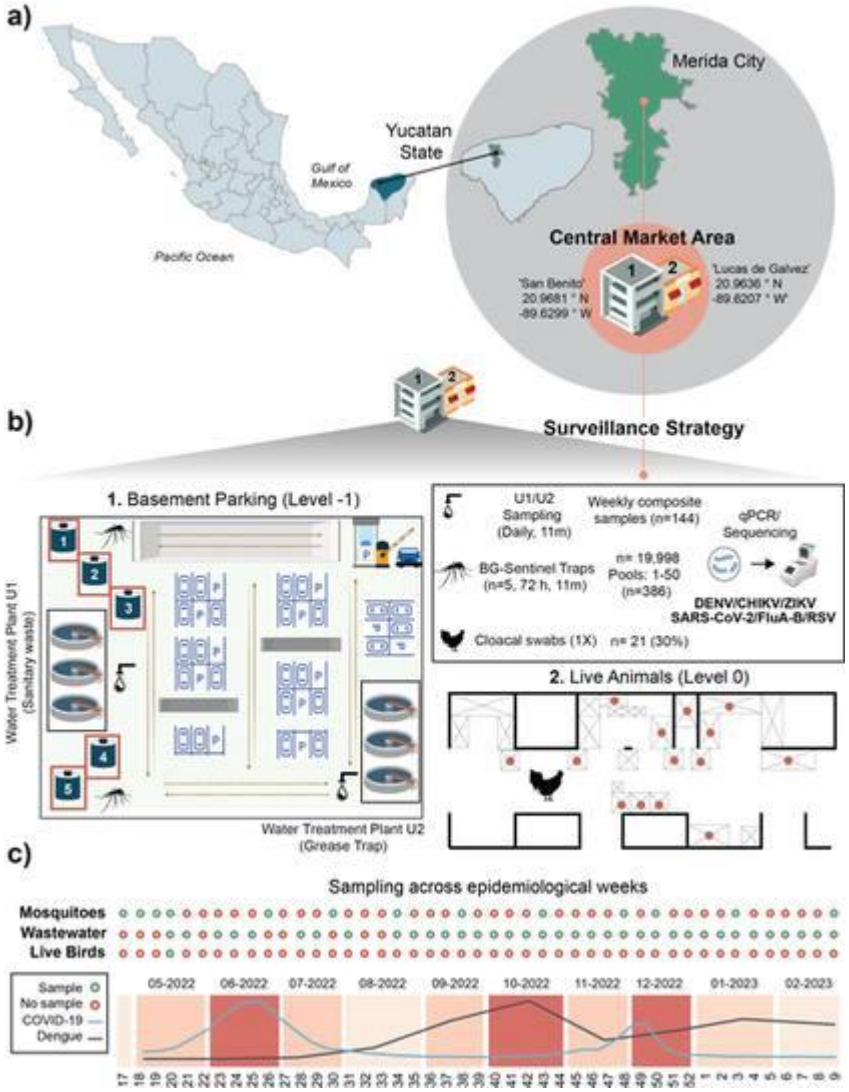
We implemented a longitudinal sampling strategy at the central market of Merida City, carried out over 11 months at 1-to-6-week intervals from April 2022 to February 2023 (Fig 1.). We used multi-type surveillance screening samples using RT-qPCR. Our approach integrated: (i) monthly mosquito sampling to screen for dengue (DENV), chikungunya (CHIKV), and Zika virus (ZIKV); (ii) weekly sampling from market's wastewater treatment plant to screen for SARS-CoV-2; and (iii) a one-time sampling event of live birds sold at the market to screen for avian influenza A viruses (AIVs). Positive samples were further sequenced and analysed under a phylogenetic approach informed by regional epidemiology.

Results

Through the entomological surveillance of over 5,000 *Aedes aegypti* mosquitoes, we report the earliest detection of DENV-3 III-B3.2 in Mexico, an emerging lineage considered a major public health concern in Latin America. Virus detection overlapped with the resurgence of DENV-3 as the predominant serotype driving the 2023 epidemic in Mexico. Phylogenetic placement informed by tip dating suggests that the lineage had likely been circulating locally for months prior to its official detection in human cases. Through wastewater surveillance, we consistently detected SARS-CoV-2 RNA, with positive signals temporally aligning with the two infection waves officially recorded at a city and state level during the study. Additionally, the putative detection of AIV RNA in two juvenile turkeys suggests continuous viral circulation within the live-animal trade network.

Conclusions

Our findings demonstrate that traditional markets can function as effective sentinel sites for monitoring viruses locally, supporting the use of entomological surveillance as an early-detection system for monitoring emerging outbreaks. Positive virus detection signals were broadly consistent with broader epidemiological dynamics officially reported. A similar strategy could complement official surveillance systems in urban settings across low and middle-income countries.



Protected Areas and One Health: Insights and the MAP-ACT-CREATE for One Health toolkit for minimizing disease risks from an IUCN WCPA Task Force

Sarah H. OLSON (1), Paulo COLCHAO (2), Amélie DESVARS-LARRIVE (3), Hannah T. FAIRBANK (4), Nina Lester FINLEY (5), David T. S. HAYMAN (6), Ziva JUSTINEK (7), Shirin KARRYYEVA (8), Renata MUYLAERT (9), Brent MITCHELL (10), Serge MORAND (11), Alexandria P. NELSON (12), Nicole NOVA (13), Anna PONTEL DE ALMEIDA (14), Paula PRIST (15), Gavrila Amadea PUSPITARANI (3), Kent REDFORD (16), Chris WALZER (1), Skylar R. HOPKINS (12)

1: Wildlife Conservation Society, Health Program, United States of America; 2: Wildlife Conservation Society, Peru; 3: University of Veterinary Medicine Vienna, Austria, Complexity Science Hub, Vienna, Austria; 4: Global Environment Facility (GEF), USA; 5: Health In Harmony, USA, London School of Hygiene and Tropical Medicine, London, United Kingdom; 6: Massey University, Molecular Epidemiology and Public Health Laboratory, School of Veterinary Sciences, New Zealand; 7: Planet Indonesia, Indonesia; 8: Conservation X Labs, Turkmenistan; 9: University of Sydney, Sydney School of Veterinary Science, Australia; 10: Quebec-Labrador Foundation (QLF), USA; 11: HealthDEEP, CNRS (French National Centre for Scientific Research) - Kasetsart University - Mahidol University, Thailand; 12: North Carolina State University, Department of Applied Ecology, USA; 13: Princeton University, USA; 14: University of Veterinary Medicine Vienna, Austria; 15: IUCN (International Union for Conservation of Nature), Forest and Grasslands Unit, USA; 16: Archipelago Consulting, USA

Land-use change, globalization, and climate change are rapidly altering wildlife-livestock-human interfaces, increasing the rate of disease emergence and spread. To combat these risks, policymakers at all scales are increasingly aligning their activities with the One Health framework and with the Joint Plan of Action, including an action track specifically for integrating the environment into One Health. One Health policy should explicitly incorporate protected and conserved areas (PCAs) because PCAs are widespread and important wildlife-livestock-human interfaces. PCAs vary in their priorities, resources,

disease risks, and other challenges, so there is an urgent need for research, funding, and support that will allow PCA managers and planners to implement context-specific actions for minimizing, mediating, and monitoring infectious disease risks. This will require collaborations among health and environment ministries and PCA managers of all kinds. Therefore, the IUCN World Commission on Protected Areas established a two-year Task Force on Protected Areas and One Health. Here, we showcase three adaptable tools that the Task Force developed for PCA managers in a peer-to-peer guide. The tools are designed to help PCA managers assess infectious disease risks (Map & Assess Pathogens), translate those assessments into tailored management actions (Analyze & Control Transmission), and evaluate and build long-term One Health capacity across multiple dimensions (Capacity, Resources, Expertise, Alliances, Training & Empowerment). Grounded in expert consensus and tested across diverse contexts, the toolkit provides flexible checklists, decision pathways, and actionable examples that enable managers with varying levels of One Health knowledge to identify existing activities, diagnose gaps, and implement context-appropriate strategies. Collectively, these tools aim to strengthen communication, coordination, collaboration, and capacity building within and among PCAs and broader One Health systems, while remaining interoperable with complementary monitoring, reporting, and conservation planning resources. We will also share lessons learned from case studies where the One Health framework was successfully used in PCAs and from interviews with PCA managers about the challenges and opportunities for operationalizing One Health. The IUCN World Commission on Protected Areas has made One Health a pillar of its conservation strategy, and we look forward to engaging and sharing the toolkit with interested attendees.

Tackling the Biodiversity-Pandemics relationship at the roots through research policy transformation

Alexandre CARON (1), Soushieta JAGADESH (2), Claire LAJAUNIE (3), Mahur TURAN (4), NIls BUNNEFELD (5), Andrew CUNNINGHAM (6), Miguel FERNANDEZ (7), Alister SCOTT (8), Norbert TCHOUAFFE TCHIADJE (9), **Serge MORAND** (10), Candice POUGET (11), Adam IZDEBSKI (12), Julie SHAPIRO (13)

1: CIRAD ASTRE - ILRI, ILRI, NAirbo, Kenya; 2: International Society for Infectious Diseases (ISID), Boston; 3: Institut national de la santé et de la recherche médicale (Inserm), UMR LPED (Aix-Marseille Université, IRD), Marseille, France; 4: TUBITAK, The Scientific and Technological Research Council of Turkiye, Turkiye; 5: Biological and Environmental Science, Faculty of Natural Science, University of Stirling, UK; 6: Institute of Zoology, Zoological Society of London, UK; 7: German Center for Integrative Biodiversity Research, Germany; 8: Department of Architecture and Built Environment, University of Northumbria, UK; 9: Pan-African Institute for Development, African Academy of Sciences and University of Ebolowa, Cameroon; 10: IRL HealthDEEP, CNRS – Kasetsart University – Mahidol University, Bangkok, Thailand; 11: Department of Conservation Biology & Social-Ecological Systems, Helmholtz Centre for Environmental Research – UFZ, Leipzig, Germany; 12: Centre for Modern Interdisciplinary Technologies, Nicolaus Copernicus University in Toruń, Poland; 13: Department of Life Sciences, Ben-Gurion University of the Negev, Be'er Sheva, Israel

Background: Human epidemics from emerging infectious diseases are increasingly frequent, often originating from the pathogen biodiversity hosted by wildlife. The most effective way to avoid significant human and societal losses from the next pandemic requires interventions that prevent disease emergence at its roots. This demands a more holistic understanding of the biodiversity-pandemic relationship, but current knowledge gaps limit the ability of policy to produce consequential interventions.

Methods: Here we used mixed methods research, combining a scoping literature review with participatory-basedconsultations to identify research gaps and policy recommendations for the biodiversity-pandemic relationship.

Resulsts: The findings highlight four main transformational recommendations to build a future strategic research agenda that will close crucial knowledge gaps and inform effective policy: (i) advancing wildlife/domestic animal/human (W/D/H) interface science to prevent pandemics at their source, where spillover occurs; (ii) fostering improved interdisciplinary collaboration across natural sciences, social sciences, and humanities, (iii) promoting transdisciplinary engagement with Indigenous Poeple and local communities and civil society to integrate diverse knowledge systems in research design and interventions. In particular, championing safe spaces where expert-led and community-led approaches can meet and codesign interventions; and (iv) and shifting from short-term funding cycles to long-term, problem-driven research programs which can track social-ecological trends and changes, including post interventions.

Conclusion: The biodiversity-pandemics relationship exposes systemic governance failures, requiring both local and global solutions. Our results yield critical insights for future design, focus and conduct of research to move beyond the biomedical-centred approach by integrating social sciences and societal actors into research projects with longer funding horizons. Such changes in research design and delivery can be transformative in improving understanding, management and evaluation of the biodiversity–health relationship through actionable research translating into effective policy. The One Health approach, as redefined recently, provides the cradle for the changes presented here, as a holistic and systemic approach to health risks. We believe that our recommendations for future research funding could support a more bottom-up and participatory One Health operationalization at W/D/H interfaces and reduce the chances of infectious disease emergence and pandemic spread.

From detection to preparedness: A One Health approach to arbovirus surveillance in Canada's changing climate

Jumari SNYMAN (1,2), Louwrens P SNYMAN (3), Carol-Anne VILLENEUVE (4), Valeria MARTINEZ (5), Priya GOUNDAR (6), Nicole WHITE (6), Naima JUTHA (7), Isabelle DUSFOUR (8), Nicolas LECOMTE (9), Patrick A LEIGHTON (4), Darcy VISSCHER (1,10), Vanessa MEIER-STEPHENSON (1,2), Emily JENKINS (5), Anil KUMAR (5), Tom C HOBMAN (1,2)

1: University of Alberta, Edmonton, Canada; 2: Li Ka Shing Institute of Virology, Edmonton, Canada; 3: Royal Alberta Museum, Edmonton, Canada; 4: Université de Montréal, Québec, Canada; 5: University of Saskatchewan, Saskatoon, Canada; 6: Government of Saskatchewan, Regina, Canada; 7: Government of the Northwest Territories, Yellowknife, Canada; 8: Institut Pasteur, Paris, France; 9: Université de Moncton, New-Brunswick, Canada; 10: The King's University, Edmonton,Canada

Arthropod-borne viruses (arboviruses) exemplify the interconnected effects of environmental change on animal and human health. In Canada, climate-driven shifts, including longer transmission seasons and northward mosquito expansion, are reshaping arbovirus risk across prairie and Arctic ecosystems. Increasing activity of West Nile virus (WNV) and California serogroup viruses (CSGV), together with the threat of non-endemic virus introduction, underscores the need for an integrated One Health surveillance approach.

From 2020–2025, mosquito samples collected through provincial government surveillance programs were analysed in collaboration with academic and public health partners. This model leveraged existing vector monitoring infrastructure while integrating molecular diagnostics, phylogenetics, and serosurveillance.

Mosquito pools were screened for WNV and CSGVs using a real-time RT-PCR assay incorporating CSGV–specific primers capable of detecting Jamestown Canyon virus (JCV), Snowshoe hare virus (SSHV), La Crosse virus (LACV), Cache Valley virus, and Tahyna virus. This assay enables broad detection of endemic CSGVs while providing early warning capacity for non-endemic viruses entering Canada, including potential northward spread of LACV. Positive samples were confirmed by Sanger sequencing, and the partial S segment was analysed phylogenetically to assess lineage diversity and geographic relationships. In parallel, plaque reduction neutralization tests (PRNTs) were performed on wildlife and human serum samples collected in Edmonton (2023–2025) to evaluate prior exposure and support evidence of local transmission.

Arctic regions (2020–2022, 2025), demonstrated continued northern circulation of JCV and SSHV. In Saskatchewan (2023–2024), JCV, SSHV, and WNV were identified, while concurrent surveillance in Edmonton, Alberta also detected JCV, SSHV, and WNV in mosquito pools. Several mosquito species tested positive that are not traditionally recognized as primary vectors, suggesting potential shifts in vector ecology and host–vector dynamics. Seasonal patterns were consistent across regions, with JCV activity peaking in early summer and WNV in late summer. Phylogenetic analyses revealed multiple JCV lineages circulating in the Arctics, whereas SSHV sequences primarily clustered within the western North American clade, supporting endemic persistence with regional connectivity. Plaque reduction neutralization tests (PRNTs) conducted on wildlife and human serum samples collected in Edmonton (2023–2025) demonstrated seropositivity consistent with prior exposure indicating active arbovirus circulation at the human–animal interface.

These findings demonstrate that arboviruses are established across diverse Canadian ecosystems. Integrating vector, wildlife, and human data illustrates transmission at the human–animal interface and reinforces the value of a One Health framework. To strengthen preparedness, we are advancing a dedicated Arbovirus Surveillance Unit to harmonize cross-sector surveillance and enable real-time data

sharing, shifting from reactive detection to proactive preparedness across Canada's interconnected ecosystems.

Global Sentinels: The Palearctic-Afrotropical Flyway as a Conduit for Antimicrobial Resistance in Wintering Little Stints (Calidris minuta)

Catherine MBUTHIA (1), Rael TOO (2), Alexanda MZULA (3), Titus IMBOMA (4), John KIIRU (2), Samuel KARIUKI (2), Abubakar HOZA (3)

1: Karatina University, Kenya; 2: Kenya Medical Research Institute, Kenya; 3: Sokoine University of Agriculture, Tanzania; 4: National Museums of Kenya, Kenya

Background: Migratory shorebirds are increasingly recognized as mobile sentinels capable of disseminating antimicrobial resistance (AMR) across intercontinental boundaries. The Little Stint (*Calidris minuta*), a long-distance migrant journeying from Arctic breeding grounds to the African Rift Valley, occupies high-connectivity wetland interfaces. In the Rift Valley, these birds forage along the shores of lakes impacted by varying degrees of anthropogenic pressure. This study assessed the frequency of multidrug-resistant (MDR) and extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales in *C. minuta* and shared environmental water sources to characterize the wildlife-livestock-human interface.

Methodology: A two-year repeated cross-sectional surveillance was conducted during birds' arrival at the Rift Valley lakes (October 2021) and pre-departure from the lakes (April 2022). Fecal samples (n=184) were collected from birds at Lake Bogoria (low anthropogenic pressure) and Lake Magadi (high anthropogenic pressure). Concurrently, 48 environmental water samples were collected from shared freshwater sources. Isolates were identified via MALDI-TOF MS and tested against 12 antimicrobials using the Kirby-Bauer method

Results: From 294 isolates, 38 (12.9%) were classified as MDR and 19 (6.5%) as ESBL producers. Additionally, 37 (12.6%) of the isolates co-expressed the ESBL-MDR phenotypes. *Enterobacter* spp. (31.0%) and *Escherichia coli* (17.3%) predominated. Resistance was highest for ampicillin (50.0%) and lowest for meropenem (1.0%). The most frequent MDR phenotype included resistance to ampicillin, tetracycline, and trimethoprim-sulfamethoxazole. *Enterobacter* spp. exhibited the highest MDR (8.2%) and combined ESBL-MDR (4.8%) frequencies. Crucially, no statistically significant differences ($p>0.05$) were found between the two lakes or migratory cohorts, indicating that MDR strains are pervasive across the landscape regardless of localized human activity.

Conclusion: Our findings demonstrate that *C. minuta* serves as a significant reservoir for AMR, suggesting that resistant strains are maintained and transported across the Palearctic-Afrotropical flyway. This underscores the necessity of including migratory wildlife in global AMR surveillance frameworks. Effective mitigation requires transboundary One Health policies to monitor these ecological bridges and protect the integrity of aquatic ecosystems vital to both animal and human health

Antimicrobial resistance - session 1

SCS10 · 14:00-15:30 · Auditorium I

Tracking Tuberculosis and Antimicrobial Resistance in Sub-Saharan Africa Through Wastewater-Based Surveillance: A One Health Approach

Hlengiwe Nombuso MTETWA (1,2), Poovendhree REDDY (1,2), Isaac Dennis AMOAH (3), Sheena KUMARI (2), Faizal BUX (2)

1: Department of Community Health Studies, Faculty of Health Sciences, Durban University of Technology, PO Box 1334, Durban, 4000, South Africa; 2: Institute for Water and Wastewater Technology (IWWT), Durban University of Technology, PO Box 1334, Durban, 4000, South Africa; 3: Department of Environmental Science, University of Arizona, Tucson, USA

Background

Tuberculosis (TB) and antimicrobial resistance (AMR) remain major public health threats in sub-Saharan Africa, where conventional surveillance systems are often constrained by delayed diagnosis, under-reporting, and limited laboratory capacity. Environmental pathways, particularly wastewater systems, are increasingly recognised as important reservoirs and transmission interfaces for drug-resistant pathogens. Wastewater-based surveillance (WBS) offers a population-level, non-invasive approach to complement clinical surveillance and strengthen One Health responses to TB and AMR.

Methods

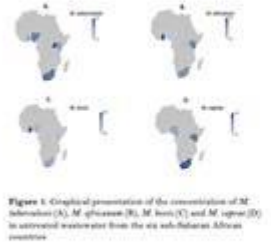
This multi-country study applied an integrated molecular and multi-omics framework to characterise *Mycobacterium* species, virulence determinants, and TB-associated antibiotic resistance genes (ARGs) in influent and effluent wastewater samples collected from six TB-endemic countries in sub-Saharan Africa (Ghana, Nigeria, Kenya, South Africa, Uganda, and Cameroon). DNA and RNA were extracted and analysed using droplet digital PCR, shotgun metagenomic sequencing, and metatranscriptomic profiling. Taxonomic, functional, and resistance profiles were compared across countries and treatment stages using non-parametric statistical analyses to assess spatial and environmental patterns.

Results

Mycobacterium tuberculosis complex (MTBC) lineages (L1, L2, L4, and L6) were detected in 85% of wastewater samples, indicating widespread community-level shedding. Non-tuberculous mycobacteria, including members of the *Mycobacterium avium* complex, accounted for 22.5% of *Mycobacterium* reads. Metatranscriptomic analyses revealed active transcription of key virulence pathways, particularly ESX-5 secretion systems and lipid metabolism-associated genes, with significantly higher expression observed in high-burden settings. ARGs associated with first-line TB drugs (rifampicin, isoniazid, pyrazinamide) and second-line agents (bedaquiline, delamanid, fluoroquinolones) were identified across all countries, including locations where some second-line drugs are not routinely used in treatment programmes. Resistance mechanisms linked to efflux pumps were highly prevalent, and ARG abundance was significantly higher in influent compared to effluent samples, indicating incomplete removal during wastewater treatment.

Conclusions

These findings demonstrate that wastewater systems act as integrative reservoirs of TB pathogens and resistance determinants, reflecting both disease burden and antimicrobial selection pressures at the community level. By combining genomic and transcriptomic evidence of pathogen presence and activity, this study highlights the value of WBS as a scalable One Health surveillance tool to support TB and AMR control, inform antimicrobial stewardship, and strengthen community resilience in sub-Saharan Africa.



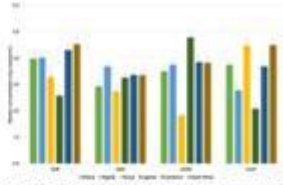


Figure 2: Median concentrations of tuberculosis-causing *Mycobacterium* spp. in untreated wastewater from the six African countries.

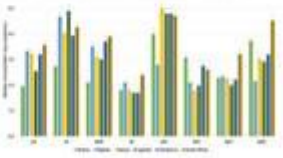


Figure 3: Median concentration (log copies/mL) of selected genes encoding resistance to the second-line TB drugs i.e streptomycin(*rrs*), aminoglycosides (*eis*), ethionamide (*ethR*), cycloserine (*alr*), delaminid (*ddn, fgd1* and *fbiA*) and bedaquiline (*atpE*) in the untreated wastewater from the six WWTPs.

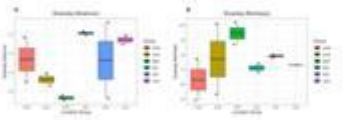


Figure 4: DNA sequencing-based boxplots revealing Alpha-Diversity measures (Simpson and Shannon Index) within the *Mycobacterium* genus across wastewater samples from six African countries

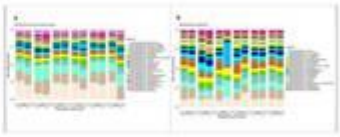


Figure 6: Heatmap depicting the intricate *Mycobacterium* genus composition from wastewater across the studied countries.

Figure 5: Beta diversity analysis using the Bray-Curtis dissimilarity index, depicting the compositional differences in microbial communities among six African countries.

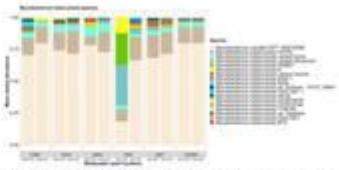


Figure 7: Heatmap diagram illustrating *Mycobacterium tuberculosis* complex profile from wastewater samples across the studied countries

From Supermarket Demands to Farm Decisions: Contextualising antibiotic use in Agriculture

Allegra SCHERMULY (4), Ri SCARBOROUGH (1), Leslie DOWSON (2), Courtney IERANO (2), Brendan MCMULLAN (3), Leanne TEOH (5), Kirsten BAILEY (1), Ruby BIEZEN (6), Brian HUR (1), **Laura HARDEFELDT** (1)

1: Melbourne Veterinary School, University of Melbourne, Australia; 2: The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia; 3: Sydney Children's Hospital, Randwick, Australia; 4: Monash University, Clayton, Australia; 5: Melbourne Dental School, University of Melbourne, Australia; 6: Department of Primary Care, University of Melbourne, Australia

Background: Appropriate antimicrobial use (AMU) carries different meanings across One Health stakeholders. Commercial, regulatory and other contexts may shape how livestock farmers and veterinarians practice antimicrobial stewardship (AMS) and influence actionable interventions to support appropriate AMU on farm.

Methods: Four qualitative focus groups involving livestock farmers, consumers, healthcare professionals and policymakers were performed in 2024.Inductive grounded theory analysis was used to identify themes.

Results: Two primary thematic domains were identified: structural and economic factors, and informational and educational factors. Structural and economic factors were prominent in participants' accounts. Farmers and agricultural veterinarians described how supermarket buying power and consumer preferences — for example for free-range or "antibiotic-free" products — materially influence production systems and AMU. Extensive and outdoor systems reported higher disease exposure, sometimes increasing reliance on antimicrobials, while supermarket-driven production specifications directed on-farm practices. The prohibitive cost of veterinary visits led many farmers to reserve in-person veterinary care for extraordinary events; routine decisions were often managed using pre-dispensed antimicrobials, written or verbal treatment protocols, quick phone consultations or retained leftovers.

These practices reflect pragmatic business survival strategies but create risk for inappropriate AMU, including antibiotic treatment of likely viral conditions.

Regulatory tensions were flagged as a major barrier. Label dose rates are frequently too low to be effective according to current evidence but withholding periods for higher (off-label) doses have frequently not been established forcing prescribers to choose between legal compliance and effective treatment. Variation between jurisdictions and gaps for niche species or small and hobby farms complicate measurement of AMU and perceptions of fairness in regulatory oversight. Policymakers and participants highlighted the need for harmonised legislation and withholding periods that accommodate evidence-based dosing.

Informational and educational factors were likewise critical. Farmers expressed a desire for practical, timely AMS education compatible with busy and geographically dispersed farm life, and for more peer-to-peer knowledge exchange within industries. Defensiveness and siloing limited information sharing. Access to consistent, trustworthy veterinary advice was variable; participants supported expanded remote or online advisory services and longer advisory consultations to discuss non-antimicrobial alternatives. Niche industries reported insufficient pharmacological data to establish appropriate doses, undermining stewardship efforts.

Conclusions: Effective AMS in livestock sectors requires interventions that address economic drivers, improve access to veterinary expertise, harmonise regulatory frameworks to support evidence-based prescribing, and deliver tailored, pragmatic education and peer learning opportunities. Engagement of commercial buyers in stewardship and policy actions to resolve legal-clinical conflicts are pivotal to make appropriate AMU feasible for veterinarians and farmers.

Environmental and Clinical Surveillance of Antimicrobial Resistance Along the Paraopeba River Basin Following a Mining Disaster in Brazil

Bruna C. LOPES (1), Gabriel R FERNANDES (2), Aline B. M. VAZ (3), Wanderson K. de OLIVEIRA (4), Paula L. C. FONSECA (1), Múcio L. P. de CASTRO (4), Carlos E. STARLING (4), Dhian R. A. CAMARGO (5), **César R. MOTA FILHO** (1), Andre B. SANTOS (6)

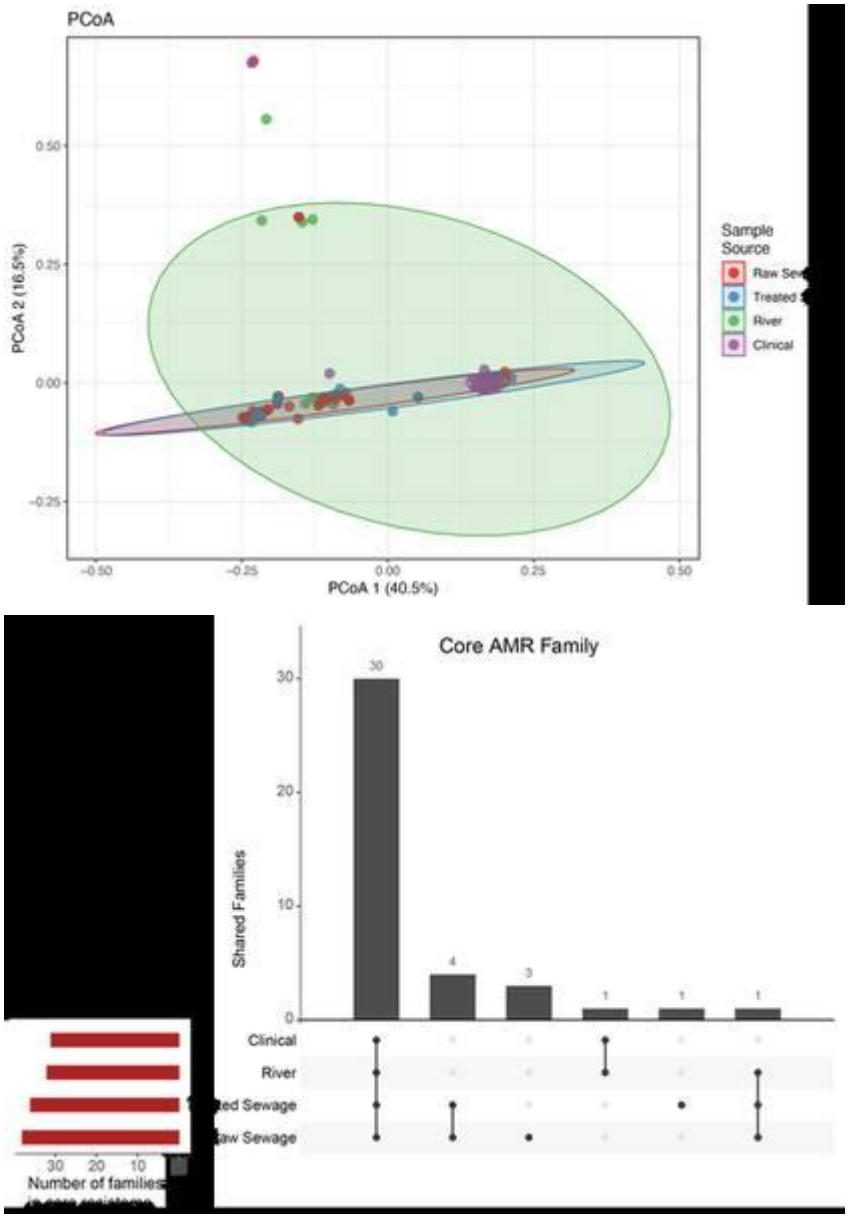
1: Federal University of Minas Gerais, Brazil; 2: Instituto René Rachou - Fiocruz Minas, Brazil; 3: Unifenas, Brazil; 4: Infection Control; 5: Ezequiel Dias Foundation; 6: Federal University of Ceara, Brazil

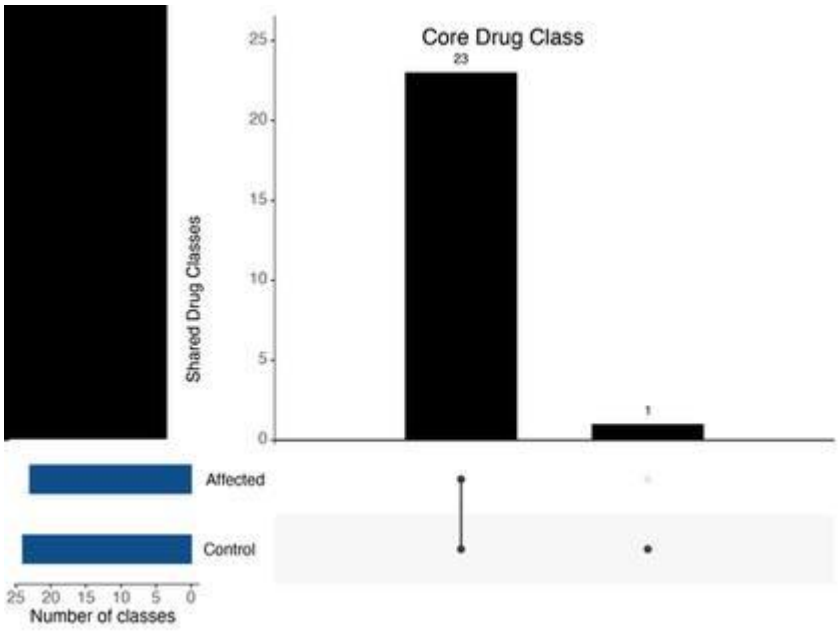
Aquatic environments are recognized as important reservoirs and dissemination pathways for antimicrobial resistance (AMR), linking microbial communities across environmental, animal, and human compartments. Environmental disturbances may alter these ecological networks and influence the distribution of antimicrobial resistance genes (ARGs). In January 2019, the collapse of a mining tailings dam in southeastern Brazil released millions of cubic meters of mining waste into the Paraopeba River basin, causing extensive environmental disruption. While the immediate ecological impacts of this disaster have been documented, its potential influence on AMR dynamics across environmental and human compartments remains poorly understood. This study applied an integrated One Health surveillance approach to investigate the distribution of antimicrobial resistance genes along the Paraopeba watershed five years after the dam collapse.

Monthly sampling campaigns were conducted throughout 2025 in areas upstream and downstream of the dam rupture site. Environmental matrices included river water, raw sanitary sewage, and treated wastewater from wastewater treatment plants (WWTPs), totaling 156 environmental samples. Clinical bacterial isolates obtained from urine samples of patients treated at healthcare facilities within the same regions were also included for comparative analysis. Culture-based methods were used to isolate antimicrobial-resistant bacteria belonging to the ESKAPEE group (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp., and Escherichia coli), focusing on resistance to carbapenems and third-generation β-lactams. Environmental and clinical isolates underwent DNA extraction followed by whole-genome sequencing using the Illumina platform. Genome assemblies were generated using SPAdes, gene prediction was performed with Prodigal, and antimicrobial resistance gene annotation was conducted using the Comprehensive Antibiotic Resistance Database (CARD). The core resistome was defined as resistance genes detected in at least 50% of the analyzed samples.

Preliminary analyses revealed a conserved core resistome shared between environmental and clinical isolates. Efflux pump genes, particularly those belonging to the major facilitator superfamily (MFS) and the resistance–nodulation–cell division (RND) family, were the most abundant resistance mechanisms. A total of 30 antimicrobial resistance gene families were detected across environmental and clinical compartments, indicating substantial overlap between aquatic environments and human-associated bacteria. Only a few genes were compartment-specific, with three detected exclusively in sewage samples, one in river water, and two in urine isolates.

Five years after the environmental disturbance, antimicrobial resistance genes remain widely distributed across aquatic environments and human clinical isolates within the Paraopeba basin. The presence of a shared resistome across environmental and clinical compartments highlights the interconnected nature of AMR dissemination within a One Health framework and reinforces the importance of integrated environmental and clinical surveillance to monitor AMR dynamics in ecosystems affected by large-scale disturbances.





Revised African Union Framework for Antimicrobial Resistance Control 2026 - 2030: Strategic shift from high-level intent to practical, measurable interventions

Nyambura MOREMI (1), Yewande ALIMI (1), Fowzia Mohamed SHEIKH (1), Molla Godi FISEHATSION (1), John OPPONG-OTOO (2), Merawi ARAGAW (1)

1: Africa Centers for Disease Control and Prevention, Ethiopia; 2: African Union – Inter-African Bureau for Animal Resources, Kenya

Background: Antimicrobial resistance (AMR) continues to threaten health security, food systems, and economic stability across Africa. Despite the notable achievements of the first version of the continental AMR framework (2020-2025) which demonstrated African Union's commitment and determination in tackling AMR, implementation gaps at country and continental level underscored the need for a more operational, results-driven approach. The revised Framework (2026-2030) initiates a strategic shift from high-level intent to practical, measurable interventions designed to work within national systems across all 55 African Union (AU) Member States.

Methods: The Framework was developed through an iterative, consultative and multi-sectoral approach. Africa CDC and AU-IBAR engaged AU member states, Regional Economic Communities and AMR partners to comprehensive assess achievements, document lessons learned, and refine strategies for the revised Framework, ensuring alignment with emerging global and continental priorities, including the 2024 United Nations General Assembly Political Declaration on AMR articulated in the AU's AMR Landmark Report, the Africa CDC's Africa Health Security Sovereignity Agenda and the Kampala Comprehensive African Agricultural Development Programme Declaration. Notable gaps in governance, financing, access to AMR countermeasures, surveillance integration and advocacy impact were systematically analyzed to inform strategic redesign.

Results: In five years (2020-2025), notable achievements include high-level political advocacy, setting up One Health coordinating mechanisms within member states, benchmarking continental laboratory capacity and antimicrobial use baseline data, institutionalizing integrated AMR surveillance, improving data quality and enhancing biosecurity and infection prevention and control measures through flagship programs. The revised Framework (2026-2030) introduces major strategic shifts including elevating governance and advocacy from enablers to primary strategic goals, placing political accountability, leadership, culturally adaptable advocacy and coordinated actions at the center of AMR control. Integration of cross-sectoral data integration linking food safety systems, environmental monitoring and wastewater surveillance into unified AMR data platforms to strengthen early warning systems. Development of a clear, data-driven AMR investment case, and addressing access to AMR countermeasures as broader health security and economic resilience goals.

Conclusion: The revised AU Framework for AMR Control (2026–2030) represents a transition from aspirational policy to actionable implementation. Its success will depend on sustained political commitment, domestic resource mobilization, impactful partnerships and coordinated action across all AU Member States. It reaffirms AU's commitment to embracing continental and global solidarity in making AMR a surmountable challenge.

Environmental Antimicrobial Resistance, Wildlife and Biodiversity in Tunisia: A One Health Approach Aligned with the Kunming-Montreal Global Biodiversity Framework

Haifa EL HENTATI (1), Hatem BEN BELGACEM (2), Wissal DEROUICH (1)

1: National Gene Bank of Tunisia- Tunisian Ministry of Environment - , Tunisia; 2: Directorate of the Ecology and Natural Areas, Ministry of Environment, Tunisia

Background

Antimicrobial resistance (AMR) poses a systemic threat to human, animal, and environmental health, increasingly affecting natural ecosystems. Soil and freshwater environments act as reservoirs of resistance genes, while wildlife exposed to contamination serves as ecological sentinels at the human–animal–environment interface. Tunisia, hosting over 7500 species across seven major ecosystems and 42 internationally significant wetlands, offers a strategic context to explore these interactions. Yet, environmental AMR surveillance remains insufficiently integrated into national biodiversity monitoring. This study aims to operationalize a One Health framework for environmental AMR surveillance in wildlife and natural habitats, contributing to the implementation of the Kunming–Montreal Global Biodiversity Framework (KM-GBF) and Sustainable Development Goal 15 (Life on Land).

Methods

This initiative, led by the Ministry of Environment through the National Gene Bank and the Directorate of Ecology and Natural Areas, applied an environmental DNA (eDNA) approach to detect antimicrobial resistance (AMR) determinants non-invasively. Five environmental samples (three freshwater and two soil) were collected from key ecosystems and analyzed using high-throughput Illumina sequencing. Bioinformatic analysis against curated resistance databases identified antimicrobial resistance genes (ARGs). Results were integrated into the National Biodiversity Strategies and Action Plans (NBSAPs), aligned with the Kunming–Montreal Global Biodiversity Framework (KM-GBF) and the National Strategy of Ecological Transition. Geospatial mapping enabled identification of high-risk areas and supported early warning mechanisms within an ecosystem-based surveillance framework, ensuring responsible genetic resource management in line with access and benefit-sharing principles.

Results

Five environmental samples (three freshwater and two soil) generated approximately 1.2 million raw reads, of which 950000 high-quality sequences were retained after filtering. Eighteen distinct antimicrobial resistance genes (ARGs) were identified, covering six antibiotic classes, including beta-lactams (blaTEM, blaOXA), tetracyclines (tetA, tetM), sulfonamides (sul1, sul2), macrolides (ermB), aminoglycosides (aadA), and quinolones (qnrS). ARG diversity was higher in freshwater than in soil, particularly near agricultural and peri-urban areas, indicating anthropogenic pressure. Co-detection of ARGs and wildlife eDNA suggests potential exposure pathways at the human–animal–ecosystem interface. Spatial integration with biodiversity monitoring identified high-risk zones and supported targeted actions aligned with KM-GBF Targets 7, 13, and 14. These preliminary findings confirm the feasibility of integrating environmental AMR surveillance within a One Health framework.

Conclusions

Environmental AMR surveillance using eDNA provides a scalable and non-invasive approach to link resistance monitoring with wildlife conservation under One Health. By integrating AMR detection with biodiversity data and policy frameworks, this initiative supports KM-GBF implementation and strengthens ecosystem resilience. This pilot establishes a foundation for expanded national surveillance and evidence-based interventions.

Understanding the potential for the Community Dialogue Approach to tackle antimicrobial resistance: Evidence from a randomised control trial and process evaluation in rural Bangladesh.

Jessica MITCHELL (1), Joseph HICKS (2), Rumana HUQUE (3), Md. Badruddin SAIFY (3), Sonnet ABDULLAH (3), Helen HAWKINGS (4), Sophia LATHAM (5), Paul COOKE (6), Rebecca KING (2)

1: Global Agriculture and Food Systems, Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK, EH25 9RG; 2: Nuffield Centre for International Health and Development, Leeds Institute for Health Sciences, University of Leeds, Woodhouse Lane, Leeds, LS2 9JT, UK.; 3: ARK Foundation, Suite: C3-C4, House No: 6, Road No: 109, Gulshan-2, Dhaka-1212, Bangladesh.; 4: Malaria Consortium. The Green House, 244-254, Cambridge Heath Road, London EC2 9DA, UK.; 5: University of Liverpool Veterinary School, Leahurst Campus, Wirral Peninsular, Liverpool, UK, L69 7ZB; 6: Center for World Cinemas and Digital Cultures, Faculty of Arts, Humanities and Culture, University of Leeds, Woodhouse Lane, Leeds, LS2 9JT, UK

Background

In Bangladesh, widespread antibiotic misuse across humans, animals, and the environment accelerates the challenge of antimicrobial resistance (AMR). The COSTAR project aimed to address this through a co-created, intervention embedded within the human health system known as the Community Dialogue Approach (CDA). The CDA is grounded in the Integrated Model of Communication for Social Change, framing dialogue as a collective process for reflection, decision-making, and action. Our objectives were to co-create, implement, and robustly evaluate an innovative community engagement intervention that addresses the contextual One Health drivers of AMR.

Methods

A two-arm, cluster-randomised trial was implemented in five sub-districts of Cumilla, Bangladesh. In the intervention clusters, trained volunteer community facilitators (n=221) delivered 11 participatory dialogues using co-developed flipbooks, dialogue guides, monitoring tools and action plans over 12 months. Supervisors were local health staff. Control clusters received no engagement.

The trial had two primary outcomes measured via cross-sectional household surveys (baseline and endline): 1) knowledge of antibiotics, antibiotic resistance, and using antibiotics for human illness based on 25 multiple-choice questions, and 2) knowledge about using antibiotics for animal health, and antibiotic-related environmental considerations based on 20 multiple-choice questions.

A process evaluation complemented the trial, examining reach, fidelity, gender inclusion, and mechanisms of change. Process evaluation employed qualitative evaluation of monitoring data, 30 dialogue observations, 24 Focus Group Discussions, and 10 Key Informant Interviews using the Medical Research Council (MRC) framework for evaluating complex interventions.

Results

The CDA significantly improved antibiotic-related knowledge at both community and individual levels. Knowledge on human antibiotic use increased by +16 percentage points (95% CI: 9, 22; p0.001), and animal/environmental antibiotic knowledge by +12 percentage points (95% CI: 5–19, p0.001). Among participants attending at least one dialogue, mean knowledge scores were 73% versus 33% among non-attenders (mean difference 40 percentage points, 95% CI: 33–47).

Implementation fidelity was high: 4,362 dialogues were delivered with 80,164 total attendees, reaching 51% of respondents' households. Communities identified and acted on 35 locally defined actions, such as consulting qualified providers, completing antibiotic courses, and improving animal husbandry, hygiene and waste disposal. Process evaluation data revealed motivation, acceptability and knowledge diffusion as mechanisms of impact, with facilitators' storytelling seen to key factor encouraging engagement.

Conclusions

This trial provides the first experimental evidence that a CDA can shift community knowledge on antibiotics and resistance from a One Health perspective. Attending a dialogue led to higher knowledge showing a clear causal pathway. However, results were stronger for human health knowledge than for animal/environment topics, highlighting the need to reflect on the One Health reach of the current intervention, particularly the impacts on embedding within the human health system only.

Strengthening One Health surveillance in animal populations and food systems through the International FAO Antimicrobial Resistance Monitoring System (InFARM)

Alejandro DORADO GARCIA, Agnes AGUNOS, Norma Sofisa HURIF, Aristeidis TSACHLARIS, Marie VERHAEGEN, Kim Anh TEMPELMAN, Eduardo MACHADO, Alina CHERKAS, Junxia SONG, **Lina AWADA**
Food and Agriculture Organization of the United Nations (FAO), Italy

Background
Antimicrobial resistance (AMR) is a growing threat to human, animal, plant and environmental health, requiring coordinated surveillance across sectors. While global surveillance systems exist for human health, AMR data from animal populations, food products and agrifood production environments remain fragmented and unevenly reported. To address this gap, the Food and Agriculture Organization of the United Nations (FAO) developed the International FAO Antimicrobial Resistance Monitoring System (InFARM), a global information system designed to support countries in generating, harmonizing, sharing and utilizing AMR data from animals and food, and antimicrobial use (AMU) data in plant production. This study presents results from the first report on the early implementation of the system and assesses its contribution to strengthening One Health AMR surveillance.

Methods
InFARM was developed through a stepwise process aligned with international standards and guidance from FAO, Codex Alimentarius, WHO and WOAH. The system's IT platform integrates standardized metadata, laboratory data structures and analytical workflows to enable harmonized reporting of antimicrobial susceptibility testing (AST) results from animals, food products and related production environments. The platform is also expanding to collect AMU data in plant production and protection. During the early implementation phase (2023–2025), countries submitted AMR datasets through annual open calls for data. Submitted datasets were curated, validated and are being analyzed to generate global indicators monitoring AMR prevalence and emerging trends.

Results
Early implementation of InFARM demonstrated rapid growth in country participation and data reporting. Between the first reporting cycle (2024) and the subsequent year (2025), participation expanded from 49 countries to 80 countries, while the number of reported datasets and bacterial isolates nearly doubled, exceeding 800,000 isolates. Data included AST results from major indicator bacteria and pathogens collected from animals and food. The system enabled the establishment of an international framework and technical guidance for generating harmonized global analyses of AMR patterns across agrifood systems. InFARM also supported countries in strengthening national surveillance through training of national focal points and improved data management and reporting capacities.

Conclusions
Early results demonstrate that InFARM provides a scalable and operational mechanism for strengthening AMR surveillance across agrifood systems within a One Health framework. By harmonizing data generation and enabling global reporting from animals and food systems, InFARM contributes critical evidence to inform risk assessment, policy development and antimicrobial stewardship. Continued expansion of the system, alongside improved interoperability with surveillance systems from WHO, WOAH and UNEP, will be essential to close remaining surveillance gaps and support integrated monitoring of AMR across human, animal, plant, and environmental interfaces.

Data, Technology & Innovative Analytics

SCS11 · 16:00-17:30 · Auditorium I

Designing the PREZODE International Platform: A Collaborative Information System for Prevention of Zoonotic Diseases within a One Health Framework

Paula CACERES (1), Lina AWADA (2), Joconiah CHIRENDA (3), Thameur BEN HASSINE (4), Amélie DESVARS-LARRIVE (11), Crawford REWIE (2), Madonna KEMP (10), Sarah OLSON (6), Romain BOUVIER (20), Sari TANIKAWA (1), Christina PETTAN-BREWER (7), Serge MORAND (17), Pablo VALDES DONOSO (8), Soushieta JAGADESH (9), Paolo TIZZANI (19), Lea ESTBERG (15), Maguelonne TEISSEIRE (1), Rafik GARNI (12), Jessie ABBATE (13), Giovanni MARINI (14), Lina MEGO (8), Margarida SIMOES (18), Anca STOICESCU (16), Fondzeyuf FOLAH (23), Ximena TOLOSA (22), Elsa LEGER (1), Ricardo SOARES MAGALHAES (21), Casey BARTON BEHRAVESH (15), Manon LOUNNAS (24), Roslyn HICKSON (10), Anne-Laure BANULS (24), Robyn ALDERS (25), Maria Fernanda VINCENTI (26), **Muhamad Fairus NOOR HASSIM** (5)

1: INRAE, France; 2: FAO; 3: University of ZImbabwe, Zimbabwe; 4: Direction Générale des Services Vétérinaires, Tunis; 5: Universiti Malaysia Terengganu, Malaysia; 6: Wildlife Conservation Society, USA; 7: University of Washington, USA; 8: Université de Montréal, Canada; 9: International Society of Infectious diseases; 10: CSIRO, Australia; 11: University of Veterinary Medicine Vienna, Austria; 12: Institut Pasteur of Algeria; 13: Geomatys, France; 14: Fondazione Edmund Mach, Italy; 15: USDA APHIS Veterinary Services, USA; 16: EFSA, Italy; 17: CNRS, France; 18: University of Évora, Portugal; 19: WOAH; 20: CIRAD, France; 21: The University of Queensland, Australia; 22: Queensland Department of Health, Australia; 23: UNEP-WCMC; 24: IRD, France; 25: Australian National University, Australia; 26: Maastricht University, Netherlands

BACKGROUND

Preventing emerging zoonotic diseases requires integrating knowledge and data from multiple disciplines, sectors and regions. However, information relevant to prevention is currently fragmented across research projects, institutions, platforms, and data systems.

As part of the international PREZODE (Preventing Zoonotic Disease Emergence) initiative, the need to develop an international platform focused on preventing zoonotic diseases using a One Health approach was underscored. The aim of this platform is to address the needs identified by the international community while reducing the duplication among existing infrastructure or initiatives.

METHODS

To design this platform, the multidisciplinary **International Data Working Group (IDWG)** was established, bringing together experts in data, research, and health information systems from international organisations, research institutes, academia, and public services.

An analysis identified 242 specific data-linked needs identified through a series of PREZODE's studies conducted in 2021-2024. These needs were grouped into 20 broad categories that could be addressed through the PREZODE platform.

Based on this evidence and the IDWG's expertise, five conceptual platform models were proposed. These models were then evaluated by the PREZODE experts using a structured, multi-criteria evaluation matrix based on three dimensions: potential impact, implementation complexity, and number of needs addressed.

RESULTS

The analysis indicated that none of the five proposed platforms would have sufficient global impact if considered individually. However, combining three of the models could significantly strengthen prevention efforts. Based on this finding, a modular architecture for the PREZODE International Platform was defined, composed of three complementary components:

CONCLUSIONS

The PREZODE International Platform aims to transform fragmented knowledge into collective intelligence for prevention. It is conceived as a collaborative information system supporting global zoonotic disease prevention within a One Health framework by improving the visibility of prevention efforts, facilitating collaboration, and enabling data integration.

IDWG experts also demonstrated the importance of analysing existing infrastructures to avoid duplication and and of learning from previous experiences, as well as involving future users in the design process. To

this end, PREZODE is currently finalizing a platform bench-marking exercise, developing an initial prototype, and establishing an international user committee to test it.

Digital Interoperability for One Health Surveillance in Guinea: Automated Information Exchange between Animal and Public Health Systems

Lisette KOHAGNE TONGUE (1), Daouda BANGOURA (1), Fassou KOUROUMA (2), Mory CISSE (3), Lionel GBAGUIDI (1), Marcel OHOUKOU BOKA (1), Sabina RAMAZZOTTO (1), Pavel NEGINSKY (1), Fernanda DOREA (1), Amy DELGADO (1), Gisela GIOIA (1), Eduardo MACHADO (1), Ismaila SECK (1)

1: Food and Agricultural Organisation for the United Nations, Guinea; 2: Ministère de l'Elevage : Direction Nationale des Services Vétérinaires; 3: Ministère de la Santé et de l'Hygiène Publique : Agence Nationale de Sécurité Sanitaire

Background Integrated surveillance systems are essential for the early detection and control of zoonotic diseases at the human–animal–environment interface. However, globally, surveillance information systems remain fragmented. In Guinea, to address this gap and strengthen implementation of the One Health approach, national authorities, with support from the Food and Agriculture Organization of the United Nations (FAO) and technical partners, initiated an interoperability strategy linking the digital surveillance system used in the public health sector, DHIS2, with the system used in veterinary services, EMA-i+. The objective was to harmonize data exchange mechanisms, enable rapid cross-sectoral notifications of zoonotic disease events, and improve epidemiological intelligence and response capacity.

Methods A national multisectoral consultation involving representatives from the human, animal, and environmental health sectors, private sector and technical partners, developed an interoperability strategy between the surveillance systems. The strategy defined operational objectives, technical protocols, exchange mechanisms, semantic and syntactic standards, priority zoonotic diseases, and an implementation roadmap under the coordination of the National One Health Platform. Two complementary data-sharing mechanisms were established. The first involved automated alert-based notifications using emails to inform predefined stakeholders when a zoonotic event is reported in either platform. The second involved system-to-system interconnection through application programming interfaces (APIs) enabling standardized data transmission between platforms. Following governmental endorsement, implementation began with a pilot phase focusing on automated alert notifications linking EMA-i+ and DHIS2. Initial activities included awareness-raising among professionals from both sectors on interoperability principles, configuration of user accounts to enable automated notification dissemination, and training of surveillance personnel. In October 2025, 102 professionals from the prefectures of Coyah (30), Forécariah (35), and Dubréka (37) were trained, and the mechanism was piloted from October 2025 to February 2026.

Results The interoperability pilot enabled near real-time sharing of zoonotic disease alerts between the veterinary and public health sectors. Within five months, the DHIS2 system reported 15 suspected human anthrax cases and 13 suspected viral haemorrhagic fever cases that were automatically communicated to animal health authorities. Additionally, 300 dog bite incidents and one cat scratch case were shared across sectors. The rapid exchange of information triggered coordinated multisectoral responses, including joint field investigations, rabies and anthrax vaccination activities, and targeted active surveillance around suspected viral haemorrhagic fever events, one of which was confirmed as Lassa fever.

Conclusions

The Guinea experience demonstrates how automated bidirectional information sharing between animal and public health systems can significantly improve early warning and multisectoral collaboration. Sustaining and expanding this approach will require continued technical development, structured governance, and institutional commitment to fully integrate digital surveillance systems and enhance preparedness for emerging zoonotic diseases.

Development and Implementation of a Nationwide Electronic Health Record-Based (EHR) Surveillance Platform for Vector-Borne, Zoonotic, and Environmentally-Transmitted Infectious Diseases: The Veterans Health Administration (VHA) as a Sentinel Network

Julienne REYNOLDS (1,2,3), Ariana PAREDES-VINCENT (4), Pankaj AGARWAL (1,2), Jack ANDERSON (1,3), Lauren EPSTEIN (5,6), Jimmy EFIRD (7), Michael GELMAN (8,9), Robert BONOMO (10,11), Maria RODRIGUEZ-BARRADAS (12,13), Christopher WOODS (1,3), Sheldon BROWN (4,14)

1: Durham VA Medical Center, Durham, NC, USA; 2: Institute for Medical Research, Durham, NC, USA; 3: Duke University, Durham, NC, USA; 4: Hudson Valley VA Healthcare System, Montrose, NY, USA; 5: Atlanta VA Healthcare System, Atlanta, GA, USA; 6: Emory University, Atlanta, GA, USA; 7: Jamaica Plain VA Medical Center, Boston, MA, USA; 8: Miami VA Medical Center, Miami, FL, USA; 9: University of Miami, Miami, FL, USA; 10: Louis Stokes Cleveland VA Medical Center, Cleveland, OH, USA; 11: Case Western Reserve University, Cleveland, OH, USA; 12: Michael E DeBakey VA Medical Center, Houston, TX, USA; 13: Baylor College of Medicine, Houston, TX, USA; 14: Icahn School of Medicine at Mount Sinai, New York, NY, USA

BACKGROUND

Vector-borne, zoonotic, and environmentally-transmitted infectious diseases (VBZEDs) are increasing in the United States due to land-use changes and shifting meteorological and ecological patterns. Existing U.S. surveillance frameworks remain disconnected, reflexive, and reliant on clinician reporting, leading to systematic underreporting and delayed detection of emerging threats at the human-animal-environment interface. U.S. military Veterans face compounded VBZED risk: global deployments exposed service members to diverse ecological and zoonotic exposure settings, while service-associated comorbidities increase susceptibility to severe disease. The Veterans Health Administration (VHA)—the largest integrated healthcare system in the United States, comprising 170 medical centers and 1,193 outpatient clinics—demonstrated during the COVID-19 pandemic that its facility-level infection trends closely mirror national surveillance data, establishing proof of concept for EHR-based sentinel surveillance at national scale.

METHODS

We created a nationwide EHR-based VBZED surveillance framework using diagnostic data from the VA Corporate Data Warehouse (CDW), accessed through the Veterans Integrated Computer Infrastructure (VINCI) and benchmarked against CDC WONDER and CDC Stacks. Using 670 ICD-9 and ICD-10 diagnostic codes, we identified incident cases of 94 VBZEDs across the VHA patient population from 1-Oct-1999 through 30-Sept-2025. Cases were summarized by sex, age group, race, ethnicity, and geographic region. Annual incidence rates per 100,000 patients were computed by state. State-level standardized morbidity ratios (SMRs) were calculated against VHA national rates for all diseases and against CDC national rates for 23 reportable diseases. We developed an interactive Power BI dashboard to enable near-real-time, per-disease reporting with dynamic filtering.

OUTPUTS

Over the 26-year study period, VHA incidence rates for Lyme disease, spotted fever rickettsiosis, babesiosis, ehrlichiosis and anaplasmosis, West Nile virus, malaria, and coccidioidomycosis closely mirrored national CDC surveillance trends, validating the EHR-based approach.

The dashboard enables exportable, six-page per-disease reports covering temporal trends, choropleth maps, regional analysis, and CDC benchmarking. Static reports with summary graphs, incidence visuals and SMR tables are presently available. We are integrating demographic stratification of incidence rates, targeting implementation in April 2026.

NEXT STEPS

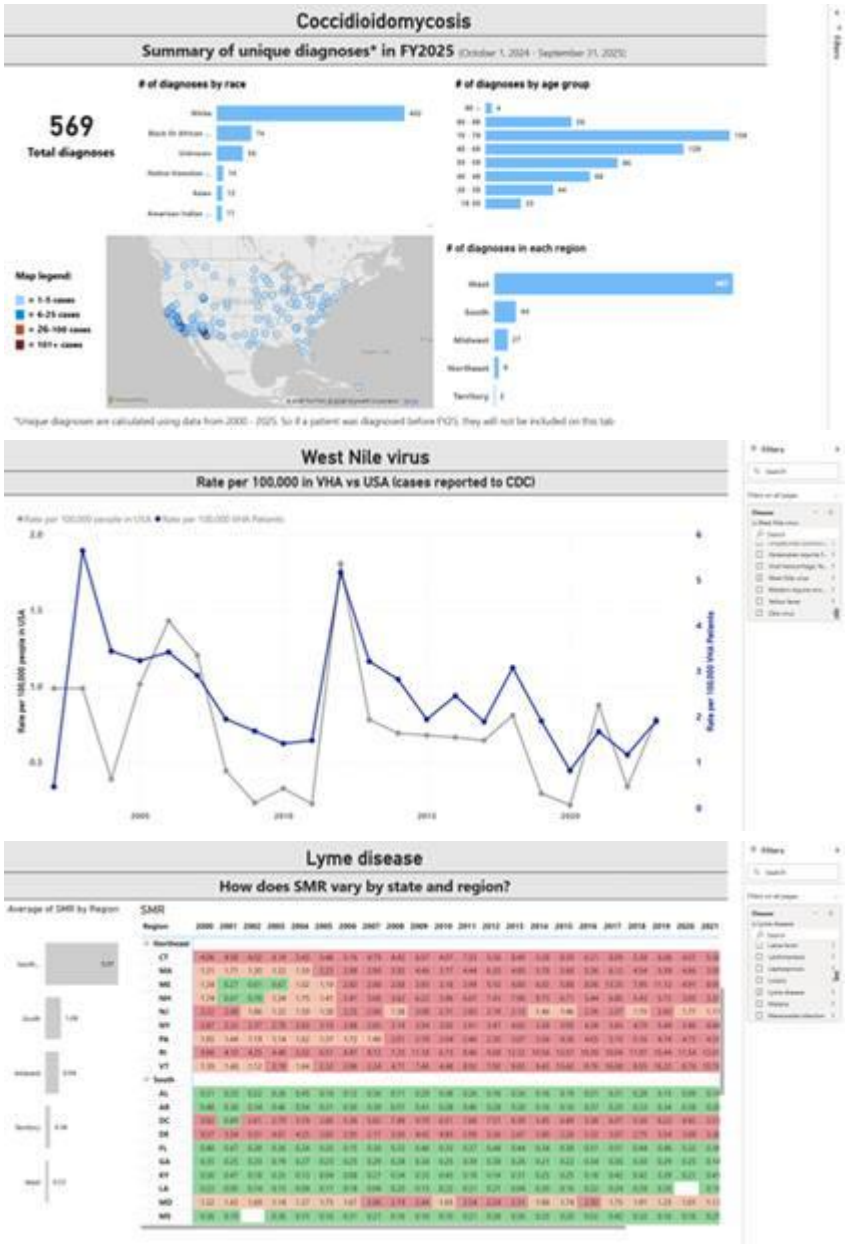
In March 2026, we received approval for prospective biospecimen collection through the VA Science and Health Initiative to Combat Infectious and Emerging Life-Threatening Diseases (VA SHIELD) biorepository—currently holding 50,000+ samples from 12 collection sites—providing a pathway for molecular validation of EHR-identified cases.

Our surveillance is also being enhanced through incorporation of clinical outcomes (e.g. hospitalization and death within 60 days of diagnosis) as well as laboratory (LOINC) and pharmacy data to validate ICD-derived incidence.

CONCLUSIONS

VHA's standardized EHR infrastructure constitutes a scalable, nationally distributed One Health sentinel surveillance network capable of detecting VBZED emergence and geographic expansion in near-real time.

Integration with the VA SHIELD biorepository creates a translational feedback loop from administrative case identification to molecular confirmation, which may otherwise be unavailable per standard of care.



EFSA's Horizon Scanning for Plant Health: Advancing OneHealth for Enhanced Early Warning

Sara Valentina TRAMONTINI (1), Adamo UBOLDI (2), Caroline BELLENOT (3), Maria RIBAYA MUNOZ (1), Florian KUNTZE (1), Zoe MARMIER (3), Sybren VOS (1)

1: European Food Safety Authority, Italy; 2: Joint Research Center of the European Commission, Italy; 3: French Agency for Food, Environmental and Occupational Health & Safety

Background

The European Food Safety Authority (EFSA) is mandated by the European Commission since 2016 to perform horizon scanning in support to early warning on plant pests. This task requires the use of scraping tools integrated by experts curation of results. Here, the key achievements of this project are presented, whose most recent and relevant expression is the constitution of the first community of plant health within the EIOS system. This represents an essential occasion to conduct horizon scanning in an integrated manner across plant, animal, and human health.

Methods

EFSA's horizon scanning is ensured by a continuous, automated workflow using the Epidemic Intelligence from Open Sources (EIOS) tool. The system includes more than 26,000 keywords and reviews nearly 32,000 information sources in 79 languages. EIOS initiative is sustained by a long-standing collaboration between the WHO and the Joint Research Centre (JRC) covering human, animal and, now, plant health. EFSA, together with ANSES, reviews the signals and prioritise them after experts' validation, in order to deliver targeted signals. The refined results are summarised in monthly newsletters and on an interactive dashboard, combined with risk screening indicators (PeMo method) in case of pest species 'new' to the EU phytosanitary framework, to timely inform EU risk managers about emerging risks. Between 2024 and 2026 EFSA and ANSES coorganised four international workshops dedicated to the horizon scanning activity and capacity building: these events fostered knowledge exchange and methodological refinement, bringing together risk managers, scientific experts, and OneHealth stakeholders.

Results

By the end of 2024, drawing on eight years of experience and feedback from its stakeholders, EFSA supported the constitution of the EIOS Plant Health Community. The launch of this joint initiative by EFSA, CABI, and JRC, established a collaborative platform for global knowledge sharing—open to institutions addressing phytosanitary risks and OneHealth challenges. The February 2025 workshop empowered risk managers to integrate horizon scanning into risk prioritisation, while the December 2025 workshop explored key risk drivers (e.g. climate change, global trade, ecological shifts), informing future research and early warning strategies that impact interconnected health domains. The next steps envisage the definition of a proper ontology to connect plant health with the other domains, the combination of new tools and datasets and the expansion of the activity toward foresight practices.

Conclusions

The establishment of the EIOS Plant Health Community marks a significant step in advancing the OneHealth agenda, enabling the sharing of methodologies, data, and tools across disciplines and borders. Ongoing refinement of risk screening and community engagement are expected to empower national and international authorities, enhance phytosanitary preparedness, and support evidence-based policy and research, reflecting the OneHealth principle of collaborative, holistic risk management.

Metagenomics, Wastewater, and One Health: A Non-Invasive Pan-Pathogen Approach for Zoonotic Surveillance in LMICs

Matt PARKER (1), Nisachon APINDA (2), Terdsak YANO (2), Kanokwan SANGKAKAM (2), Anucha MUENTHAISONG (2), Angkana HUANG (3), Sarah OLSON (4), Nathan GRUBAUGH (5), Karyna ROSARIO (7), **Juliana GIL** (6), Patipat SUSUMPOW (1)

1: Opendream, Thailand; 2: Faculty of Veterinary Medicine, Chiang Mai University, Thailand; 3: Department of Genetics, University of Cambridge, Cambridge, UK; 4: Wildlife Conservation Society, Health Program, Bronx, NY, USA; 5: Department of Epidemiology of Microbial Diseases, Yale School of Public Health, CT, USA; 6: Rapid Response group, Chan Zuckerberg Biohub San Francisco, CA, USA; 7: Chan Zuckerberg Initiative, Redwood City, CA, USA

Background

Early detection of emerging and zoonotic viral pathogens is critical for pandemic prevention, yet metagenomic surveillance remains limited by cost and sensitivity, particularly in complex, high-background samples like wastewater. Wastewater has shown promise in LMICs as an equitable approach to pathogen surveillance, but the fragmentation of genomes in wastewater poses considerable challenges for genomic sequencing. While environmental surveillance has expanded rapidly in human health contexts, agricultural and animal-associated environments—key interfaces for zoonotic spillover—remain underrepresented. Our broad objective is to implement affordable and effective early-warning systems which can detect outbreaks of zoonotic disease at animal-human interfaces in high-risk regions of the world before they spread to humans. Our specific objective is to design and evaluate the optimal protocol for researchers in LMICs to implement metagenomic surveillance of zoonoses for high background, low target complex samples collected from rural non-sewered settings.

Methods

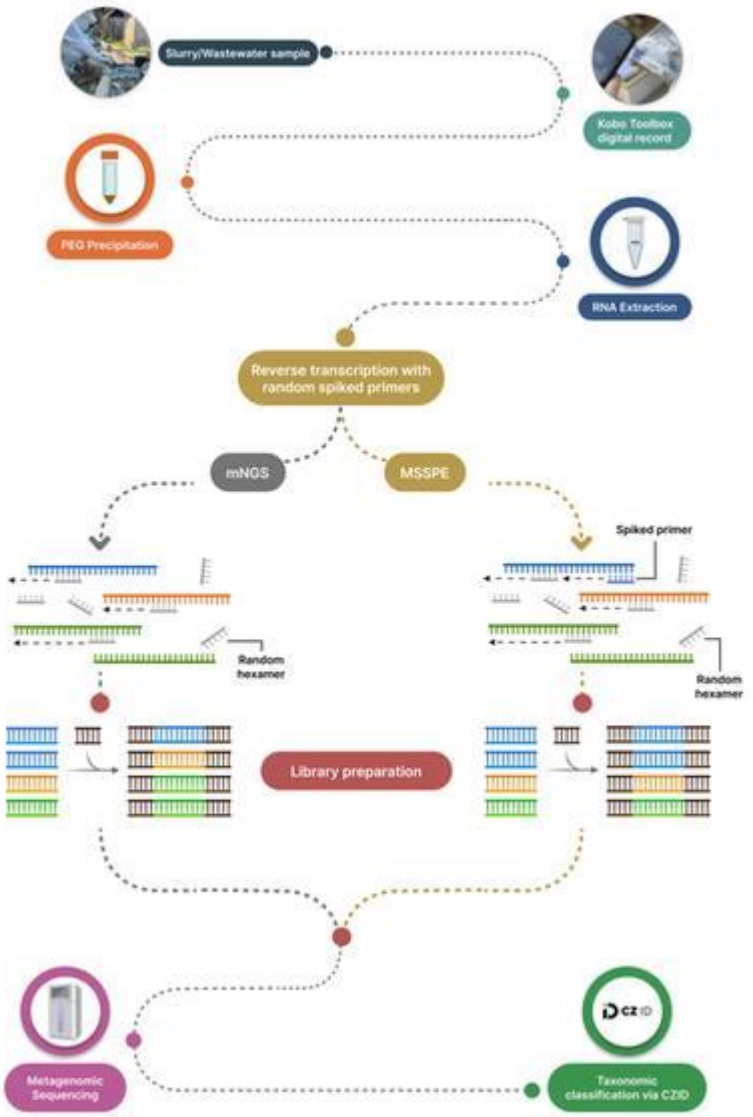
We developed Open-MSSPE-Design, a non-invasive assay for detecting low abundance, high priority DNA and RNA pathogens from wastewater using shallow metagenomic sequencing. We generated fifteen primer sets targeting high-priority DNA and RNA viral pathogens affecting human and animal health in Southeast Asia using our open-source primer design algorithm. We compared performance of untargeted metagenomic sequencing (mNGS) to Metagenomic Sequencing with Spiked Primer Enrichment (MSSPE). Farm slurry and agricultural wastewater samples were collected from mixed-livestock smallholder farms in Northern Thailand. Samples were prepared for untargeted mNGS or enriched via MSSPE, sequenced using Illumina sequencers, and analyzed using Chan Zuckerberg ID (CZ ID).

Results

We detected multiple high-risk DNA and RNA viruses in wastewater samples from smallholder farm operations. MSSPE achieved substantial viral enrichment for pathogenic DNA and RNA viruses in both reads and genome coverage, while retaining sensitivity for untargeted pathogens. MSSPE also increased the odds of detecting targeted viruses, with the greatest advantage at shallow sequencing depths where MSSPE required fewer reads to identify targeted viral taxa relative to mNGS.

Conclusion

In this research we demonstrate a new method to improve detection of priority viruses without substantially increasing workflow time or cost. This open-source workflow supports cost-effective metagenomic viral surveillance for resource-constrained settings, providing a non-invasive method for detecting low-abundance viruses. By lowering financial and technical barriers, this approach expands access to viral metagenomics across environmental, agricultural, and potentially clinical contexts. The development of a surveillance approach specifically designed for resource-limited settings addresses a critical gap in global pathogen surveillance infrastructure.



Interoperable Digital Surveillance Tools for One Health Early Warning in Animal Health Systems

Justine ASSENGA (1), Fredrick KIVARIA (2), **Gisela GIOIA** (3), Lisette KOHAGNE TONGUE (4), Crawford REVIE (5), Beatrice MOUILLE (3), Ercole DEL NEGRO (6), Kora Brice LAFIA (7)

1: FAO Tanzania, Tanzania; 2: FAO: Food and Agriculture Organization of the United Nations, Kenya; 3: Food and agriculture organization for the United Nations (FAO), Italy; 4: Food and Agricultural Organisation for the United Nations, Guinea; 5: UN FAO, United Kingdom; 6: IZSAM, Italy; 7: FAO, Democratic Republic of the Congo

Background: Timely detection, verification, and response to animal and zoonotic disease events require surveillance systems that connect community signals, field epidemiology, laboratory diagnostics, public health platforms, and global disease intelligence. Fragmented data flows can delay early warning at the human-animal-environment interface. FAO's Event Mobile Application Plus (EMA-i+) and EMPRES-i+ platforms support countries to digitalize animal health surveillance while maintaining national data ownership. This abstract synthesizes operational experiences from Africa to describe how EMA-i+, EMPRES-i+, AfyaData, DHIS2, SILAB, and global intelligence mechanisms are strengthening One Health surveillance.

Methods: Evidence was drawn from implementation and interoperability use cases in Tanzania, Guinea, Ghana, the Democratic Republic of the Congo (DRC), and EMPRES-i+ operations. Approaches included

cascade training of veterinary and wildlife officers; community-based syndromic reporting through AfyaData; real-time, georeferenced field reporting through EMA-i+; national data management and visualization through EMPRES-i+; bidirectional alert exchange between EMA-i+ and DHIS2; and linkage of field reports with SILAB laboratory workflows. Country platforms were configured for national veterinary services, with decisions on data access and sharing retained by governments. Operational outputs, training records, reported events, and response actions were summarized descriptively.

Results: EMA-i+ deployment improved field reporting capacity and accelerated transmission of standardized animal health information. In Tanzania, 107 district officers from 92 councils across 13 regions were trained through a national cascade model, strengthening reporting from community to national levels and identifying needs for further data management, QGIS, ward-level training, and laboratory interoperability. In Guinea, automated EMA-i+-DHIS2 notifications piloted from October 2025 to February 2026 enabled near real-time cross-sector sharing of 15 suspected human anthrax cases, 13 suspected viral haemorrhagic fever cases, 300 dog bites, and one cat scratch, triggering joint investigations, vaccination, and active surveillance; one event was confirmed as Lassa fever. AfyaData-EMA-i+ interoperability demonstrated how community observations from trained frontline actors can be routed to official veterinary authorities for verification and follow-up. EMA-i+-SILAB interoperability, pilot tested in Ghana in April 2026, created a feedback loop linking outbreak reports, sample tracking, validated diagnostic results, and targeted field investigations. In DRC, EMA-i+ wildlife surveillance supported early reporting of 52 hippopotamus and seven buffalo deaths in Virunga National Park, facilitating anthrax confirmation, WOAH notification, cross-sectoral information sharing, and risk communication.

Conclusions: Across diverse African surveillance contexts, EMA-i+ and interoperable digital tools strengthened early warning by improving timeliness, completeness, and cross-sector use of surveillance data. Connecting community, field, laboratory, public health, national, and global intelligence systems can close critical surveillance loops while respecting country data governance. Sustained impact will require institutional commitment, technical maintenance, workforce training, interoperability standards, and integration into routine One Health decision-making.

TREADS: A Scalable, Interoperable One Health Security Ecosystem for Early Warning and Decision Support

Lauren CHARLES (1,4), Tracey MCNAMARA (2), Louise GRESHAM (3)

1: Pacific Northwest National Laboratory, United States of America; 2: Washington State University Paul Allen School for Global Health, United States of America; 3: Western University of Health Sciences College of Veterinary Medicine, United States of America; 4: PAX sapiens, United States of America

Background: Early detection of threats at the human–animal–environment interface requires integrating health signals across domains. Despite broad consensus on One Health (OH) approaches, biosurveillance data remain fragmented — siloed across jurisdictions and sectors, stored in incompatible formats, and described using inconsistent terminology. These barriers limit cross-sector analytics and early warning for zoonotic spillover events, antimicrobial resistance trends, and environmentally mediated health risks.

Methods: Pacific Northwest National Laboratory (PNNL) developed an interoperable OH security ecosystem built on their Threat Risk Event Analysis, Detection & Surveillance (TREADS) framework. The architecture integrates multisector data while supporting mission-specific platforms for distinct user communities. The National Wildlife Disease Database supports wildlife health monitoring by wildlife agencies and rehabilitation networks; OH-TREADS integrates public, agricultural, wildlife, and environmental health biosurveillance; and MedINT supports medical operations and situational awareness. All platforms operate on a shared standardized data model and analytical infrastructure, enabling interoperability and cross-domain analytics at scale.

Central to the system is a curated OH data model with standardized taxonomies harmonizing key elements including health conditions, clinical signs and syndromes, pathogens and laboratory findings, host species taxonomy, geospatial locations, and event-level metadata encompassing impacts, dynamics, and countermeasures.

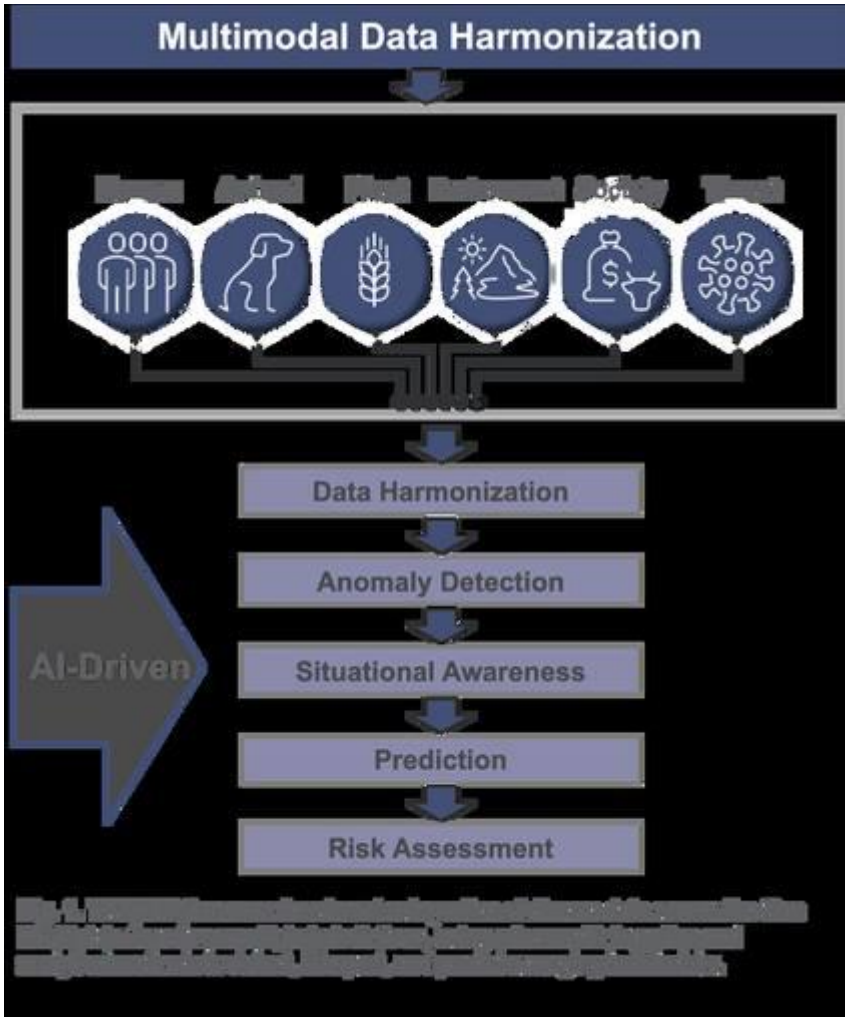
The platform features flexible data onboarding pipelines ingesting both manual and automated submissions across diverse formats, including laboratory reports, agency spreadsheets, structured

databases, and open-source situational reports. PNNL Automated Helpers leverage large language models to extract entities (pathogens, host species, conditions, locations) from semi-structured and unstructured sources, reducing manual curation burden and accelerating integration.

Results: Integrated analytics combine human health data (e.g., influenza surveillance, and notifiable disease systems); animal health data from wildlife and agricultural networks; environmental data (e.g., wastewater) with contextual layers (e.g., climate, land cover, biodiversity and population density) to support machine-learning–based anomaly detection, geospatial risk modeling, and early warning analytics designed to identify emergent signals before they escalate.

Tiered governance preserves data-owner authority while secure collaborative analysis. International engagement through the Global Wildlife Data Sharing Conferences supported by PAX sapiens has advanced shared standards and expanded cross-border wildlife health data exchange. PNNL, Western University of Health Sciences, and PAX sapiens have been established as trusted connectors across 16+ countries with growing partnerships in US, Europe, Canada, and globally.

Conclusions: The TREADS ecosystem demonstrates a scalable model for bridging human, animal, and environmental biosurveillance by harmonizing data standards, leveraging AI for efficient integration, and embedding governance that respects data sovereignty. This work offers a replicable pathway toward integrated OH security infrastructure needed to strengthen global preparedness, early detection, and evidence-informed decision-making.



Biodiversity, Wildlife & Pathogen Interfaces - session 2

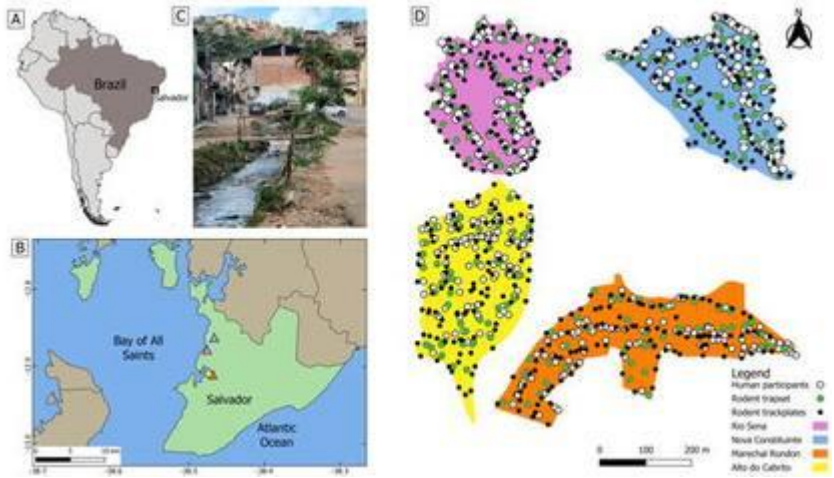
SCS13 · 08:00-08:50 · Auditorium I

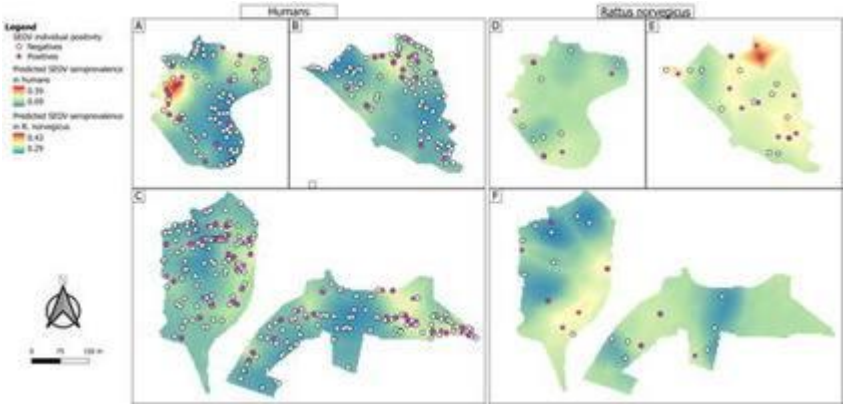
From rats to residents: Orthohantavirus at the human–rodent–environment interface in informal urban settlements in Brazil

Ana Maria BARRETO (1), Hernán D. ARGIBAY (1), Caio G. ZEPPELINI (1,2), Adedayo M. AWONIYI (1), Fábio N. SOUZA (1), Fabiana ALMERINDA G. PALMA (1), Bárbara Inês ARCANJO XAVIER (1), Diogo C.C. SANTIAGO (3), Luciana H.B.V. DE MATTOS (4), Jorlan FERNANDES (4), Mitermayer G. DOS REIS (3,5,6), Max T. EYRE (7), Michael BEGON (8), Renata C DE OLIVEIRA (4), Hussein KHALIL (2), Federico COSTA (1,6)

1: Instituto de Saúde Coletiva, Universidade Federal da Bahia, Salvador, Brazil; 2: Swedish University of Agricultural Sciences, Umeå, Sweden; 3: Faculdade de Medicina da Bahia, Universidade Federal da Bahia, Salvador, Brazil; 4: Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil; 5: Instituto Gonçalo Moniz, Fundação Oswaldo Cruz, Salvador, Brazil; 6: School of Public Health, Yale University, New Haven, Connecticut, USA; 7: London School of Hygiene and Tropical Medicine, London, United Kingdom; 8: University of Liverpool, Biosciences Building, Liverpool, United Kingdom

Background: Urban informal settlements create ecological conditions that intensify interactions between humans, rodents, and the built environment, facilitating zoonotic pathogen transmission. The global spread of Rattus norvegicus and its close association with humans have facilitated the transmission of pathogens such as Orthohantavirus seoulense (SEOV), estimated to affect 30,000 people annually. However, evidence on SEOV prevalence and associated risk factors in urban informal settlements remains scarce. Methods: Using a One Health approach, we integrated human serological data, rodent surveillance, and environmental indicators to investigate SEOV exposure in urban communities. We conducted a cross-sectional study in four urban informal settlements in Salvador city, Brazil. We collected demographic, environmental, and serological data from participating residents and from rats captured during the study. Human and rodent serum samples from these settlements were tested using IgG ELISA. We performed automated model selection to identify the set of variables that best explained SEOV exposure in urban communities. Results: Orthohantavirus antibodies were detected in 32% of rodents (37/117) and 14% of humans (91/646). Rodent seropositivity was associated with higher body weight, female sex, sexual maturity, absence of zoonosis-control visits, and proximity to stored construction materials. Among humans, older age, visible garbage near the household, and employment in construction work were associated with exposure. Conclusions: These findings indicate sustained Orthohantavirus circulation among rats and spillover to humans in urban informal settlements, representing one of the highest human seroprevalence estimates reported in South America. The risk of Orthohantavirus infection is not only biological but also shaped by environmental and socioeconomic conditions that increase human exposure in vulnerable communities. From a One Health perspective, these results highlight how interactions between human populations, synanthropic rodents, and degraded urban environments drive zoonotic transmission. Our findings underscore the urgent need for integrated surveillance and cross-sectoral interventions that simultaneously address rodent ecology, environmental management, and social determinants of health in vulnerable urban settings.





Land-use change restructures mammal communities and reshapes zoonotic pathogen dynamics in Amazonian landscapes

Maricruz JARAMILLO (1), Gabriela ALIAGA SAMANEZ (2), Luz Dary ACEVEDO (1), Fabián BELTRÁN-SAAVEDRA (1), Erika GARCÍA-BONILLA (3), Glenda AYALA (1), Charles C.Y. XU (2,4), Mathieu PRUVOT (4), Robert WALLACE (1), German FORERO (1), Mailyn GONZALEZ (3), Lucy KEATTS (1), Sarah OLSON (1), Alex GREENWOOD (2)

1: Wildlife Conservation Society; 2: Leibniz Institute for Zoo and Wildlife Research; 3: Instituto de Investigación de Recursos Biológicos Alexander von Humboldt; 4: University of Calgary, Faculty of Veterinary Medicine

Background

Preventing future pandemics requires understanding pathogen dynamics at their source, including wildlife hosts and environmental drivers of spillover. Rapid land-use change (LUC) across the Amazon is transforming biodiverse forests into fragmented landscapes dominated by agriculture and cattle ranching. These shifts alter wildlife communities and create new interfaces among wildlife, domestic animals, and humans, potentially increasing zoonotic disease risk. Despite recognition that LUC contributes to disease emergence, the ecological mechanisms linking habitat degradation, wildlife hosts, and pathogen circulation remain poorly understood. We investigated whether deforestation alters wildlife distributions and interactions, reshaping host communities and influencing pathogen circulation.

Methods We conducted ecological and molecular surveys across rapidly changing Amazonian landscapes in Colombia and Bolivia. Using a space-for-time design, we sampled conserved forest, recently deforested areas, and transformed habitats, during both wet and dry seasons. Bats and rodents were surveyed to quantify species richness, abundance, and community composition, using hierarchical models to account for imperfect detection and variation in sampling effort. Biological samples were tested with molecular techniques, including PCR-based pathogen screening, to characterize viral diversity and prevalence.

Results Bats showed consistent responses to habitat degradation, with species richness and abundance declining from intact forest to disturbed and transformed habitats. Occupancy models indicated lower probabilities of species occurrence in degraded habitats, while detection probability varied with survey effort. Current analyses of rodent communities suggest more variable responses among sites, showing no clear patterns across habitat zones, suggesting that broader landscape context shapes community structure. Initial pathogen screening revealed heterogeneous viral prevalence and host-specific variation. In the Colombian datasets, viral prevalence in bat communities varied across habitat zones and seasons, with patterns differing among virus groups, suggesting that environmental conditions and habitat characteristics may influence viral circulation. In contrast, rodent communities showed no clear differences in viral prevalence across habitat zones or seasons for the pathogens evaluated.

Conclusions Land-use change restructures wildlife host communities, though effects vary by taxonomic group and landscape context. Shifts in species composition and interactions may influence host–pathogen dynamics, with bats particularly responsive to habitat conditions. Variation in viral prevalence among bat communities highlights the role of environmental and habitat factors in pathogen circulation, whereas rodent pathogens appear less affected by local habitat changes. Integrating ecological community analyses with pathogen detection provides a framework for understanding how environmental transformation shapes disease dynamics. Incorporating these ecological drivers into land-

use planning and conservation strategies is critical to anticipate and mitigate zoonotic spillover risks in rapidly changing tropical regions.

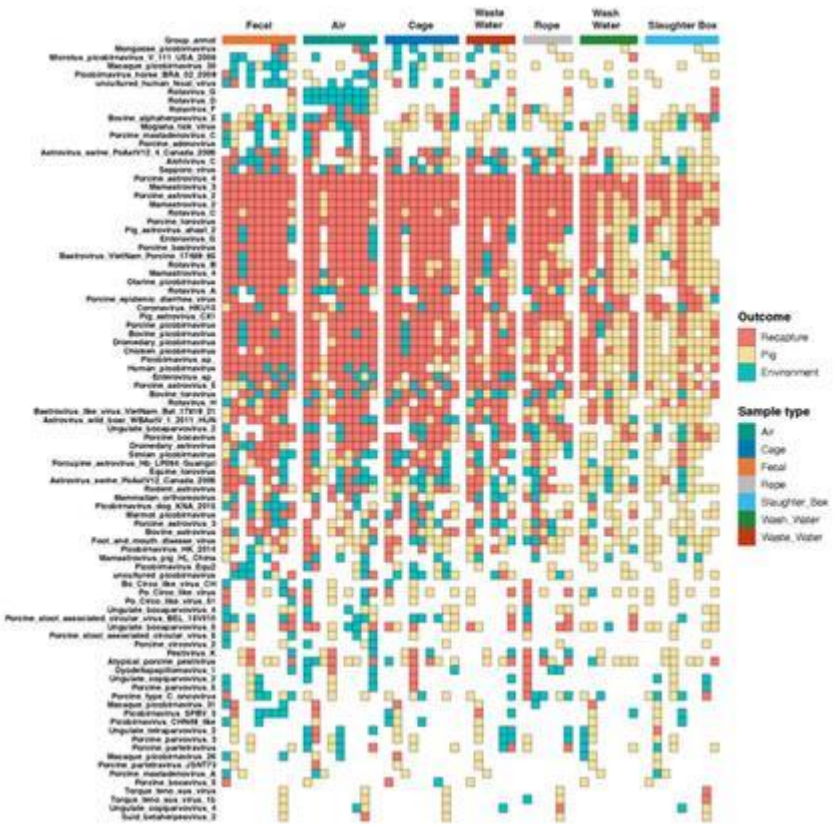
Air sampling coupled with metagenomics accurately captures zoonotic virus diversity emerging from pig slaughterhouses in Cambodia

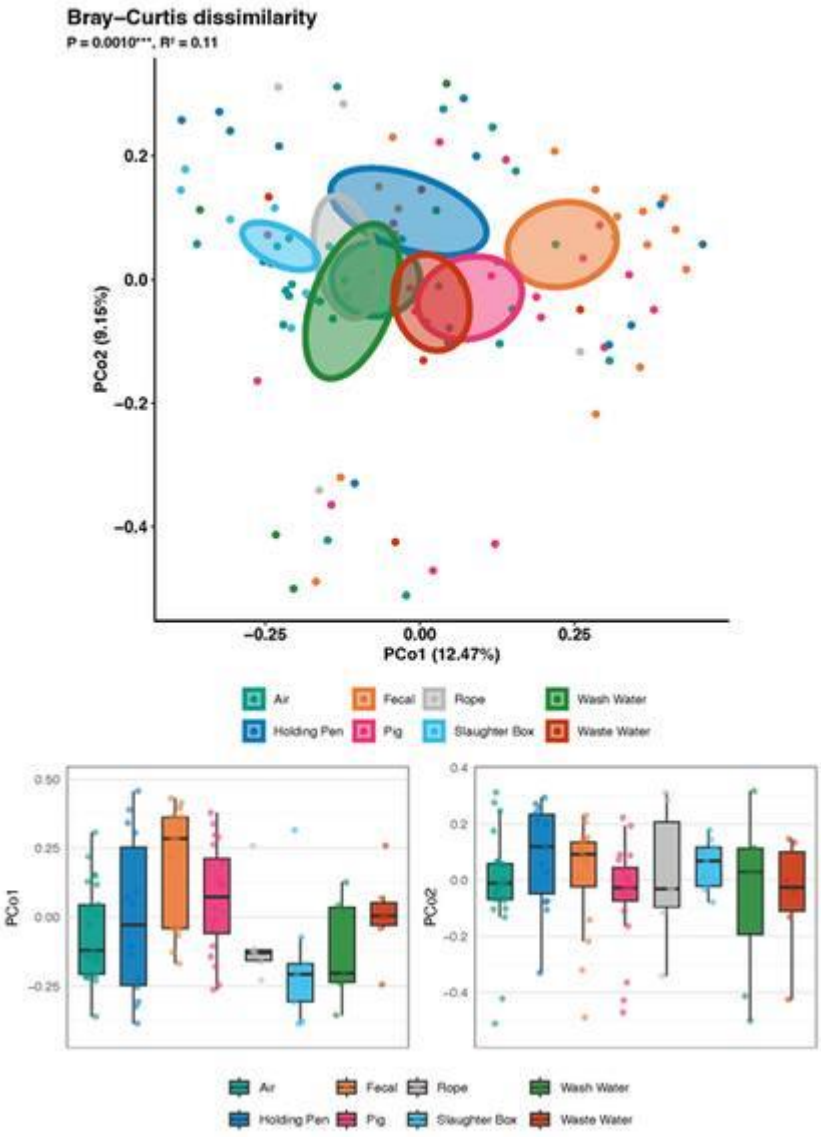
Peter CRONIN (1), Vireak HEANG (2), Jurre SIEGERS (2), Dolyce LOW (1), Yvonne SU (1), Gavin SMITH (1), Erik KARLSSON (2)

1: Programme in Emerging Infectious Diseases, Duke-National University of Singapore Medical School, Singapore; 2: Virology Unit, Institute Pasteur du Cambodge, Pasteur Network, Phnom Penh, Cambodia

The global intensification of swine production has increased the risk of zoonotic virus spillover to humans. Effective surveillance at human-swine interfaces is essential to enhance pandemic preparedness, particularly in Southeast Asia which is marked by the prevalence of both endemic and emerging infectious diseases of One Health importance. To date, the majority of surveillance efforts rely on the sampling of individual pigs which is time-consuming, expensive, and poses significant occupational safety risk. Recently, environmental metagenomics has emerged as a powerful strategy to complement traditional surveillance methods by providing broader coverage and more comprehensive pathogen detection. Here, we assessed the performance of metagenomics on environmental samples (ES) versus nasal swabs from pigs for detecting viral pathogens at two slaughterhouse locations in Cambodia. Sampling was conducted across 9 separate visits between November 2022 and March 2023. ES, including air, holding pen swabs, faeces, carcass wash water, waste water, rope and slaughter box swabs were collected alongside samples from pigs. Overall, we found a clear association between viruses identified from pig swabs and those detected in the surrounding environment. ES demonstrated high sensitivity in recovering important swine pathogens including those from virus families *Astroviridae*, *Coronaviridae*, *Reoviridae* and *Orthomyxoviridae*. Air samples in particular consistently recaptured most of the virus diversity observed in pigs while also detecting numerous additional viruses missed by traditional sampling methods. Species-level profiling and beta-diversity confirmed that other ES types including holding pen swabs, faeces and rope, also performed well, exhibiting high similarity having to pig swabs and sharing a high number of the same species. Viral contigs from ES showed high sequence similarity and uniform coverage relative to pig swab contigs when aligned to the same genes. Our findings show metagenomics on ES can effectively augment traditional surveillance, offering broader coverage and improved pathogen detection. This approach could be pivotal for mitigating zoonotic spillover and enhancing pandemic preparedness.

Mongoose_picobirnavirus
Microtus_picobirnavirus_V_111_USA_2008
Macaque_picobirnavirus_30
Picobirnavirus_horse_BRA_02_2009
uncultured_human_fecal_virus
Rotavirus_G
Rotavirus_D
Rotavirus_F
Bovine_alphaherpesvirus_5
Mogiana_tick_virus
Porcine_mastadenovirus_C
Porcine_adenovirus
Astrovirus_swine_PoAstV12_4_Canada_2006
Aichivirus_C
Sapporo_virus
Porcine_astrovirus_4
Mamastrovirus_3
Porcine_astrovirus_2
Mamastrovirus_2
Rotavirus_C
Porcine_torovirus
Pig_astrovirus_ahast_2
Enterovirus_G
Porcine_bastrovirus
Bastrovirus_VietNam_Porcine_17489_85
Rotavirus_B
Mamastrovirus_4
Otarine_picobirnavirus
Rotavirus_A
Porcine_epidemic_diarrhea_virus
Coronavirus_HKU15
Pig_astrovirus_CX1
Porcine_picobirnavirus
Bovine_picobirnavirus
Dromedary_picobirnavirus
Chicken_picobirnavirus
Picobirnavirus_sp_
Human_picobirnavirus
Enterovirus_sp_
Porcine_astrovirus_5
Bovine_torovirus
Rotavirus_H
Bastrovirus_like_virus_VietNam_Bat_17819_21
Astrovirus_wild_boar_WBAstV_1_2011_HUN
Ungulate_bocaparvovirus_2
Porcine_bocavirus
Dromedary_astrovirus
Simian_picobirnavirus
Porcupine_astrovirus_Hb_LP084_Guangxi
Equine_torovirus
Astrovirus_swine_PoAstV12_Canada_2006
Rodent_astrovirus
Mammalian_orthoreovirus
Picobirnavirus_dog_KNA_2015
Marmot_picobirnavirus
Porcine_astrovirus_3
Bovine_astrovirus
Foot_and_mouth_disease_virus
Picobirnavirus_HK_2014
Mamastrovirus_pig_HL_China
Picobirnavirus_Equ2
uncultured_picobirnavirus
Bo_Circo_like_virus_CH
Po_Circo_like_virus
Po_Circo_like_virus_51
Ungulate_bocaparvovirus_4
Porcine_stool_associated_circular_virus_BEL_15V010
Ungulate_bocaparvovirus_5
Porcine_stool_associated_circular_virus_5
Porcine_circovirus_2
Pestivirus_K
Atypical_porcine_pestivirus
Dyodeltapapillomavirus_1
Ungulate_copiparvovirus_2
Porcine_parvovirus_5
Porcine_type_C_oncovirus
Macaque_picobirnavirus_31
Picobirnavirus_SPBV_3
Picobirnavirus_CHN49_like
Ungulate_tetraparvovirus_2
Porcine_parvovirus_3
Porcine_partetravirus
Macaque_picobirnavirus_26
Porcine_partetravirus_JSNT73
Porcine_mastadenovirus_A
Porcine_bocavirus_5
Torque_teno_sus_virus
Torque_teno_sus_virus_1b
Ungulate_copiparvovirus_4
Suid_betaherpesvirus_2
Outcome
Recaptured
Environment
Pig


Fecal
Air
Cage
Waste Water
Rope
Wash Water
Slaughter Box
Outcome
Recapture
Pig
Environment
Sample type
Air
Cage
Fecal
Rope
Slaughter_Box
Wash_Water
Waste_Water



Health hazards in Peru's wildlife trade: Toward Operationalizing One Health

Paulo COLCHAO-CLAUX (1), Carlos CALVO-MAC (2), Micaela DE LA PUENTE-LEON (2,3), Jorge Luis MARTINEZ (1), Rosa VENTO (1), Yovana MURILLO (4), Lucy KEATTS (5)

1: Wildlife Conservation Society, Peru; 2: ONG ConservAccion; 3: Universidad San Ignacio de Loyola; 4: Wildlife Conservation Society, Andes Amazonia Orinoquia; 5: Wildlife Conservation Society, Health Program

Background: The ability of pathogens to infect multiple hosts is influenced by interspecific contacts, environmental alterations, and pathogen evolution. Legal and illegal wildlife trade increases interspecific exposure and facilitates pathogen introduction and dissemination, creating high-risk interfaces for animal, human and ecosystem health. In Peru, sanitary risks along wildlife trade remains underestimated and undermanaged despite the large number of traded and trafficked wildlife. Between 2011–2020 authorities recorded 8,731 seizures involving 53,908 live wildlife. This study aimed to generate evidence-based recommendations to reduce health risks associated with wildlife trade and management.

Methods: We compiled, systematized, and analyzed information on wildlife trade and health in Peru from scientific and gray literature, institutional databases, and interviews. Analyses covered (i) national and international regulations governing trade; (ii) international trade flows and tariff traceability; (iii) sanitary requirements for export, import, and captivity; (iv) documented detections of etiologic agents in free-ranging, seized, or captive wildlife; and (v) wildlife pathogen diagnostic capacity and laboratory gaps.

Etiologic agents were prioritized according to transmission probability, relevance, local presence, and policy considerations. Based on these findings, we developed proposals to strengthen health management across wildlife trade and rescue.

Results: We identified 166 regulatory documents related to international trade and 121 relevant to rescue centers. From 2015–2024, 1,190 exports were documented (7,827 products), dominated by reptiles and capybaras; an additional 105 primates were exported by April 2025. Under-reporting and low data specificity limit traceability and sanitary oversight. Across the literature and records, 187 pathogen-detection events were identified in wildlife, involving 116 etiological agents, with most evidence from the Amazon and Lima regions. We cataloged 138 laboratories with uneven certification, quality assurance, and diagnostic capacity. Prioritization highlighted pathogens of concern: rabies virus, *Leptospira spp*., influenza A (HPAI), *Mycobacterium spp*., *Brucella spp*., *Salmonella spp*., *Echinococcus spp*., and *Campylobacter spp*. Responsibilities among authorities for wildlife health remain unclear, and requirements are inconsistent across regions. Biosafety practices varied across actors and facilities; critical high-risk disease transmission nodes were identified across trade and rescue operations, and limited traceability constrains risk assessment and management.

Conclusions: Wildlife trade and trafficking in Peru create high-risk interfaces for pathogen transmission affecting animal, human and ecosystem health. We recommend institutionalizing integrated One Health surveillance, clarifying the competent sanitary authority for wildlife, and standardizing minimum sanitary requirements for export and import. Biosafety and traceability protocols strengthened and formalized across trade and rescue processes. Expanding the national diagnostic network through inter-institutional agreements would improve surveillance and risk assessment capacity. Finally, strengthening rescue centers as integrated pathogen-surveillance nodes with clear health-management guidelines and sustained financing is critical. These findings highlighted the importance of coordinated wildlife health surveillance systems embedded within One Health platforms to prevent infectious diseases at the source.

Preparedness, Resilience & Economic Evaluation

SCS15 · 11:00-12:30 · Auditorium I

What surveillance misses: indigenous disease knowledge and ontologies could enable early detection of emerging diseases in remote rural areas

Peregrine ROTHMAN-OSTROW (1), James WOOD (1), Jonathan RUSHTON (2)

1: University of Cambridge, United Kingdom; 2: Universty of Edinburgh, United Kingdom

Introduction: Infectious diseases that pose threats to global trade and biosecurity elicit swift political attention and resource mobilisation. The COVID-19 pandemic brought the risk of pathogen emergence and spillover from animals into public dialogue, and efforts to strengthen surveillance for early detection of novel diseases in remote rural areas is a renewed priority for global health security. Remote rural areas typically fall outside the bounds of health systems infrastructure, rendering passive surveillance frameworks, effectively moot. Integrated One Health approaches to syndromic surveillance, grounded in training community representatives to identify and report externally defined observable signs of prioritised diseases, have been promoted as a pragmatic solution. While such approaches may improve identification of recognised events, they are far less equipped to capture unanticipated or ambiguous indicators that do not conform to prescribed reporting frameworks. We present findings from a study conducted among Maasai pastoral communities that examined how locally constituted ways of identifying, distinguishing, and labelling patterns of illness, which may diverge from biomedical disease categories, could provide early indicators that remain otherwise invisible under contemporary surveillance frameworks.

Methodology: We undertook an 8-month study in a remote rural area in southwestern Kenya, using cattle as a case study species. Following an ethnographic approach, semi-structured interviews and participatory methods were employed. Thematic analysis was undertaken in MAXQDA.

Results: Maasai pastoralists organise knowledge of cattle diseases through locally situated indigenous ontologies which conceptually link clinical signs, transmission patterns, ecologies, and postmortem findings. Disease recognition follows a logic of interpretation, grounded in the observation of animals, landscapes, vectors, and seasons, in the context of lived experiences and risk. Risk perceptions are driven by the intrinsic value and individuality ascribed to cattle which governs how people notice, respond to, and conceptualise diseases as threats. Maa names assigned to patterns of illness foreground salient attributes or peculiarities that differentiate diseases. These knowledge systems are adaptive and context-specific, shaped by local ecologies, shared histories, and dialects across geographies. Thus, indigenous language disease ontologies, which function as a system of pattern recognition, offer pivotal insights for contextually relevant disease surveillance, outbreak response, and health service delivery.

Conclusion: Indigenous disease ontologies are sophisticated knowledge frameworks that offer crucial insight into how communities recognise, interpret, and respond to disease. Current means of engaging communities, even those that integrate participatory methods, often adopt top-down approaches from positions of biomedical hierarchy; this delegitimises local knowledge, priorities, and framings of disease. Raising issues of equity and inclusion, this fundamentally weakens capacity to detect and prevent epidemics. We suggest that recognising and engaging with indigenous disease ontologies as legitimate, valuable knowledge systems, creates opportunities for bidirectional knowledge exchange between communities and scientists, improving equitable engagement, while strengthening early detection and response to emerging threats.

Source control or downstream prevention? A One Health cost-effectiveness analysis of rabies interventions

Martha M LUKA (1), Zinia Thajudeen NUJUM (2), Dan HAYDON (1), Elaine FERGUSON (1), Harikumar S (3), Miqdad ASARIA (4), Rony Ray JOHN (5), Katie HAMPSON (1)

1: University of Glasgow, United Kingdom; 2: Kerala University of Health Sciences, Kerala, India; 3: Directorate of Health Services, Kerala, India; 4: London School of Economics and Political Science, United Kingdom; 5: Directorate of Animal Husbandry, Kerala, India

Background: Rabies kills an estimated 59,000 people annually, with dogs responsible for 95% of human cases. Effective interventions exist across the human-animal interface: mass dog vaccination (MDV) interrupts transmission at the source, post-exposure prophylaxis (PEP) protects individuals after exposure, and pre-exposure prophylaxis (PrEP) primes immunity before exposure. Despite this toolkit, human rabies persists even in settings with strong health systems. Kerala, India, provides PEP free of charge to up to 940,000 people annually, with over 90% regimen completion rates, but reported 5–33 human rabies deaths each year between 2012 and 2025. We evaluated the comparative cost-effectiveness of MDV, PEP schedule optimisation, and routine childhood PrEP to inform resource allocation in support of WHO's goal to end dog-mediated human rabies deaths.

Methods: We adapted a probabilistic decision-tree model to simulate rabies transmission and prevention in Kerala over a 10-year horizon (2026–2035), capturing dog-to-human transmission, healthcare-seeking, and PEP and PrEP uptake and adherence. The model was calibrated against Kerala surveillance data. We evaluated 12 intervention scenarios varying MDV coverage in owned and unowned dogs, and contrasted PEP and PrEP regimens. Each scenario was run with 1,000 stochastic realisations. We compared rabies deaths, deaths averted relative to a no-intervention counterfactual, and average cost-effectiveness ratios expressed as cost per quality-adjusted life year (QALY) gained, from the government healthcare provider perspective.

Results: Under the status quo, 309 rabies deaths (95% prediction intervals (PI): 144–525) were projected over 10 years at a total programme cost of US$49 million, with PEP accounting for 91% of costs and MDV driving 76% of deaths averted. Scaling unowned dog vaccination to 70% coverage reduced deaths by 89% to 33 (95% PI: 9–92) over 10 years, but annual deaths to almost zero from year four onwards, at US$97 per QALY gained. Introducing routine childhood PrEP under any regimen added US$11–36 million in costs while reducing cumulative deaths by fewer than 12 over the 10 years, while uncertainty intervals overlapped with the status quo. Adopting WHO's abbreviated 1-week PEP schedule was cost-saving relative to India's current 4-dose regimen, saving US$6 million over 10 years with equivalent mortality outcomes. If PrEP investment displaced MDV funding, deaths increased relative to the status quo. Sensitivity analyses confirmed MDV coverage and healthcare-seeking as dominant determinants of mortality, with PrEP coverage having minimal impact across a wide range of parameter values.

Conclusion: In a One Health framework, intervening at the animal reservoir through MDV substantially outperforms human-directed downstream interventions in both epidemiological impact and cost-effectiveness. Even in a setting with exemplary PEP delivery, unvaccinated dogs remain the proximate driver of human deaths. Rabies elimination requires prioritising source control, and PrEP should not be considered where it competes with MDV for limited resources.

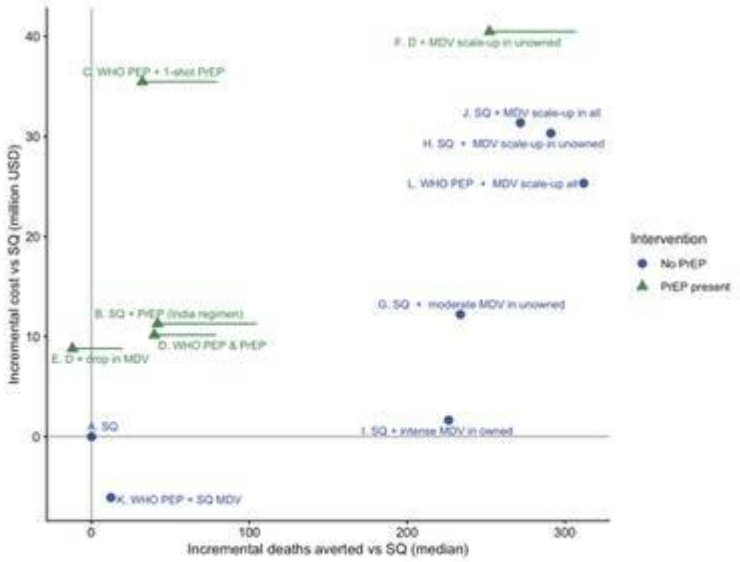


Figure 1. Cost-effectiveness plane comparing rabies prevention strategies relative to the status quo in Kerala, India (2026–2035). Each point represents a scenario, plotted by the incremental median number of deaths averted (x-axis) and the incremental programme cost (y-axis), relative to the status quo. Blue circles indicate scenarios without pre-exposure prophylaxis (PrEP) and green triangles indicate scenarios with PrEP. For PrEP scenarios, the green horizontal line shows the range of incremental deaths averted when the assumed effectiveness of PrEP in the absence of subsequent PEP (*PrEP_effectiveness*) is varied from 0 to 1, holding all other parameters constant; the point corresponds to the base-case assumption (*PrEP_effectiveness* = 0).

Abbreviations: SQ = status quo, MDV = mass dog vaccination, PEP = post-exposure prophylaxis, PrEP = pre-exposure prophylaxis, WHO = World Health Organisation

Strengthening Collaborative Systems to Address Local to Global One Health Challenges: Systems Mapping to Support One Health and Sustainable Development Goals Implementation

Katey PELICAN (1), Tracey DUTCHER (2)

1: University of Hawaii, United States of America; 2: Office of Health Security, Department of Homeland Security, United States of America

Background: The One Health Systems Mapping and Analysis Resource Toolkit (OH-SMART) was developed in 2014 through a collaboration between the University of Minnesota and the U.S. Department of Agriculture. Its purpose is to support participatory decision-making among government agencies and improve collaboration for the prevention, detection, and control of infectious disease threats.

Methods: The OH-SMART toolkit consists of six steps, drawing from social science and business improvement methodologies:

Stakeholder Mapping and Policy Field Analysis

Semi-structured Interviews and Qualitative Analysis

Multi-sectoral Participatory Process Mapping

Collaborative System Analysis and Identification of Pain Points

Solutions Identification

Action Planning

These steps are highly adaptable and have been used to address a wide range of complex challenges globally. A key component of OH-SMART's success is its paired Implementor training, which builds facilitation skills as a core competency for One Health program development. Trainees who complete implementer training and support country-level implementation can advance to become Master Facilitators.

Results: Since its launch in 2014, OH-SMART has been applied in 29 countries at local, sub-national, national, and international levels. Its use has expanded beyond infectious disease to include:

Indigenous communities, improving collaboration for food security, youth engagement, and wildlife co-stewardship

Non-governmental organizations and industry partners, supporting seed and medical device value chains

Intergovernmental agencies, addressing cross-border One Health and Sustainable Development Goal (SDG) challenges

Academic institutions, integrating One Health competencies into undergraduate, graduate, and continuing education programs

Government agencies at various levels, enhancing collaborative systems for disaster preparedness, community resilience, climate and health, antimicrobial resistance, zoonotic and vector-borne diseases, food access, and environmental contaminants

To date, over 200 professionals have been trained in OH-SMART, and at least 12 Master Facilitators in 7 countries across 4 continents are using the toolkit to support One Health implementation in their regions.

Conclusions: This presentation will highlight key results and lessons learned on how organizations and institutions can strengthen One Health collaboration and better manage complex threats. It will address strategies for improving coordination both horizontally among peer agencies and vertically across organizations, enabling effective management of challenges from the local to the global level.

Educational Outcomes:

Comprehend Systems Mapping for One Health: Participants will understand the principles and steps of the OH-SMART toolkit and how systems mapping can be used to analyze and improve collaboration in One Health initiatives.

Identify and Address Collaboration Challenges: Participants will be able to recognize common barriers and pain points in multi-sectoral One Health collaborations and propose evidence-based solutions to overcome these challenges.

Translate Workshop Learning into Practice: Participants will leave with practical skills and actionable strategies to strengthen One Health systems in their own contexts, supporting the implementation of One Health and Sustainable Development Goals at various levels.

Responding to Clade Ib Mpox in Africa: Vaccine Strategy During Sustained Human Transmission

Charles IBENEME (1), Glory ONYEUGO (1), Yap BOUM (1), Nebiyu DEREJE (1), Lilian MALIRO (2), Ngashi NGONGO (1)

1: Africa Centers for Disease Control and Prevention (Africa CDC), Addis Ababa, Ethiopia; 2: Expanded Programme on Immunization (EPI), Malawi ministry of Health (MOH)

Background The 2024 resurgence of mpox driven by Clade Ib prompted declarations of a Public Health Emergency of Continental Security and a Public Health Emergency of International Concern. Unlike prior outbreaks, vaccines were mobilized within weeks. We describe progress, operational challenges, and policy lessons from Africa's first year of coordinated continental mpox vaccination.

Materials and Methods

We conducted a descriptive analysis of vaccine policy, regulatory processes, allocation decisions, delivery data, pharmacovigilance reports, and monitoring dashboards from August 2024 to December 2025. Data sources included the Continental Incident Management Support Team (IMST), national reports from 16 countries, allocation records, and deployment tracking systems.

Results By December 2025, over 5 million mpox vaccine doses (MVA-BN and LC16m8) had been shipped to 16 African countries. Fourteen countries-initiated vaccination, prioritizing contacts of confirmed cases and other high-risk groups in hotspot areas. Regulatory harmonization through AVAREF accelerated emergency authorizations, while global prequalification enabled multilateral procurement. Gavi-supported operational financing facilitated early rollout; however, broader operational funding gaps affected speed and scale in some settings. Vaccine utilization ranged widely (0–100%), influenced by epidemiologic context, competing outbreaks, surveillance capacity, and stigma affecting case detection and demand generation. No serious vaccine-attributable safety signals were identified.

Conclusions The mpox response demonstrates strengthened regional coordination and faster vaccine access compared to prior emergencies. Future preparedness must integrate regulatory agility, proactive operational financing, surveillance strengthening, and context-specific effectiveness research to optimize outbreak vaccination in Africa.

A BEACON for Novel Disease Threats: Leveraging Artificial Intelligence for Informal Event-Based Outbreak Surveillance

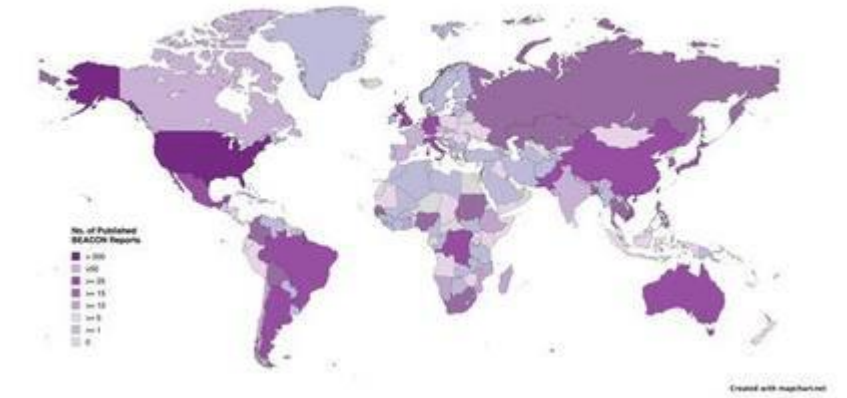
Nahid BHADELIA (1), John BROWNSTEIN (2), Yannis PASCHALIDIS (1), **Larry MADOFF** (1), Britta LASSMANN (1)
1: Boston University, United States of America; 2: Boston Children's Hospital, United States of America

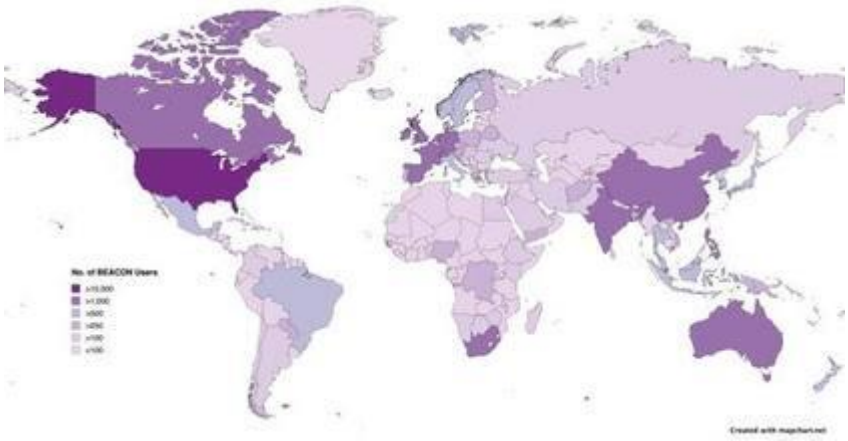
Background: Event-based surveillance systems have proven critical for early detection of disease outbreaks by analyzing informal data sources. The integration of artificial intelligence (AI) offers new opportunities to enhance these capabilities at scale. We describe the Biothreats Emergence, Analysis and Communications Network (BEACON), a novel open access platform that combines a domain-adapted large language model (LLM) within an expert human workflow to provide rapid, contextualized outbreak reporting on both animal and human disease outbreaks across the globe.

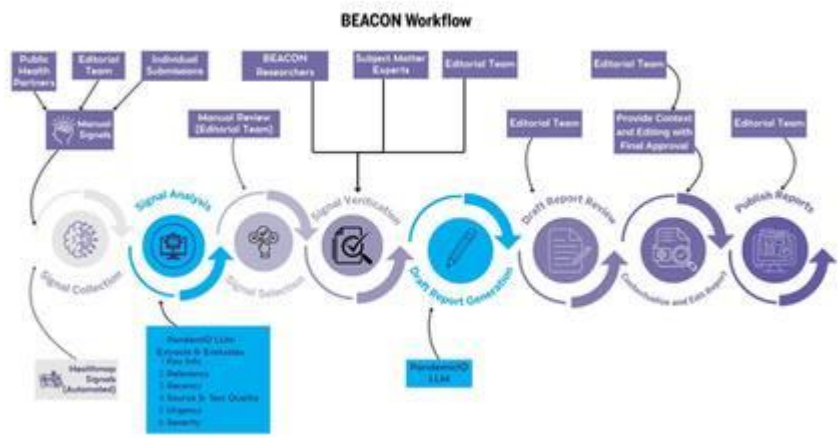
Methods: BEACON utilizes a domain-adapted LLM (PandemIQ), which is specifically trained to understand infectious diseases (both human and animal) and perform information extraction, risk assessment, and preliminary reasoning. The LLM ingests outbreak reports from the web (including from HealthMap) and from the globally based human subject matter experts (SMEs) on the program team. The platform leverages this multidisciplinary and regional expertise of SMEs and outbreak analysts in 14 countries to identify new threats, review LLM outputs, make editorial decisions on reporting, and verify disease signals. The team then uses the LLM to generate draft reports that it edits and contextualizes before publication. BEACON outbreak analysts select signals for reporting when they meet one or more of the following criteria: 1) sporadic cases and “firsts”; 2) unknown diseases; 3) pattern shifts; 4) high-risk events; and 5) under-reported areas.

Results: When evaluated against commercially available LLMs and established baselines, PandemIQ performed better in various tasks on public datasets, including answering questions on reports in the Biomedical Alert News and Disease (BAND) dataset and classifying news snippets in the Multi-label Disease Event Classification dataset. Supported by the PandemIQ's initial categorization and information extraction, the BEACON team of subject matter experts have analyzed over 60,000 signals in just 10 months. The average time from the public posting of a signal to its ingestion in the platform is 6 hours at which point it will be reviewed the same day by an outbreak analyst and, if it meets the reporting criteria, published in a report within 24-48 hours on the BEACON website. BEACON averages 5,000 active users per week with users located in 222 countries and territories. The platform has been adopted by the WHO EIOS initiative and utilized by over 200 hospital systems and local, state, national, and multi-national public health agencies for their disease surveillance.

Conclusions: As of February 2026, BEACON has reported nearly 800 outbreaks in more than 1,800 disease reports, covering nearly 200 diseases and over 100 species in 169 countries and territories. The platform has been adopted by numerous public health agencies showing its early utility for epidemic surveillance efforts. The platform offers a nimble, complementary approach to traditional surveillance by leveraging recent AI advancements while retaining the benefits of informal reporting.







Community-Based Farmer Platforms Improve Livestock Vaccination Uptake, Reduce Losses, and Enhance Wellbeing: a Cluster-Randomized Trial in Ghana

Francis Sena NUVEY (1,2,3), Günther FINK (2), Jan HATTENDORF (2), Tontie Inusah SULBEIN (4), Daniel T. HAYDON (5), Gilbert FOKOU (3), Kennedy Kwasi ADDO (6), Jakob ZINSSTAG (2), Clemence ESSE-DIBBY (3), Bassirou BONFOH (3)

1: Friedrich-Loeffler-Institut, Germany; 2: Swiss Tropical and Public Health Institute, Switzerland; 3: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Côte d'Ivoire; 4: School of Nursing and Midwifery, University of Ghana, Ghana; 5: School of Biodiversity, One Health and Veterinary Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, United Kingdom; 6: Noguchi Memorial Institute for Medical Research, University of Ghana, Ghana

Background: Infectious livestock diseases remain a major constraint to productivity, food security, and farmer wellbeing across sub-Saharan Africa. In Ghana, Contagious Bovine Pleuropneumonia and Peste

des Petits Ruminants have been identified as the diseases with the greatest negative impact on ruminant production and wellbeing of livestock dependent populations. Despite the availability of effective vaccines, uptake remains low due to barriers in access, affordability, and service coordination. Formative participatory research suggested that localized farmer platforms, which organize farmers together and coordinate vaccination scheduling, share information, and pool resources, could address these constraints. We conducted a cluster-randomized controlled trial to evaluate the effectiveness of these decentralized platforms on vaccination uptake, antimicrobial use, livestock losses, and farmer wellbeing in three districts in Ghana.

Methods: Forty-six communities (46 clusters) were randomized 1:1 to intervention or control arms. About ten households per cluster were enrolled and surveyed at baseline, 6 months, and 12 months. In intervention communities, two trained local leaders established farmer platforms to coordinate vaccine information exchange, schedule vaccination services, and share vaccination costs. Analyses followed an intention-to-treat approach using mixed-effects models with random intercepts for clusters. Endline analyses were limited to households with at least one prior observation (baseline or 6 months). The primary outcome was livestock vaccination uptake at 12 months. Secondary outcomes included antimicrobial use in the past month, livestock losses over 12 months, and wellbeing measured using the WHOQOL-BREF across physical, psychological, social, and environmental domains.

Results: A total of 1,090 observations were collected across three survey waves, with 211 households contributing endline data. At 12 months, the predicted probability of vaccinating was 96% (95% CI: 86–99%) in the intervention arm versus 47% (95% CI: 25–70%) in controls (adjusted OR: 26.8; 95% CI: 5.1–141.0; *p*0.001). In intervention communities, 2% of farmers reported livestock losses compared with 31% in controls (adjusted OR: 0.045; 95% CI: 0.01–0.23; *p*0.001). Antimicrobial use remained low in both groups, with no significant difference at endline (OR: 0.81; $p=0.823$). Wellbeing scores were modestly higher in the intervention arm (mean difference=2.69; $p=0.053$).

Conclusions: This decentralized community-led platform intervention led to a significant increase in vaccination uptake and marked reduction in livestock mortality over 12 months. These findings demonstrate that leveraging local coordination capacity of communities can improve utilization of existing vaccines in resource-constrained settings. Although no effect was observed on antimicrobial use, and wellbeing gains were modest, the evidence shows that such local-driven initiatives have potential to overcome persistent demand- and supply-side barriers to livestock vaccination, offer a pragmatic pathway to strengthen preventive health service delivery, and enhance household wellbeing.

Climate change, Environment, Ecosystems Health - session 2

SCS16 · 14:00-15:30 · Auditorium I

NOAA One Health: Integrating Marine Ecosystem Drivers and Environmental Intelligence To Enhance the Health Sector

Alice LAU

National Oceanic and Atmospheric Administration, United States of America

Background

The National Oceanic and Atmospheric Administration (NOAA) is a U.S. government agency established in 1970 to unify and leverage the country's expertise in ocean, weather, hazards, and water science, holding a unique, ever-evolving role in the One Health approach. As a global leader in oceanographic, meteorological, and atmospheric predictive science, NOAA is at the forefront of efforts to promote marine ecosystem health and environmental intelligence initiatives. Recognizing its crucial role, the NOAA Science Advisory Board established the Oceans and Health Working Group (OHWG) in 2010 to guide agency-wide health sector contributions, mitigate threats to ocean health, and highlight underrepresented opportunities across multiple sectors. With leading organizations within the One Health framework primarily focusing on human or animal health, NOAA is well-positioned to fill this gap in ecosystem health and play a crucial role in advancing global One Health efforts.

Methods

The NOAA One Health Group is an essential, multidisciplinary nexus convening experts across NOAA, other federal agencies, researchers, non-governmental partners, and international organizations with cross-cutting expertise in the environment and health space. With ten thematic areas encompassing NOAA's diverse One Health portfolio, such as leading initiatives in air quality monitoring, sustainable aquaculture, weather forecasting, ocean health benefits, and vector-borne diseases management, NOAA One Health provides authoritative meteorological, ecological, and marine health data, research, and initiatives at the intersection of environmental drivers and health outcomes.

Results

NOAA produces a suite of predictive models, forecasts, and weather-driven tools for infectious diseases and environmental hazards across aquatic and terrestrial ecosystems. Examples include sea surface temperature products and a Vibrio harvest calculator to ensure safe shellfish harvesting and food security nationwide, the NOAA-funded AeDES system that forecasts vector-borne disease risk in the Americas by tracking environmental conditions and mosquito life cycles to support public health interventions, and the experimental pollen forecast that provides estimates and high-risk times of daily, location-specific pollen concentration by modeling weather impacts. The delivery of integrated advanced modeling tools enables actionable environmental health applications. NOAA One Health further builds capacity in One Health solutions through robust cross-sector partnerships, leadership, and engagement in professional and intergovernmental organizations, such as the Group on Earth Observations, the U.S. One Health Coordination Unit, and the American Meteorological Society.

Conclusion

From extreme conditions to emerging infectious diseases, developing environmentally based, weather-driven health outlooks and interdisciplinary action are paramount to tackling unprecedented, rapidly evolving public health and ecosystem threats. Focused on synthesizing, analyzing, and refining environmental data, NOAA provides critical environmental intelligence through its observing systems and models to support ecological and epidemiological forecasts and modeling across timescales. Through its mission, legislative mandate, and partnerships, NOAA holds a critical role in contributing to environmental protection and marine ecosystem health initiatives within the One Health framework.

Rain, Rats, and Residents: Understanding Zoonotic transmission in Urban Brazilian Slums

Hussein KHALIL (1), Federico COSTA (2), Fabio NEVES SOUZA (2)
1: Swedish University of Agricultural Sciences, Sweden; 2: Federal University of Bahia

Rapid urbanisation and inadequate sanitation in low-income (slum) communities put more than a billion residents in a cycle of poverty and disease. In these environments, zoonotic disease transmission exemplifies the core challenges addressed by a One Health approach, where risk depends on the interaction between reservoir ecology, human behaviour, and environmental contamination. This risk is exacerbated by climate change and extreme weather events, such as heavy rainfall. For example, leptospirosis, a globally distributed bacterial disease transmitted in urban areas by Norway rats (*Rattus norvegicus*), peaks following severe rain and flooding. Previous research links infection to point-in-time environmental risks or rat presence, but the spatial and temporal mechanisms linking animal, human, and pathogen movement remain poorly understood.

In this ongoing study set in urban slums in Salvador, Brazil , we present an interdisciplinary One Health approach to partition and map these interacting dimensions of risk. To capture reservoir dynamics, we monitor rat movement and distribution using a combination of camera traps and Bluetooth Low Energy (BLE) tags. Simultaneously, we evaluate seasonal environmental contamination by collecting water samples to test for *Leptospira* presence. Finally, we map human exposure vulnerability by deploying GPS trackers and conducting exit interviews with residents, stratified by age, gender, and socioeconomic status. All sampling is stratified by season (dry versus wet and within season, rain-free and rainy days).

We investigate how heavy rainfall mobilises bacteria and whether it drives rat dispersion into higher elevation areas, altering the landscape of risk for residents of these areas. Preliminary observations indicate that rainfall variability influences rat activity and distribution. Concurrently, precipitation alters daily human mobility patterns, increasing the spatial overlap between rodent and human movements. Socioeconomic status and gender differences further dictate these spatial constraints and subsequent infection vulnerabilities.

By partitioning disease risk into its interconnected animal, environmental, and human movement components, this study operationalises the One Health framework in urban slums, moving beyond traditional static epidemiology. Understanding these seasonal patterns is improtant for identifying precise and time-sensitive interventions, including timing rodent control, implementing localised drainage improvements, or establishing safe movement corridors to effectively mitigate future climate-driven zoonotic outbreaks.

Seasonally Structured Bidirectional Microbiota Exchange between Humans and a Climate-Vulnerable Lake Ecosystem

Yaovi Mahuton Gildas HOUNMANOU (1), Julie SEGRE (2), Anders DALSGAARD (1)
1: University of Copenhagen, Denmark; 2: National Institutes of Health

Background: Environmental reservoirs remain underrepresented in many One Health investigations of infectious disease dynamics. Climate-driven hydrological variability may substantially reshape microbial communities in aquatic settlements and influence human exposure to environmental microbiota and pathogens. This study examined microbial connectivity between humans and a climate-sensitive lagoon ecosystem to evaluate seasonal patterns of microbiota exchange and potential pathogen emergence.

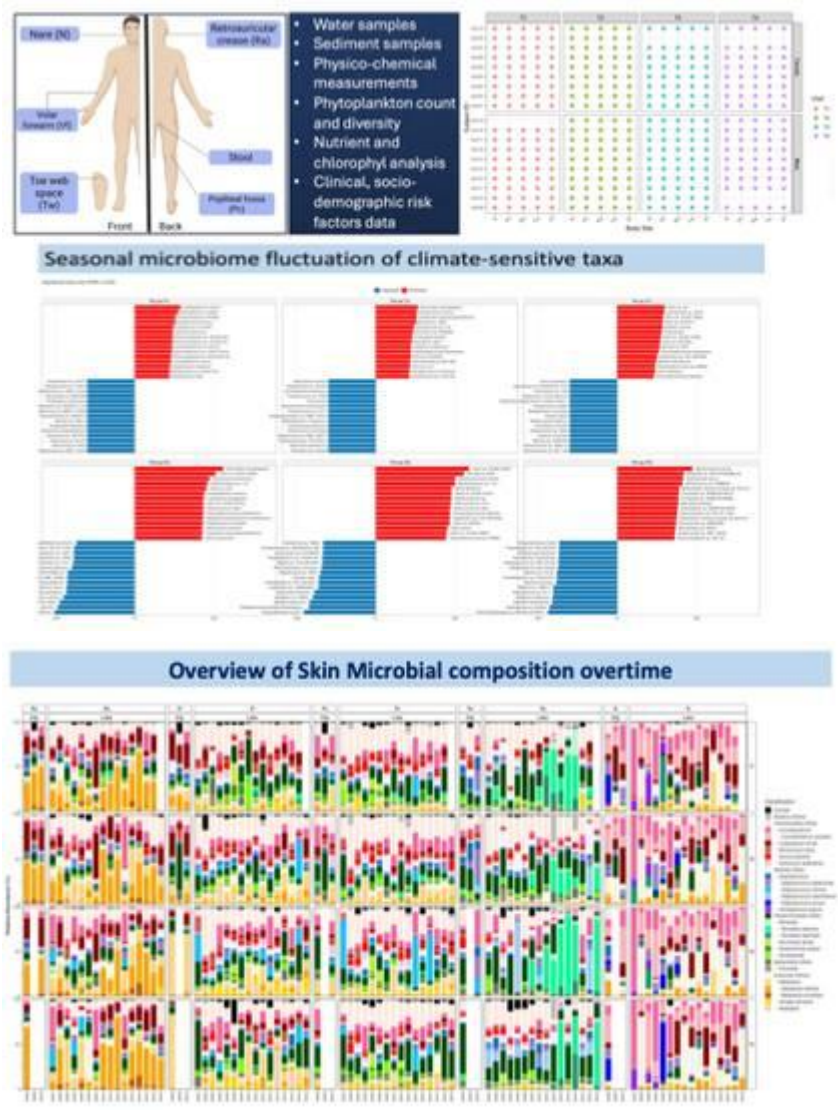
Methods: A longitudinal multi-omics study was conducted in Lake Nokoué, Benin, a densely populated lagoon system experiencing seasonal flooding, salinity fluctuations, and eutrophication. A total of 1,176 paired human and environmental samples were collected quarterly from 20 lake residents and non-lake controls across five sites. Environmental samples included water and sediment, while human samples comprised stool, four skin sites, and nasal swabs. Clinical, behavioural, and environmental metadata were collected, including water contact, occupation, hygiene practices, antibiotic use, and physicochemical parameters such as nutrient concentrations, chlorophyll-a, and phytoplankton diversity. Genome-resolved metagenomics, metatranscriptomics, and ecological modelling were applied to characterize microbial community dynamics and cross-ecosystem connectivity.

Results: Environmental microbiomes followed reproducible seasonal trajectories associated with hydrological transitions and eutrophication gradients. One densely populated site displayed persistent microbial divergence across seasons, consistent with chronic anthropogenic loading interacting with

climate forcing. Genome-resolved analyses identified bidirectional microbiota exchange between the lake ecosystem and humans. Lake water was consistently enriched with human gut-associated taxa, including Prevotella, suggesting sustained fecal inputs. Conversely, lake residents exhibited seasonal acquisition of environmentally associated taxa across skin, nasal, and gut microbiomes, whereas non-lake controls maintained relatively stable microbial profiles. Environmental microbial signatures in humans increased with occupational water contact and limited hygiene practices. Seasonal peaks of clinically relevant lineages, including Vibrio spp., were detected in environmental samples. Nasal RNA viromics additionally revealed temporally structured viral carriage, including influenza A(H1N1), accompanied by host antiviral transcriptomic activation.

Conclusions:

Climate-sensitive aquatic settlements function as coupled human–environment microbial systems in which seasonal environmental forcing drives reciprocal microbiota exchange and temporally structured pathogen exposure. Longitudinal multi-omics surveillance in such environments may support early warning of climate-associated infectious disease risks and strengthen One Health monitoring strategies.



Nature for Health: Reframing Upstream Prevention through Systems Thinking

Katie WOOLASTON (1), **Rumbidzai GONDO** (2), Christina PETTAN-BREWER (3), Ntish DEBNATH (4), Serge MORAND (5), Julius NZIZA (6), Marcela M UHART (7), Andrea CHAVES (8), Alexandre CARON (9), Pag-Tendu M YENTCHARE (10), Lisa CRUMP (11)

1: KW Green Governance Solutions, Australia; 2: Zimbabwe Youth Biodiversity Network, Harare, Zimbabwe; 3: School of Medicine, University of Washington, Seattle, USA; 4: One Health Bangladesh; EpiC Project FHI 360 Bangladesh; 5: HealthDEEP, CNRS – Kasetsart University – Mahidol University, Bangkok, Thailand.; 6: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Scotland; 7: Karen C. Drayer Wildlife Health Center, Weill School of Veterinary Medicine, University of California, Davis; 8: Centro Nacional de Innovaciones Biotecnológicas (CENIBiot), CeNAT, Conare, San José 1174-1200, Costa Rica; 9: ASTRE, CIRAD, INRAE, University of Montpellier, Montpellier, France; 10: Graduate School of Public and International Affairs, University of Ottawa; 11: Swiss Tropical and Public Health Institute, Allschwil, Switzerland

Background: Nature4Health (N4H) is a global initiative designed to reposition biodiversity conservation and environmental integrity at the centre of One Health prevention efforts. Although One Health has gained prominence in global policy, its environmental dimensions remain unevenly integrated, with biodiversity frequently peripheral to governance, surveillance and financing frameworks. Converging scientific evidence demonstrates that environmental degradation amplifies health risks, including emerging infectious diseases, climate-sensitive transmission dynamics, and broader determinants of wellbeing such as food, water and mental health security. However, persistent methodological, institutional and normative barriers continue to constrain the integration of biodiversity into health governance. These include fragmented sectoral mandates, short-term funding cycles, limited ecological surveillance, and valuation frameworks that privilege near-term human health outcomes over long-term ecological resilience. This paper examines how N4H seeks to address these barriers by operationalising biodiversity-centred prevention within the One Health framework.

Methods: This study draws on organisational learning and early implementation experiences from the Nature4Health initiative, supported by the International Climate Initiative (IKI) and implemented in partnership with IUCN, UNDP, UNEP, WHO and WOAH. Using a systems-based analytical approach, the study examines programme design, the initiative's Theory of Change, and emerging insights from locally grounded interventions in low- and middle-income countries. Qualitative analysis was conducted to identify how governance arrangements, evidence systems and financing mechanisms are being structured to address upstream ecological and socio-political drivers of health risk.

Results: The analysis shows that N4H operationalises systemic thinking through three primary mechanisms: strengthening cross-sectoral governance arrangements, developing mixed evidence systems that integrate ecological and health data, and mobilising prevention-oriented financing that supports biodiversity conservation as a health intervention. Early implementation experiences indicate that these approaches can help identify leverage points for prevention, support adaptive management, and facilitate collaboration across environmental, animal health and public health sectors. The initiative also demonstrates how catalytic funding and locally grounded interventions can support integrated governance approaches that address the root causes of emerging health risks.

Conclusions: The Nature4Health initiative illustrates how biodiversity-centred prevention can be operationalised within the One Health framework through governance reform, integrated evidence systems and targeted financing mechanisms. These findings highlight the importance of addressing ecological drivers of health risk as part of global health security strategies. Lessons emerging from early implementation provide practical insights for governments, funders and practitioners seeking to strengthen environmental integration within One Health and advance more systemic, prevention-oriented approaches to health governance.

Nature-Based Solutions for Health: Applying a One Health Lens to Regenerative Agriculture

Catherine MACHALABA (1), Nadia ALSADI (2), Sasha GENNET (3), Clare E. KAZANSKI (4), Shamitha KEERTHI (2), Briene LERMITTE (2), Alison LOVDAL (3), Matthew SHUPLER (1), Stephen A. WOOD (3), Philip A. LORING (1)

1: The Nature Conservancy, Global Science; 2: The Nature Conservancy, North America Agriculture; 3: The Nature Conservancy, Provide Food and Water; 4: The Nature Conservancy, North America Region

Background: Nature-based solutions (NbS) provide an array of benefits for biodiversity and climate, but their contributions to human and animal health have been generally overlooked in disease prevention and preparedness efforts. With increasingly intensified and multi-hazard environmental and health crises at local and global scales, scaling NbS is critical and can benefit from a One Health approach to generate multiple benefits and minimize trade-offs. Regenerative agriculture offers a suite of nature-based solutions aimed at transitioning unsustainable agricultural systems to resilient, nature-aligned practices while maintaining the essential values and services agricultural practices provide.

Methods: An exploratory project examined agriculture-environment-health connections to assess the role and enabling conditions for regenerative agriculture practices on health outcomes. Literature review, policy analysis, and worked case studies were leveraged to examine the state of knowledge along specific pathways at the agriculture-environment-health nexus and evaluate needs for a research agenda. Implications for burden of disease studies are also discussed.

Results: We identified fourteen potential NbS that can help to prevent or mitigate health impacts identified from agriculture-environment pathways: Nitrate-attributable disease, Particulate matter driven respiratory and cardiovascular disease, Infectious disease outbreaks and antimicrobial resistance, and Cancer, neurological disorders, endocrine disruptions from pesticide exposure. While these hold promise, at present the potential benefits of NbS are limited by 1) a fragmented policy landscape, which provides limited opportunity and incentive to work across sectors; 2) different geographic and temporal scales and scope of data availability across sectors, which hinders agriculture-health attribution science and assessment of the scale of impact interventions may have; and 3) imprecise understanding of the conditions in which they deliver optimal benefits or could generate adverse impacts, while acknowledging their general high potential as context-tailored solutions, as well as interactions with other hazards on human and animal health, such as extreme heat.

Conclusion: Overall, NbS appear to have high potential to provide population-level health benefits. However, there is limited work to date on the contribution of regenerative agriculture in reducing human and animal disease burden. Estimating and quantifying these impacts – as well as any potential trade-offs - could provide a meaningful return on investment studies for agriculture, conservation, and health to optimize investment outcomes. There are also opportunities to expand this work, including potential linkages to mental health outcomes, nutrition, mitigation of health effects of climate emergencies, and more.

A multi-endosymbiont approach to monitoring sentinel species as bioindicators of tropical ecosystem health

Klara Judita PETRZELKOVA (1,2,3), Peter SAMAS (1), Dušan ROMPORTL (4), Eva NOSKOVA (1), Martin KVAC (2,5), Alex PIEL (6,7), Fiona Anne STEWART (6), Eddy KAMBALE SYALUHA (8), Anne LAUDISOIT (9), Matthew MCLENNAN (10), Vicent KIIZA (10), Nicholas MPANGA (10), Johnmary BARUZALIIRE (10), Edison MUGANYIZI (10), Johnson MPANGIRE (10), Isaac KUGONZA (10), John BUSINGE (10), Thierry AEBISCHER (11), Daniel SEMPEBWA (1,12,13), David ERYENYU (12), Caroline ASIIMWE (12,14), Fred BABWETEERA (12), Klaus ZUBERBUHLER (12), Josephine Nadezda MSINDAI (6), Nicole M. SIMMONS (15), Catherine HOBAITER (16,17), Thibaud GRUBER (17,18), Chie HASHIMOTO (19,20), Takeshi FURUICHI (19), Dennis BABAASA (21), Eva MARESOVA (1), Barbora CERVENA (1), Bethan MASON (1), Jakub KREISINGER (22), Barbora PAFCO (1)

1: Institute of Vertebrate Biology, Czech Academy of Sciences, Czech Republic; 2: Institute of Parasitology, Biology Centre, Czech Academy of Sciences, Czech Republic; 3: Liberec Zoo, Czech Republic; 4: Department of Physical Geography and Geoecology, Faculty of Science, Charles University, Czech Republic; 5: Faculty of Agriculture and Technology, University of South Bohemia, Czech Republic; 6: Dept. of Anthropology, University College London, UK; 7: Max Planck Institute for Evolutionary Anthropology, Germany; 8: Gorilla Doctors, MGVP, Inc., USA; 9: EVECO group, University of Antwerpen, Belgium; 10: Bulindi Chimpanzee and Community Project, Uganda; 11: AP-RCA_Chinko, Chinko Conservation Area, African Parks, Central African Republic; 12: Budongo Conservation Field Station, Uganda; 13: University of Veterinary Sciences Brno, Czech Republic; 14: Uganda Wildlife Authority; 15: Kyambura Chimpanzee Project, Makerere University, Uganda; 16: Wild Minds Lab, School of Psychology and Neuroscience, University of St Andrews, UK; 17: Bugoma Primate Conservation Project, Uganda; 18: Swiss Center for Affective Sciences and Faculty of Psychology and Educational Sciences, University of Geneva, Switzerland; 19: Wildlife Research Center, Kyoto University, Japan; 20: Center for Primate Field Studies, Kyoto University, Japan; 21: Institute of Tropical Forest Conservation, Mbarara University of Science and Technology, Uganda; 22: Department of Zoology, Faculty of Science, Charles University, Czech Republic

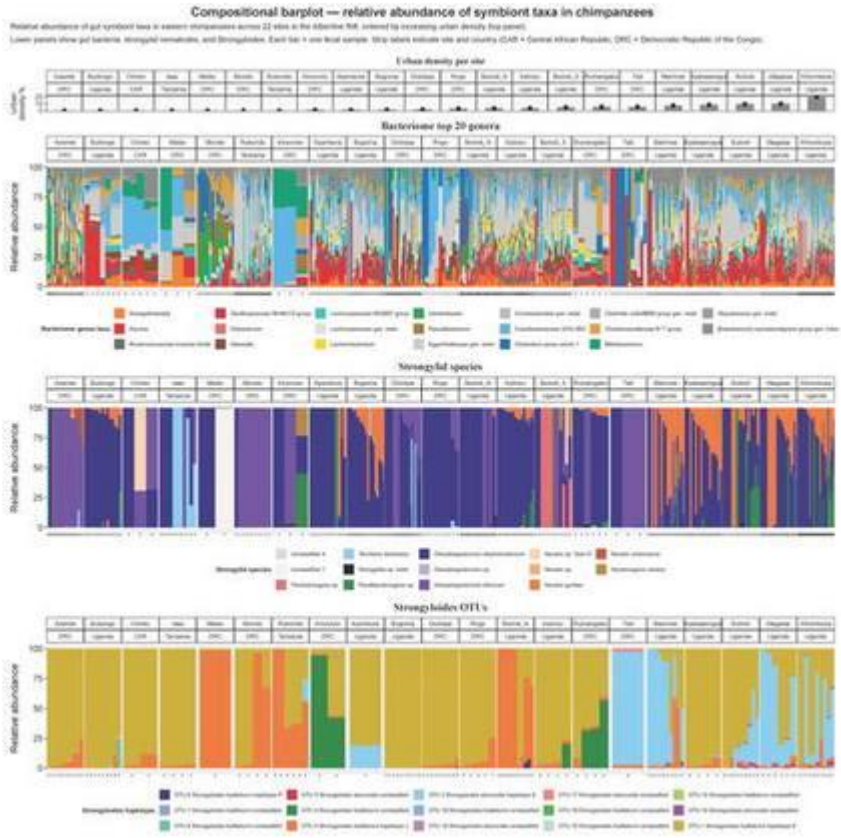
Anthropogenic environmental change, including habitat fragmentation, biodiversity loss and increasing human–wildlife interactions, is reshaping ecological communities and altering infectious disease dynamics. These processes may influence not only host populations but also the diversity and structure of their associated symbiont communities. Great apes, due to their ecological sensitivity, long lifespan, and phylogenetic proximity to humans, represent valuable sentinel species for monitoring ecosystem health within a One Health framework.

In this study, we investigate whether gastrointestinal symbiont communities of eastern chimpanzees (*Pan troglodytes schweinfurthii*) reflect gradients of anthropogenic disturbance across 21 sites, the majority of which are located in the Albertine Rift, one of the most biodiverse regions of Africa. We analysed non-

invasively collected faecal samples from chimpanzee populations across 21 sites spanning a broad geographic and ecological range, from relatively intact forest ecosystems to fragmented landscapes with varying levels of human influence. Using high-throughput sequencing approaches and spatial and habitat analyses, we characterized three major components of the chimpanzee gut symbiont community: bacteria (16S rRNA metabarcoding), strongylid nematodes (ITS-2 metabarcoding), and *Strongyloides* spp. (HVR-IV of 18S rDNA) to test the hypothesis that proximity to anthropogenic disturbance (manifested through urban density) and altered biodiversity (expressed as habitat heterogeneity via Normalized Difference Vegetation Index) in tropical ecosystems affect the taxonomic and functional structure of chimpanzee gastrointestinal symbiont communities.

Analyses of alpha diversity and community composition using Generalised Additive Models (GAMs) and permutational MANOVA (PERMANOVA) on Aitchison distances show that anthropogenic disturbance is associated with a restructuring of the bacterial fermentative core of the chimpanzee gut and with changes in helminth community structure. In particular, several key fiber-fermenting and butyrate-producing genera within the families Lachnospiraceae and Oscillospiraceae (e.g. *Roseburia*, *Agathobacter*, *Coprococcus*) declined with increasing urban density. These bacteria play central roles in the fermentation of complex plant polysaccharides and the production of short-chain fatty acids, suggesting reduced fermentative capacity in individuals that live near disturbed environments. Conversely, bacterial taxa often associated with low-fiber or human-impacted bacteriomes (e.g. *Collinsella*) increased in relative abundance. Strongylid communities also shifted across the landscape, although these patterns were primarily associated with habitat heterogeneity and temperature. Notably, the zoonotic genotype A of *Strongyloides stercoralis* emerged as a potential bioindicator of anthropogenic disturbance and, consequently, of broader ecosystem health, with urban density identified as a significant predictor of *Strongyloides* community structure. This finding is particularly relevant given that strongyloidiasis is a neglected tropical disease requiring improved surveillance and control in endemic regions.

Our findings highlight that combining bacterial and eukaryotic symbionts of sentinel wildlife species can provide sensitive indicators of ecosystem disturbance. Multi-symbiont monitoring frameworks may therefore offer valuable early warning signals of ecological degradation and emerging zoonotic risks in rapidly changing tropical landscapes.



African pastoral commons, OECMs and agroecology principles for healthy savanna social-ecological systems

Alexandre CARON (1), **Salome BUKACHI** (2), Jason SIRCELY (3), Prisca MUGABE (4), Jean-Daniel CESARO (5), Musso MUNYEME (6), Flora PULE-MEULENBERG (7), Richard FYNN (8), Peter TYRRELL (9), Peadar BREHONY (10), Jacques VAN ROOYEN (11)

1: CIRAD,UMR ASTRE - ILRI, ILRI, Nairobi, Kenya; 2: Institute of Anthropology, Gender and African Studies University of Nairobi, Nairobi, Kenya; 3: Livestock, Climate, and Environment, International Livestock Research Institute (ILRI), Nairobi, Kenya; 4: Department of Livestock Sciences, Faculty of Agriculture Environment and Food Systems, University of Zimbabwe, Harare, Zimbabwe; 5: CIRAD UMR SELMET, Montpellier, France; 6: Department of Disease Control, School of Veterinary Medicine, The University of Zambia, Lusaka, Zambia; 7: Department of Crop and Soil Sciences, Faculty of Agriculture, Botswana University of Agriculture and Natural Resources, Gaborone, Botswana; 8: Okavango Research Institute, University of Botswana, Maun, Botswana; 9: Sustain, East Africa, Nairobi, Kenya; 10: Sustain, East Africa, Arusha, Tanzania; 11: REHERD Africa

Background: African pastoral cultures are rooted in extensive mobile livestock production systems, intricately linked to ecological processes in rangelands of Western, Eastern and southern Africa. These rangelands, when sustainably managed, can be rich in soil, wild plants and animal biodiversity, store CO2, and offer a good quality of life for pastoral communities. They can promote health eocsystems with healthy humans, plants and wild and domestic animals as the new One Health definition promotes.

However, like most biomes, rangelands currently face significant threats including climate change, land use changes, biodiversity loss and invasive species. Due to their size and biological and cultural richness, pastoral landscapes could significantly contribute to the achievement of international agreements including targets 3 from the Global Biodiversity Framework and multiple Sustainable Development Goals. Despite their potential, these landscapes are currently under recognized in this context and would benefit from a holistic landscape One Health approach.

Methods: In complement to existing land-sparing approaches to biodiversity conservation and agriculture, land-sharing approaches offer a theoretical framework that posits pastoral landscapes as shared spaces that contribute to healthy livelihoods, biological connectivity and diversity across healthy rangeland.

By leveraging the concept of “Other Effective area-based Conservation Measures” (OECMs), we critically review how pastoral landscape can achieve long-term and effective in-situ biodiversity conservation outside of protected areas, while also targeting pastoral livelihoods well-being.

For the first time, we adapt and apply agroecological principles to African pastoral systems, recognizing pastoral communities as custodians of pastoral landscape. We emphasize their knowledge systems as foundational to the management of pastoral landscapes. Utilizing agroecological transition theory, we propose sustainable and environmentally friendly pathways for pastoral systems in the Anthropocene, interweaving pastoral and scientific knowledge.

Results*:* By integrating the OECM framework for pastoral landscapes and the pastoral ecology principles emerging from agroecology, we present a robust applied framework that establishes comprehensive support and monitoring guidelines for ecology-based pastoralism. This framework promotes shared landscapes grounded in just governance, sustainable livelihoods and nature-based solutions for biodiverse ecosystems. It can serve as an instrumental resource for managers, professionals and researchers aiming to advocate for African rangelands as shared landscapes.

Conclusions: This framework borrows from the One Health approach in its social-ecological and holisitc dimension to deliver mutiplie dimesnions of health in pastoral savannas. It showcases how agroecology and One Health are closely related concepts that can deliver bottom-up One Health operationalisaiton approach.

Antimicrobial resistance - session 2

SCS17 · 16:00-17:30 · Auditorium I

Defining 'appropriate' antimicrobial use in One Health: a global consensus survey

Ri SCARBOROUGH (1,2), Leslie DOWSON (1,2), Courtney IERANO (1,2,3), Brendan MCMULLAN (4), Leanne TEOH (1,2), Kirsten BAILEY (1,2), Ruby BIEZEN (1,2), Brian HUR (1), Allegra SCHERMULY (5), Glenn BROWNING (1,2), Karin THURSKY (1,2,3), Laura HARDEFELDT (1,2)

1: The University of Melbourne, Australia; 2: The Peter Doherty Institute for Infection and Immunity, Melbourne, Australia; 3: The Royal Melbourne Hospital, Parkville, Australia; 4: Sydney Children's Hospital, Randwick, Australia; 5: Monash University, Clayton, Australia

Aim

To develop a shared One Health description of 'appropriate' antimicrobial use (AMU).

Background

There is increasing agreement that antimicrobial stewardship (AMS) efforts should take a One Health approach and focus on increasing appropriateness of AMU, rather than reducing AMU.

One Health AMS implementation requires a shared understanding of 'appropriate AMU' across stakeholders in human and animal health, and across countries of different income levels.

Methods

Four focus groups were held with diverse stakeholders including pharmacists, doctors, dentists and livestock producers, to develop detailed statements that could describe appropriate (systemic) AMU across all One Health contexts. Additional statements were gathered from a literature review.

Statements were presented in a four-round Delphi survey. The survey was circulated to antimicrobial stewardship experts in human and animal health globally, including low-and middle-income countries.

The consensus level was set at 80%; in the first three rounds, statements that reached this threshold were included in the consensus description. In the final round, participants rated how feasible it would be to measure each consensus item, in the context with which they were most familiar.

Results

Sixty-two percent (243/391) of invitees from 44 countries responded to at least one survey round. Human health respondents made up the majority (63%), with 25% from animal health and 11% from environmental health or other. Twenty-two percent of participants were from low- and middle-income countries and 63% had an influence on their national AMR strategy.

The 76 statements presented covered several topics, including why, when and how AMU should be initiated, and the selection of drug, route, dose and duration. Forty-three of the proposed statements reached consensus in the first round, rising to 51 in subsequent rounds. There was minimal difference between responses from participants from human health and those from animal health.

Examples of the consensus statements to describe appropriate antimicrobial use included:

The final list of 51 statements underlined the importance of avoiding systemic antimicrobial use where possible. When antimicrobials were unavoidable, patient safety and effectiveness were prioritised. Participants endorsed the use of prescribing guidelines and prudent use principles, including using the narrowest spectrum antimicrobial for the shortest effective duration. Notably, using antimicrobials to improve livestock production was *not* considered appropriate, by a large majority.

For each statement, the proportion of participants who thought it was feasible to measure concordance (in their context) ranged from 33% to 84%. The most frequent reason for a statement being considered 'not feasible' was data recording issues (82%).

ConclusionsThe consensus items represent the first detailed, One Health description of appropriate AMU and will stimulate discussion around unified measures of appropriateness.

Genomic Surveillance Reveals One Health Transmission Pathways of MDR Escherichia coli and Klebsiella pneumoniae in Northern Spain

Leticia CARBALLEIRA (1,2), Vanesa GARCÍA (1,2,3), Xenia VAZQUEZ (4,5), Carlos RODRÍGUEZ-LUCAS (6,7,8), Javier FERNÁNDEZ (9), M. Rosario RODICIO (6), **Azucena MORA** (1,2,3)

1: Laboratorio de Referencia de Escherichia coli (LREC), Dpto. de Microbioloxía e Parasitoloxía, Universidade de Santiago de Compostela (USC), Lugo 27002, Spain.; 2: Aquatic One Health Research Center (ARCUS), Universidade de Santiago de Compostela (USC), Santiago de Compostela 15782, Spain; 3: Instituto de Investigación Sanitaria de Santiago de Compostela (IDIS), Santiago de Compostela 15782, Spain; 4: Group of Functionality and Ecology of Beneficial Microorganisms (MicroHealth), Dairy Research Institute of Asturias (IPLA-CSIC), Oviedo, Asturias, Spain; 5: Health Research Institute of Asturias (ISPA), Oviedo, Asturias, Spain; 6: Dpto. de Biología Funcional, Área de Microbiología, Universidad de Oviedo, Oviedo 33006, Spain; 7: Servicio de Microbiología, Hospital Universitario Central de Asturias (HUCA), Oviedo 33006, Spain; 8: Grupo de Microbiología y Patología Infecciosa, Instituto de Investigación Sanitaria del Principado de Asturias (ISPA), Oviedo 33006, Spain; 9: Research and Innovation, Artificial Intelligence and Statistical Department, Pragmatech AI Solutions, Oviedo 33006, Spain

Background: The global rise of multidrug-resistant (MDR) *Escherichia coli* and *Klebsiella pneumoniae* represents a growing public health burden within the One Health framework. Both species are leading causes of urinary tract infections (UTI) and are increasingly associated with extended-spectrum β-lactamases (ESBL) and carbapenemases. This study investigates the genomic diversity, resistance determinants, and clonal relationships of isolates from humans, companion animals, wildlife, food, and wastewater treatment plants (WWTPs) in Oviedo (northern Spain) to identify high-risk clones with potential epidemiological relevance across reservoirs.

Methods: A total of 239 isolates (196 *E. coli*, 43 *K. pneumoniae*) collected between 2023 and 2025 underwent Illumina whole-genome sequencing (WGS). Assemblies were generated using SPAdes and quality assessed with FastQC/MultiQC. *In silico* characterization using the Center for Genomic Epidemiology (CGE) tools ResFinder, VirulenceFinder, and MLST was performed to identify resistance genes, virulence determinants, and sequence types. Clonal relatedness was assessed through cgMLST and core genome SNP distance analyses (Figure 1).

Results: ESBL genes were detected in 72 *E. coli* and 26 *K. pneumoniae* isolates, while carbapenemase genes were identified in 12 and 17 isolates, respectively. *E. coli* displayed high genetic diversity with 78 sequence types (ST), including three novel STs, whereas *K. pneumoniae* comprised 11 STs, including one novel ST. Sixteen STs previously associated with human infections were also identified in animal and environmental sources.

Among *K. pneumoniae*, more than 60% of isolates clustered in four high-risk STs, with SNP analyses revealing close genomic relatedness across reservoirs: ST147 (159 SNPs human–WWTPs), ST392 (273 SNPs human–companion animal), ST307 (194 SNPs human–wild boar meat), and ST469 (57 SNPs human–WWTPs). The most frequent resistance genes were CTX-M-15 (19/26) and OXA-48 (11/26).

In *E. coli*, 83 isolates (42%) belonged to 12 high-risk STs (Table 1). Virulence profiling identified 9 uropathogenic (UPEC), 4 extraintestinal (ExPEC), and 17 ExPEC-UPEC isolates among non-human sources, suggesting potential to cause human extraintestinal infections. ESBL (CTX-M-1, -14, -15, -27, -55 and SHV-12), AmpC (CMY-2), and carbapenemase (OXA-48 and NDM-7) determinants were detected in 36, 2, and 8 isolates, respectively. ST131 was the most prevalent clone (43 isolates), encompassing multiple phylogenetic clades (A, B, B1, C1-M27, C2) and seven virotypes.

Conclusions: Genomic analysis revealed the circulation of closely related MDR clones of *E. coli* and *K. pneumoniae* across human, animal, and environmental compartments, highlighting interconnected transmission pathways. High-risk clones shared among the three One Health sectors were identified, carrying clinically relevant resistance and virulence determinants. These findings underscore the value of genomic surveillance to support integrated monitoring and targeted interventions aimed at limiting their further dissemination.

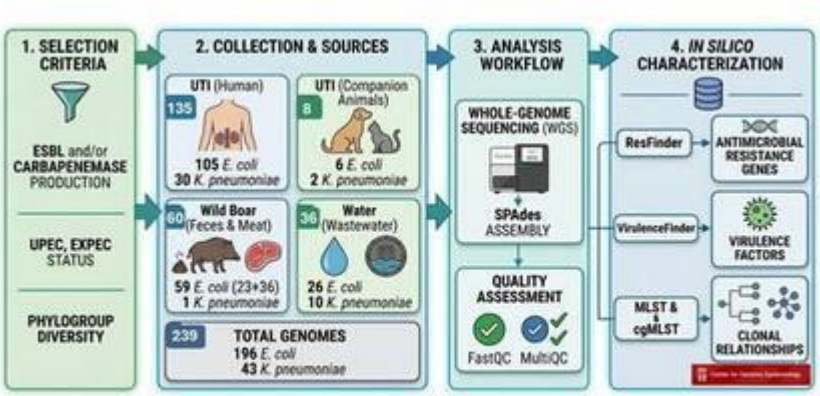


Figure 1: Overview of the isolate collection and study workflow.

Table 1. Distribution and genomic characterization of 63 high-risk clones of *E. coli*.

Clonal Complex (CC)	O:H antigens-Phylogroup-ST (Genotype)-CC	cgMLST (No. isolates)					ESBL/AmpC/carbapenemase-Abl gene typing (No. isolates)
ST 73 CC	O50:(02:H1-B2-ST73 (CH24-10)-CC73	ST69454 (1)		ST30940 (2)			
	O50:(02:H4-B2-ST10320 (CH24-10)-CC73	ST116928 (1)					CTX-M-15
	O25:H1-B2-ST73 (CH24-12)-CC73		ST95644 (1)				
	O25:H1-B2-ST73 (CH24-697)-CC73		ST46473 (1)				
	O8:H1-B2-ST73 (CH24-10)-CC73	ST71035 (1)					SHV-12
	O8:H1-B2-ST73 (CH24-30)-CC73	ST 23422 (1)					CTX-M-15
	O8:H1-B2-ST73 (CH24-103)-CC73		ST2006261 (1)				
	O6:H4-A-ST93 (CH11-0)-CC168	ST140861 (1)			*ST48009 (3)	*ST168377 (1)	*CTX-M-1 *CTX-M-14
ST 168 CC	O7:H4-A-ST93 (CH11-30)-CC168	ST195969 (1)					
	ONT:HNT-A-ST93 (CH11-0)-CC168	ST188200 (1)					
None	O114:H4-G-ST117 (CH45-97)	ST46690 (1)				*ST46690 (1)	*SHV-12
	O33:H4-G-ST117 (CH45-97)			ST94223 (1)			CTX-M-1
None	O6:H31-B2-ST127 (CH14-180)	ST9934 (1)					
	O6:H31-B2-ST127 (CH14-136)	ST114899(1)					
	O6:H31-B2-ST127 (CH14-224)		ST135188 (1)				
	O6:H31-B2-ST127 (CH14-2)				ST6940 (1)		
ST 469 CC	O160:H19-B1-ST162 (CH65-32) CC469	ST186982 (1)					
	ONT:H10-B1-ST162 (CH65-32) CC469	ST186036 (1)					
	O33:H25-B1-ST162 (CH65-32)-CC469			ST136573 (1)			CTX-M-15, CMY-2
	O8:H25-B1-ST162 (CH65-32)-CC469			ST199761 (1)			CTX-M-15
None	O83:H31-B2-ST372 (CH103-9)		ST195120 (1)			*ST100342 (1)	*OXA-48
ST 10 CC	O101:H10-A-ST744 (CH11-54)			ST186376 (1)			CTX-M-15
	ONT:H9-A-ST744 (CH11-54)					ST208263 (1)	CMY-2, NDM-7
None	O48:H8-B2-ST1236 (CH195-253)	ST32929 (1)		ST32929 (1)	ST172487 (1)		
None	O133:H5-B2-ST8184 (CH195-1033)			ST97334 (1)	ST90005 (2) ST62178 (2)		
ST 131 CC	O25:H4-B2-ST131 (CH40-30)-CC131	*ST 122338 (2) *ST 10774 (1) *ST 188324 (2) *ST122285 (3) ST 136431 (1) ST 144414 (1) *ST 180368 (2) *ST 201886 (1) *ST 33983 (1) *ST 46230 (1) ST 50256 (1) *ST 76547 (2) *ST 7808 (1) *ST 80947 (1) *ST 8116 (1) ST 93848 (1)				*ST 69493 (1) *ST 200823 (1) *ST 16150 (5)	*CTX-M-15 (12) *CTX-M-27 (5) *CTX-M-55 (1) *OXA-48 (6)
	O25:H4-B2-ST9126 (CH40-30)-CC131	ST207487 (1)					CTX-M-15
	O25:H4-B2-ST131 (CH40-22)-CC131	ST 190772 (1) ST9613 (1) ST 203333 (1)		ST21180 (1)			
	O16:H5-B2-ST131 (CH40-41)-CC131	ST139232 (1) ST146942 (1) *ST 101551 (2) ST26966 (1) ST3883(1)				*ST71646 (1)	*CTX-M-27 (4)
	O25:H4-B2-ST131 (CH40-682)-CC131	ST 23434 (1)					
	O25:H4-B2-ST131 (CH40-96)-CC131	ST 114086 (1)					CTX-M-27
	O25:H4-B2-ST131 (CH40-5)-CC131	ST 93247 (1)					CTX-M-15

Integrating Metagenomics and Microbiology to Characterise AMR Dissemination Across Wildlife, Livestock and Environmental Interfaces

Hayley THOMPSON (1), Stacey DUVENAGE (1), Judy BETTRIDGE (2), Heleen DE WEERD (3)

1: Natural Resources Institute. University of Greenwich, UK; 2: Bristol Veterinary School, University of Bristol, UK; 3: Edinburgh Genomics, The University of Edinburgh, UK.

Background: Integrated and biodynamic farming systems bring livestock, wildlife, crops and environmental reservoirs into close contact, creating ecological interfaces where antimicrobial resistance (AMR) may circulate even when on-farm antibiotic usage is low. Understanding how resistance genes and

multidrug-resistant (MDR) microorganisms are distributed across these interconnected compartments is essential for One Health–aligned surveillance.

Methods: We conducted a metagenomic and microbiological investigation of AMR across 21 samples from a mixed pig–arable farm. Samples included pig and rodent faeces, soil, irrigation and surface water, and manure. Shotgun sequencing produced over 1.8 billion paired-end reads, which were quality-filtered, host-depleted, and analysed using MetaPhlAn4 for taxonomic profiling and HUMAnN3 for functional annotation. AMR determinants were identified using MEGARes with the AMR++ pipeline. Metagenome-assembled genomes (MAGs) were recovered using MEGAHIT-based assemblies. Complementary selective culture and antimicrobial susceptibility testing were performed on Enterobacterales from matched compartments.

Results: Across the farm ecosystem, we identified a rich and diverse microbial community comprising 2,389 species, including important zoonotic and foodborne pathogens such as *Escherichia coli*, *Campylobacter* spp. and *Clostridium perfringens*. Functional profiling revealed ~5 million gene families and 625 pathways, reflecting substantial metabolic capacity. ARG screening recovered 1,449 unique ARGs, with samples containing an average of 437 ARGs (range: 38–802). Resistance mechanisms spanned multiple antimicrobial classes, including macrolides, fluoroquinolones, tetracyclines, beta-lactams, and heavy metals. PCoA analyses showed limited separation by sample type for AMR mechanisms, but clearer grouping appeared when ARGs were analysed at the gene level, with manure samples showing greater internal variability. Assembly-based analysis generated an average of 269 MAGs per sample, indicating high genomic complexity and the presence of many uncultured organisms contributing to the farm resistome. Culture-based screening revealed widespread MDR *E. coli* and ESBL-producing Enterobacterales across animal, manure, soil, and water samples. High rates of resistance were observed to ampicillin, tetracycline, cephalosporins, fluoroquinolones and carbapenems, despite historically low antimicrobial inputs on the farm.

Conclusion: This case study demonstrates that even low-antibiotic-use biodynamic farms can harbour a complex and highly interconnected resistome. The presence of conserved ARGs, MDR Enterobacterales and shared resistance signatures across wildlife, livestock and environmental compartments suggests multiple potential transmission routes within the farm system. Combining shotgun metagenomics, MAG reconstruction and traditional microbiology provides a powerful framework for One Health AMR monitoring and for identifying high-risk pathways for onward transmission into food chains and the wider environment.

Environmental Drivers of Antimicrobial Resistance in Aquaculture: A Comparative Governance Analysis of Canada and Norway

Shauna THOMAS
University of Ottawa, Canada

Background: Antimicrobial resistance (AMR) is increasingly recognized as a One Health challenge driven by environmental, agricultural, and regulatory factors. In aquaculture, antimicrobials are widely used to manage infectious disease associated with intensive production systems, yet a significant portion enters surrounding marine environments through uneaten medicated feed and fish waste. At the same time, climate and biodiversity pressures are driving structural reform in aquaculture production. In British Columbia (Canada), marine finfish production is transitioning from open-net pens toward semi-contained marine systems intended to reduce biodiversity impacts such as escapes and waste dispersal. However, early evidence suggests these systems may require more frequent antimicrobial use due to higher stocking densities and altered disease dynamics. This research evaluates whether Canada's current aquaculture governance framework adequately addresses the environmental AMR implications of this transition and explores lessons from Norway's aquaculture regulation.

Methods: The study uses a qualitative comparative legal and policy analysis combined with a literature review. Sources were identified through iterative searches in Omni Libraries, HeinOnline, LexisNexis, and Google using Boolean search strategies related to aquaculture, antimicrobial resistance, and governance. Priority was given to in-force legislation, followed by peer-reviewed literature and policy reports. Canadian governance was analyzed through the Pacific Aquaculture Regulations and Aquaculture Activities Regulations under the Fisheries Act, focusing on antimicrobial oversight and environmental

discharge provisions. A comparative policy analysis was conducted with Norway's aquaculture regulatory framework and antimicrobial stewardship policies.

Results: Findings indicate that Canada's regulatory framework manages environmental drug deposits primarily through procedural discharge authorizations rather than explicit antimicrobial stewardship objectives. As a result, climate-driven infrastructure changes, such as the shift to semi-contained systems, do not trigger regulatory reassessment of antimicrobial use risks. In contrast, Norway's EU-aligned governance framework combines strict veterinary prescription controls, vaccination strategies, and upstream pharmaceutical regulation, resulting in dramatically lower antimicrobial reliance in aquaculture production.

Conclusions: The study identifies a governance gap in Canada's aquaculture regulation: environmental adaptation policies are not currently integrated with antimicrobial stewardship objectives. Comparative evidence from Norway demonstrates that stronger upstream antimicrobial regulation can reduce environmental AMR risks without undermining aquaculture productivity. Embedding antimicrobial stewardship within environmental regulatory reform will be essential to ensure that climate-driven aquaculture transitions do not unintentionally exacerbate AMR risks. This study provides a useful policy-reference for other aquaculture nations facing a similar transition.

Migratory Sentinels: The Role of Little Stints (Calidris minuta) in the Intercontinental Dissemination of blaCTX-M-15 within the Palearctic-Afrotropical Flyway

Catherine MBUTHIA (1,2,3,4), Rael TOO (2), Alexanda MZULA (3), Anita CHEPKEMEI (2), John KIIRU (2), Samuel KARIUKI (2), Abubakar HOZA (3)

1: Karatina University, Kenya; 2: Kenya Medical Research Institute, Kenya; 3: Sokoine University of Agriculture, Tanzania; 4: SACIDS Foundation for One Health, Tanzania

Background: The escalation of antimicrobial resistance (AMR), particularly among extended-spectrum β-lactamase (ESBL)-producing bacteria is a global health priority. While human and livestock reservoirs of the *bla*CTX-M-15 allele are well-mapped, the role of long-distance migratory birds in the transboundary movement of these alleles remains under-characterized. This study investigated whether migratory little stints (*Calidris minuta*), and their aquatic ecosystems in the Kenyan Rift Valley lakes act as reservoirs for this critical clinical allele.

Method: A total of 232 samples (184 avian fecal and 48 water, from our previous work) from *C.minuta* foraging at Lakes Bogoria and Magadi shores and from their peripheral freshwater drinking sources were screened. From these, 294 bacterial isolates were recovered, with 56 showing phenotypic resistance to third-generation cephalosporins. ESBL production was confirmed via Double-Disk Synergy Testing (DDST). Molecular screening for *bla*CTX-M-15, *bla*TEM, *bla*SHV, and *bla*OXA was performed using gene-specific polymerase chain reaction (PCR).

Results: Of the 56 ESBL producers, 12 (21.4%) harbored the *bla*CTX-M-15 variant, with 10 (83% of carriers) exhibiting a multidrug-resistance (MDR) phenotype. Resistance to commonly used antimicrobials was high: ampicillin (10/12, 83.3%), tetracycline (8/12, 66.7%), sulfamethoxazole-trimethoprim (7/12, 58.3%) and amoxicillin-clavulanic acid (3/12, 25%). Crucially, resistance was detected against critically important antimicrobials (CIAs) for human medicine: aminoglycosides (gentamicin) at 50% (6/12), fourth-generation cephalosporins, cefepime (5/12, 41.7%), fluoroquinolones (ciprofloxacin) at 16.7% (2/12) and carbapenems (meropenem) at 8.3% (1/12).

Regarding co-carriage, the *bla*CTX-M-15-producers frequently carried additional β-lactamase genotypes with *bla*TEM and *bla*OXA detected at 58.3% and 16.7% respectively; notably, *bla*SHV was not co-expressed. The *bla*CTX-M-15 frequency was uniformly distributed across both avian fecal and water samples in the two study areas. Predominant carriers were *Enterobacter cloacae* (1.7% of total samples), *Escherichia coli* (1.3%), and *Klebsiella pneumoniae* (0.9%), alongside *Providencia rettgeri*, *Leclercia adecarboxylata*, and *Acinetobacter soli* (0.4% each).

Conclusion: Our findings confirm that *C. minuta* serves as a high-fidelity global sentinel for the intercontinental spread of *bla*CTX-M-15. The high frequency of ESBL-MDR co-expression suggests significant co-selection potential, facilitating the environmental maintenance of these allelic variants The detection of these clinical alleles at the wildlife-water interface in relatively remote Kenyan lakes

suggests a massive environmental "spill-over" from anthropized landscapes into the Palearctic-Afrotropical Flyway. These birds act as mobile bioreactors, facilitating the transboundary "spill-back" of high-priority resistance genes to human and livestock populations. This necessitates an urgent shift toward genomic-based, transboundary One Health surveillance to mitigate the global circulation of ESBLs.

Strengthening UK Antimicrobial Resistance Surveillance Through a Public–Private Partnership with Veterinary Laboratories

Sophie SPALDING (1), April LAWSON (2), Gina PINCHBECK (2), Vanessa SWINSON (3), Hayley WIGHTON (3), Richard NEWTON (4), Charlotte BARBER (4), Athina PAPADOPOULOU (5), Daniela OLIVERA MESA (6), Tamsin DEWE (1)

1: Veterinary Medicines Directorate (VMD); 2: Small Animal Veterinary Surveillance Network (SAVSNET), University of Liverpool; 3: Animal and Plant Health Agency (APHA); 4: Equine Infectious Disease Surveillance (EIDS), University of Cambridge; 5: Centre for Environment, Fisheries and Aquaculture Science (CEFAS); 6: Imperial College London

Background: Antimicrobial resistance (AMR) is a major One Health (OH) threat. Effective surveillance across the OH spectrum is essential for detecting emerging resistance, understanding transmission pathways and supporting evidence-based stewardship. In the UK, while surveillance in healthy livestock at slaughter is routine, most animal antimicrobial susceptibility testing (AST) is performed by private veterinary laboratories (PVLs) and not routinely shared with government, creating blind spots particularly in companion animal, equine, and aquaculture sectors.

The Private Laboratories Initiative (PLI) was established to evaluate whether PVL-generated AMR data can be consistently collected, standardised and integrated into national surveillance. France's RESAPATH programme, pioneered in 1982, evidences the long-term value of PVL-enabled surveillance, but detailed start-up guidance for today's conditions is sparse. PLI therefore provides current, transferable implementation lessons on successful engagement, governance, onboarding, and data standards for integrating PVL clinical data across all major animal sectors: farm, companion, equine and aquaculture.

Methods: A mixed-methods implementation and feasibility study was conducted across the UK veterinary diagnostics landscape, delivered through a public–private–academic partnership. Activities included national mapping; structured engagement (interviews, surveys, workshops); and extraction of bacteriology/AST results from diverse laboratory information systems. Data were standardised through bespoke cleaning scripts and a prototype large-language-model-assisted extraction tool, with secure short-term transfers for onboarding. Analyses included data-quality assessment against gold-standard methods (MIC testing and whole genome sequencing), review of diagnostic variability, governance evaluation, and feasibility testing of engagement incentives such as proficiency testing, dashboards and isolate comparison. An implementation-science and co-design approach underpinned iterative learning with PVLs.

Results: More than 40 PVLs were identified; 27 were successfully onboarded across farmed, companion, equine, and fish sectors. Tailored data-sharing agreements improved trust and ensured secure, routine data flow. Automated extraction and validation pipelines demonstrated strong technical feasibility.

Approximately 973,000 AST result lines (Apr 2024–Dec 2025) were collated. Early analyses and validity assessments revealed clear variation in diagnostic methods, AST panel selection, and metadata completeness, identifying priority areas for data-quality improvement. Individual sectors were at different stages of maturity, affecting participation, data completeness and overall quality of early outputs. Programme-level coordination accelerated cross-sector learning and ensured alignment to overall project aims.

Conclusions: Integrating AMR data from PVLs is feasible and offers clear potential to strengthen national surveillance. Through a public–private partnership, PLI has unlocked clinical datasets and improved representativeness of national data. By establishing a two-way feedback loop valued by participating laboratories, PLI is generating evidence on requirements for sustainable, high-quality data flows. Key challenges remain: heterogeneous methods, inconsistent metadata, and reliance on voluntary participation. Nonetheless, PLI offers transferable lessons where private diagnostics dominate: building trust, proportionate data-sharing, and mutual incentives that overcome access barriers are essential.

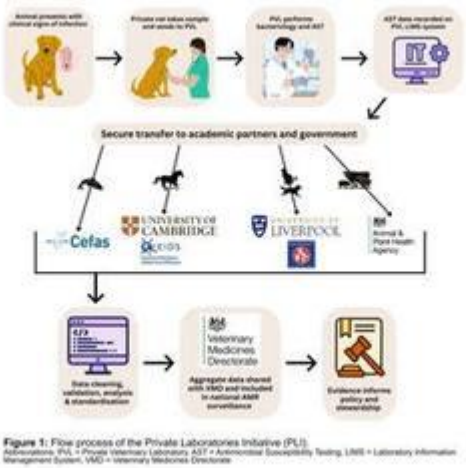


Figure 1: Flow process of the Private Laboratories Initiative (PLI).

Impact of reducing colistin use in livestock on colistin resistance in human and poultry in Indonesia (COINCIDE)

Soe Yu NAING (1), Anis KARUNIAWATI (2), Juliëtte SEVERIN (3), Kuntaman KUNTAMAN (4), Annisa RACHMAWATI (5), Sunandar SUNANDAR (5), Imron SUANDY (6), Nofita NURBIYANTI (5), Alicia WIDYA (4), Laela FITRIAH (2), Lili HASANAH (2), Tri WIDAYATI (7), Ully Indah APRILIANA (7), Puji RAHAYU (8), Dhini Rahayu NINGRUM (9), Tri NURDIANTI (9), Mohammad JOKAR (10), Diego NOBREGA (10), Mathieu PRUVOT (10), Koen PEETERS GRIETENS (9), Aldert ZOMER (1), Mira Leonie SCHNEIDERS (9), Jaap A. WAGENAAR (1), Coincide CONSORTIUM (11)

1: Division of Infectious Diseases and Immunology, Department of Biomolecular Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands; 2: Department of Clinical Microbiology, Faculty of Medicine, Universitas Indonesia; 3: Department of Medical Microbiology and Infectious Diseases, Erasmus MC University Medical Center Rotterdam, Rotterdam, the Netherlands; 4: Department of Clinical Microbiology, Faculty of Medicine Universitas Airlangga Dr. Soetomo General Academic Hospital, Surabaya, Indonesia; 5: Center for Indonesian Veterinary Analytical Studies, Bogor, Indonesia; 6: Balai Besar Veteriner (BBV) Denpasar, Denpasar, Indonesia; 7: Balai Besar Veteriner (BBV) Wates, Yogyakarta, Indonesia; 8: National Quality Control and Certification for Animal Products Laboratory (BPMSPH), Ministry of Agriculture, Bogor, Indonesia; 9: Department of Public Health, Institute of Tropical Medicine, Antwerp, Belgium; 10: Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada; 11: COINCIDE Consortium

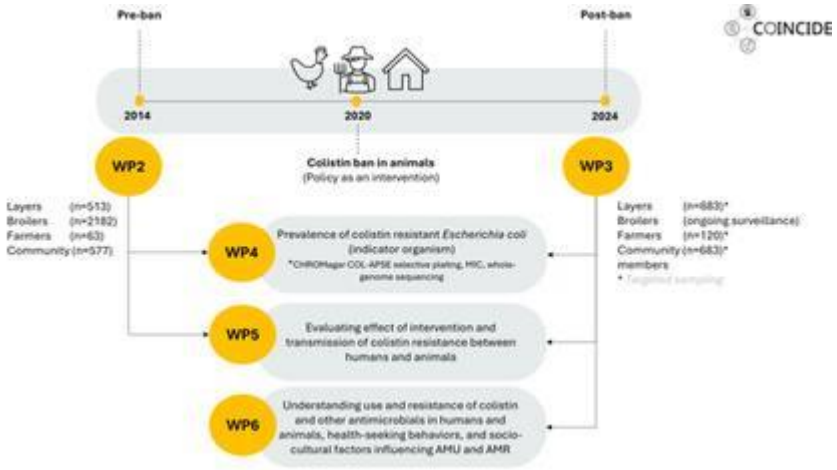
Background: Colistin is a last-resort antibiotic used to treat infections caused by multidrug-resistant Gram-negative bacteria in humans. In Indonesia, detection of colistin use and resistance in commensal *Escherichia coli* from poultry led to a national ban on its use in livestock, effective since July 1st, 2020. However, the impact of this policy intervention on colistin resistance in both humans and livestock has not yet been fully evaluated. The COINCIDE study investigates the effect of the ban by assessing compliance with the colistin ban, resistance patterns, and transmission dynamics of colistin-resistant *E. coli* between humans and poultry.

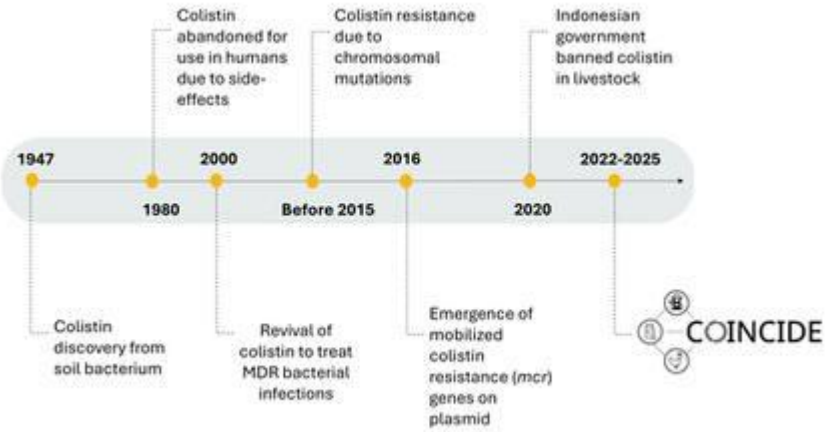
Method: This mixed-methods study triangulated pre- and post-ban microbiological and epidemiological data with social science findings in Central Java, Indonesia. A total of 2,522 *E. coli* isolates were collected from community members at primary healthcare (PHC) centers (n=1,069), layer farmers (n=175), and layer chickens (n=1,278). Phenotypic resistance was screened using CHROMagar™ COL-APSE, confirmed by microbroth dilution testing and whole-genome sequencing (WGS). In parallel, qualitative ethnography work included participant observation and informal conversations during field visits, alongside in-depth interviews (n=36) with healthcare professionals and other stakeholders. The participatory "Drug bag" method interviews (n=36) assessed antibiotic use, access, and drivers at the community level. Simulated patient visits to pharmacies and local shops (*warung*), and interviews with agrovet outlets and poultry shops were conducted to evaluate compliance with antibiotic sales regulations.

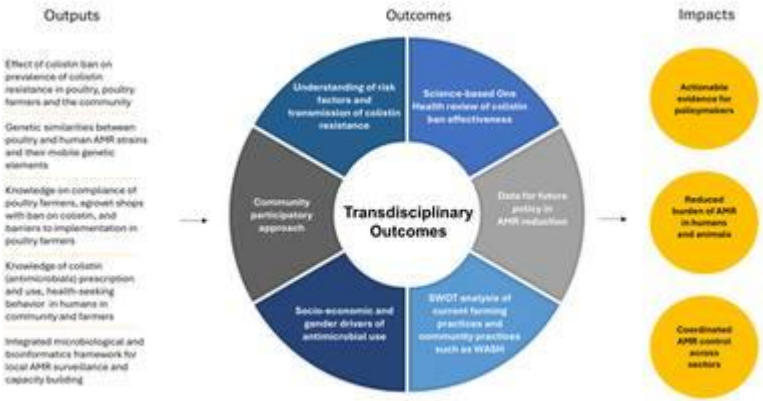
Results: Colistin-resistant *E. coli* prevalence was less than 1% in both humans and layer chickens, with the *mcr*-1 variant present, confirmed by WGS. Except for a single case of topical colistin use in the community, no colistin use or resistance was found post-ban. In the community, other antibiotics were not only widely accessible without prescription but also deeply embedded in everyday life, from practices of self-medication, 'hereditary' repurposing and sharing to the casual use of topical and candy-like antibiotics. The interviews with PHC staff reported barriers to rational prescribing of antibiotics in PHC due to a lack

of proper diagnostic facilities, high workload, and lack of awareness of the urgency of antimicrobial resistance in PHC settings.

Discussion: Colistin resistance was detected only in pre-ban samples, with a prevalence of less than 1% in both layer chickens and humans in the community. Indonesia took an important policy initiative by banning colistin. As a result, colistin resistance is very low compared to other Asian countries. By integrating microbiological data from two One Health domains (humans and animals), molecular epidemiology, policy analysis, and qualitative ethnography, COINCIDE's transdisciplinary and locally grounded approach can serve as a scalable model for AMR cross-sectoral surveillance and policy evaluation in Asia.







Antimicrobial resistance - session 3

SCS20 · 11:00-12:30 · Auditorium I

Rapid Antibiotic Susceptibility Testing Directly from Urine: A One Health Perspective

Mariana SOUSA-PINHEIRO (1,2), Francisco PASSOS-CARNEIRO (3), Patrícia POETA (4,5,6), Cidália PINA-VAZ (1,7), António J. SOARES (1)

1: RISE-Health, Faculty of Medicine, University of Porto, Portugal; 2: University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal; 3: UNILABS, Porto, Portugal; 4: Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal; 5: CECAV – Veterinary and Animal Research Centre, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal; 6: Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Portugal; 7: FASTinov SA, Porto, Portugal

Background. Urinary tract infections (UTIs) are among the most common bacterial infections associated with significant morbidity, great use of antimicrobials and even leading to urosepsis. Conventional microbiological workflows for pathogen identification and antimicrobial susceptibility testing (AST) typically require up to 48 hours to generate results, leading clinicians to initiate empirical broad-spectrum antibiotic therapy. This practice contributes to the emergence and dissemination of antimicrobial resistance, a critical challenge addressed within the One Health framework. The objective was to evaluate a new rapid AST developed by FASTinov to obtain a 2 h identification and phenotype profile of the microorganism responsible for UTI, directly from urine.

Methods. 101 urine samples were analysed including 11 inoculated with ATCC samples in urine of healthy volunteers and 90 urine samples collected from patients at UNILABS from July to September of 2026. The urine samples were analysed as routinely on Sysmex UF5000 and selected when bacteria were >40000/ml (contaminations were excluded). The QUICKprep kit from FASTinov® was used to produce a concentrated pellet in less than 5 min. This pellet was used immediately for identification (ID) on MALDI and then inoculated on FASTinov kits ® for AST testing based on phenotype in less than 2 h based on flow cytometry analysis, looking for cell lesions and not for cell growth. The same samples follow the conventional protocol; subculture on CLED, identification on MALDI from the over-night colonies and the phenotype evaluation on Vitek bioMérieux at 48 h after sample collection. Both results were compared

Results. ID with the QUICKprep and from colonies were similar in all cases obtained direct from QUICKprep (Table 1) except in 6 samples (6.3%) where MALDI gave no identification directly; those samples showed more than one microorganism on culture. On those cases, the rapid susceptibility with FASTinov was not performed as rapid phenotypes needs rapid identification. All the bacteria identified were Gram-negative so, FASTgramneg galleries from FASTinov® were inoculated. No Gram-positive during this study period were considered as UTI agent. The results obtained with the Machine Learning algorithm of FASTinov were compared with the obtained with routine procedures. The CA was 99.4% with very few errors (Table 2).

Conclusions. From a One Health perspective, accelerating diagnostic workflows in human healthcare has broader implications for controlling antimicrobial resistance across interconnected human, animal, and environmental systems. Integrating such technologies into routine practice may therefore play a crucial role in global efforts to preserve antibiotic effectiveness and mitigate the spread of resistant microorganisms.

Table 1- Identification of the bacteria identified by classic methodology from urine

Identification	Inoculated	Clinical	Total
Escherichia coli	4	58	62
Klebsiella pneumoniae	4	16	20
Proteus mirabilis		4	4
Pseudomonas aeruginosa	1	1	2
Enterobacter cloacae	1	1	2
Klebsiella aerogenes		1	1
Providentia rettegeri	1		
Citrobacter koseri		2	
Morganella morgannii		1	
Total	**11**	**84**	**95**

Table 2. Characterization of the phenotype of the studied strains and the categorical agreement (CA) between the results of the test of FASTinov ® obtained after 2 h and the routine method after 48h

Antimicrobial agent	n	S	I	R	CA%	mE	ME	VMR
Ampicillin	93	47	0	46	100			
Amoxicillin/clavulanic acid	93	78	0	15	98.9	1		
Cefotaxime	93	76	0	17	100			
Ceftazidime	95	81	0	14	100			
Cefepime	95	85	3	7	98.9	1		
Ceftazidime/avibactam	95	88	0	7	100			
Ceftolozane/tazobactam	95	88	0	7	100			
Piperacillin/tazobactam	95	85	0	10	98.9		1	
Meropenem	95	89	0	6	100			
Ciprofloxacin	95	70	11	14	96.8	3		
Gentamicin	95	81	0	14	98.9			1
Amikacin	95	94	0	1	98.9		1	
Nitrofurantoine	62	62	0	0	100			
Fosfomicin	62	62	0	0	100			
TOTAL	1258	1086	14	176	99.4	0.44%	0.18%	0.57%
ESBL+	7							
AmpC	1							
Carbapenemases	2							

N = number of strains; S = Susceptible; I = Intermediate; R = Resistant

mE = minor error; ME = major error; VMR = very major error

Beyond Policy to Practice: A political economy analysis of integrating gender and equity in the policy framework and governance of national Antimicrobial Resistance responses in Bangladesh

Syeda Tahmina AHMED (1), Farha Musharrat NOOR (1), Sneha PAUL (1), Sally THEOBALD (2), Rosie STEEGE (2), Katy DAVIS (2), Meenakshi MONGA (2), Bachera AKTAR (1), Syed Masud AHMED (1), Sabina Faiz Rashid RASHID (1)
1: BRAC University, Bangladesh, People's Republic of; 2: Liverpool School of Tropical Medicine

Background Antimicrobial resistance (AMR) is a complex, multisectoral challenge that extends beyond clinical settings, deeply intertwined with social determinants, governance structures, and health-seeking behaviors. However, the political and governance environment for integrating gender equity into AMR policies remains critically understudied. This research examines the upstream governance factors—including policy processes, institutional coordination, financing, and diplomacy—that enable or constrain the integration of gender and equity considerations into Bangladesh's AMR policy frameworks, aligning with the One Health governance agenda.

Methods We conducted key informant interviews (KIIs) with 14 national-level stakeholders, and health and technical experts in the private sector, from all one health domains- human, animal and environment health sectors and involved in AMR policy formulation and implementation. Qualitative data were collected, coded thematically, and synthesized into a narrative analysis examining policy landscapes, institutional processes, and actor dynamics.

Findings While Bangladesh possessed strong national strategies and stewardship guidelines, no existing AMR policies explicitly integrated gender or addressed socioeconomic vulnerabilities. High-level policymaking did not mandate women's leadership across AMR sectors, reflecting a fundamental governance gap. In tertiary hospital-based AMR surveillance systems, identification of vulnerable populations by age, geography, or marginalized conditions was not prioritized; thus, data were often underutilized for policy feedback, developing clear data-sharing framework. Governance of equitable AMR measures was found crippled by weak inter-ministerial coordination, including irregular AMR committee meetings and slow decision-making. Regulatory enforcement failures persisted, such as weak implementation of standard Infection Prevention and Control (IPC) guidelines in hospitals, and non-recommended antibiotic prescribing and dispensing by healthcare professionals and informal providers continue unchecked. Women's representation in regulatory and pharmaceutical professions remained negligible. Health system staff lacked a basic understanding of AMR's disproportionate impact on women, with no periodic refresher training on rational antibiotic use or One Health interlinkages. AMR programs demonstrated historical dependency on external funding; recent contractions in global AMR research and development financing threaten sustainability. Diplomatic imbalances persisted, with animal and environmental health sectors receiving lower priority and negotiating power compared to human health, their agendas heavily influenced by international donors.

Conclusion Addressing AMR's disproportionate burden on women requires fundamental governance reforms. Policy tools must mandate gender integration and equity audits across all AMR action plans. Surveillance systems urgently need sex-disaggregated data to identify vulnerable populations. Regulatory frameworks require strengthening to enforce IPC standards and antibiotic prescribing practices, including engagement with the informal private sector. Workforce development must include mandatory gender-sensitive AMR training and strategies to increase women's leadership in regulatory and pharmaceutical professions. Sustainable financing mechanisms and balanced diplomatic engagement across all One Health sectors are essential. This study demonstrates that achieving justice and equity in AMR mitigation is fundamentally a governance challenge requiring political commitment, institutional reform, and inclusive policy processes.

Integrating Digital Monitoring and Biological Interventions to Reduce Antimicrobial Use and Greenhouse Gas Emissions in Vietnamese Aquaculture: A One Health Field Trial

Chaokun HONG (1,2), Sonia LEWYCKA (1,2), Kim Dang HOANG (2), Hai Ngo Hoang TUAN (2)

1: University of Oxford; 2: Oxford University Clinical Research Unit

Background

Climate change and antimicrobial resistance (AMR) represent converging global crises disproportionately affecting low- and middle-income countries. Rising temperatures intensify aquatic disease outbreaks, compelling farmers to increase antimicrobial use and creating conditions for AMR proliferation. Simultaneously, intensive aquaculture practices generate substantial greenhouse gas (GHG) emissions, further accelerating climate change. Despite growing recognition of these interlinked challenges, interventions addressing both AMR and GHG reduction simultaneously remain absent from the evidence base. Vietnam, the world's fourth-largest aquaculture producer, exemplifies this dual crisis at farm level, where climate-driven extreme weather events increasingly destabilize small-scale production systems dominated by household operations with limited environmental management capacity, threatening both food security and rural livelihoods.

Methods

We implemented a matched-pair exploratory field trial across six small-scale fishponds in Ninh Binh Province, Vietnam, from September 2025 to May 2026. The integrated climate-smart intervention combined: (1) Internet-of-Things sensors providing continuous environmental monitoring (dissolved

oxygen, pH, temperature, ammonia) at 20-minute intervals; (2) automated rule-based decision support generating real-time risk alerts; (3) probiotic supplementation (Bacillus subtilis, Lactobacillus plantarum) delivered through automated feeders triggered by environmental deterioration; and (4) biochar water treatment modules. Three intervention ponds were compared against matched controls following conventional farmer practices. Primary outcomes included antimicrobial use intensity (mg/kg biomass), AMR gene abundance (intI1, sul1, blaTEM, tetM, tetW) quantified via qPCR in water and sediment, and GHG emissions (CH_4, N_2O) measured using static floating chambers. Secondary outcomes assessed fish survival, growth performance, economic viability, and farmer acceptability through mixed-methods evaluation.

Results

Preliminary findings will characterize the magnitude and consistency of intervention effects on antimicrobial use and AMR gene abundance—generating critical variance estimates for powering future definitive trials. Comparative GHG flux data will provide the first field evidence on whether hypothesized co-benefits between AMR mitigation and climate outcomes materialize under smallholder conditions. Process metrics will identify operational enablers and barriers to digital system adoption, while economic analysis quantifies cost-benefit trade-offs essential for viability assessment. Farmer perspectives on system usability and continued adoption intentions will illuminate implementation pathways for potential scaling beyond research contexts.

Conclusions

This study provides the first field-based evidence examining whether integrated digital and biological management can simultaneously reduce antimicrobial use and GHG emissions without compromising productivity in small-scale tropical aquaculture. By linking environmental sustainability with antimicrobial stewardship within a One Health framework, findings will contribute pilot evidence toward developing integrated AMR-climate interventions that support both climate change mitigation and resilience to extreme weather events. The trial establishes a methodological foundation for data-driven, climate-responsive aquaculture management addressing interconnected planetary health challenges, with implications for future policy-relevant research in Vietnam and the region.

---

eAMR CONNECT: An AI-Driven One Health Platform for Data Integration and Decision Support in Ethiopia

Workeabeba TAYE (9), Getachew ALEMKERE (1), Tigist WONDIMNEW (2), Wondimagegn TAMIRU (1), Ataklti HADUSH (3), Tesfaye GABRIEL (4), Alemu TADESSE (5), Betelhem LEMMA (1), Birhanu NEGERI (6), Umer TESHOME (6), Redet GETACHEW (7), Betsegaw Lemma AMERSHO (2), Yordanos Tadesse KIDANEMARIAM (8), Mirgissa Kaba SERBESSA (8)

1: Department of Pharmacology and Clinical Pharmacy, School of Pharmacy, College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia; 2: Addis Ababa Institute of Technology, Addis Ababa University, Addis Ababa, Ethiopia; 3: Veternary Drug Standardization and Drug Information, Ethiopian Agricultural Authority, Addis Ababa, Ethiopia; 4: Department of Pharmaceutics and Industrial Pharmacy, School of Pharmacy, College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia; 5: Department of Pharmaceutical Chemistry and Pharmacognosy, School of Pharmacy, College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia; 6: Ethiopian Roads Administration, Addis Ababa, Ethiopia; 7: Department of Computer Science, College of Informatics, University of Gondar, Gondar, Ethiopia; 8: School of Public Health, Addis Ababa University, Addis Ababa, Ethiopia; 9: Pediatric Infectious Disease Unit, Department of Pediatrics, School of Medicine, College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia

Background: Ethiopia faces a substantial antimicrobial resistance burden, with an estimated 85,000 AMR-associated deaths reported in 2019. Efforts to address this challenge are constrained by fragmented data systems, with information dispersed across the human, animal, and environmental health sectors. This lack of integration, together with concerns about data quality and accessibility, limits the ability of One Health (OH) stakeholders to generate coordinated, evidence-based responses. This project aimed to design and implement eAMR CONNECT, an AI-enabled, web-based platform that integrates multisectoral AMR information through an OH lens and provides accessible, context-specific insights to support clinical and policy decision-making.

Methods: eAMR CONNECT was developed in Ethiopia using an iterative software development lifecycle. The platform is based on a Retrieval-Augmented Generation architecture that combines document retrieval with large language models to generate context-aware responses. OpenAI and Gemini APIs were

integrated with domain-specific guardrails to filter irrelevant queries and reduce hallucinations. A curated collection of AMR-related research articles was processed, converted into semantic embeddings, and indexed in a vector database. When a user submits a query, the system retrieves the most relevant document segments and generates structured responses organized according to the OH framework, presenting findings from human, animal, and environmental perspectives. Core functionalities include a mobile-optimized user interface, session-based contextual memory, and a “Select Perspective” feature that allows users to focus on specific OH domains. To improve transparency, generated responses are linked to their source documents. The platform also supports automated collection of information from accessible peer-reviewed journals and validated local repositories. Ethical safeguards include consent prompts, a dedicated Terms of Use and Privacy Policy interface, and alignment with national data governance requirements that prohibit unauthorized external storage or sharing of user data.

Results: eAMR CONNECT was successfully developed, deployed on an institutional domain, and launched on 2 September 2025. Initial engagement during a stakeholder workshop included participation from government institutions and development partners. The platform generated concise, topic-specific responses in accessible language, with optional expanded detail for technical users. By combining semantic retrieval and generative AI, it improved the accessibility and interpretability of AMR-related information. Source attribution strengthened transparency, while structuring outputs by OH domain highlighted cross-sectoral relationships relevant to AMR prevention and control. The system was designed to support future interoperability with Public Health Institute systems and electronic medical records. Planned improvements include integration of additional datasets, stronger response-validation mechanisms, and data visualization tools to further support evidence-informed decision-making.

Conclusions: eAMR CONNECT demonstrates the potential of AI-enabled tools to harmonize fragmented OH data in Ethiopia. Immediate integration into national surveillance and clinical workflows is recommended. Future priorities should include optimizing the institutional domain for high-traffic public access, expanding automated source validation protocols, and embedding visualization tools to strengthen long-term reliability and clinical accuracy.

One Health molecular surveillance of methicillin and vancomycin resistance genes in Gram-positive cocci from companion animals in Southern Brazil

Jorge de Souza FRANCISCO JUNIOR (1), Ana Paula DE SA TOMELIN (1,2), Barbara SCHMINSKY DE FRANCA (1), Letícia MOURA DIONISIO (1), Mariane BATISTI (1), Vanessa CRISTINE KOBS (1), Roseneide CAMPOS DEGLMANN (1), Eleine KUROKI ANZAI (3), **Paulo FRANCA** (1)

1: Universidade da Região de Joinville - Univille, Brazil; 2: Genolab – Laboratório de Análises Genéticas, Imunogenéticas, Clínicas, Pesquisas e Vacinas Ltda, Brazil; 3: Fundação Universidade Regional de Blumenau, Brazil

Background: Antimicrobial resistance (AMR) in companion animals represents an increasingly relevant interface among veterinary practice, zoonoses and human health. Methicillin-resistant staphylococci (MRSA) and vancomycin-resistant enterococci (VRE) are of particular concern due to their capacity to circulate across hosts and persist in domestic settings. However, molecular data on resistance genes in clinical isolates from companion animals in Southern Brazil remain limited. This study aimed to assess the genotypic AMR profile of Gram-positive cocci isolated from diseased dogs and cats receiving veterinary care in Santa Catarina State, within a One Health framework. **Method:** A cross-sectional laboratory-based study was performed using bacterial isolates from two veterinary diagnostic laboratories in Joinville and Blumenau, Brazil. Clinical samples originated from diseased dogs (n = 119) and cats (n = 26), collected from multiple anatomical sites, yielded 157 Gram-positive cocci isolates. Phenotypic antimicrobial susceptibility data were retrieved from routine laboratory records. Species level identification was performed by MALDI-TOF MS. Genomic DNA extraction was extracted using a commercial kit (PureLink, Thermo Fisher Scientific, USA). DNA integrity was confirmed by partial amplification of the 16S rRNA gene. PCR assays were also used to investigate the *mecA* gene in staphylococcal isolates and *vanA* and *vanB* genes in enterococci. **Results:** Among the 157 isolates, 128 belonged to *Staphylococcaceae* and 29 to *Enterococcaceae*. The predominant staphylococcal species were *S. pseudintermedius* (n = 79) and *S. schleiferi/coagulans* (n = 30), while *E. faecalis* (n = 17) and *E. faecium* (n = 8) predominated among enterococci. Resistance to penicillin G (n = 41/86) and oxacillin (n = 13/123) was frequently observed among staphylococcal isolates. The *mecA* gene tested positive in 20 (15.6%) isolates. Among the *mecA* positive strains, there were isolates resistant to oxacillin (n = 8), susceptible (n = 10) or

not assessed (n = 2). No enterococcal isolates exhibited vancomycin resistance or harbored *vanA* or *vanB* determinants. **Conclusions:** The presence of *mecA*-positive staphylococci in clinical isolates from companion animals underscores the circulation of clinically relevant resistance determinants within shared human-animal environments. Although *vanA* and *vanB* genes were not detected, the findings reinforce the need for integrated molecular and phenotypic surveillance strategies. Companion animals should be considered key components in regional One Health frameworks to monitor and mitigate the dissemination of mobile AMR elements across veterinary, human, and environmental domains.

Integrating environmental data into an integrated assessment model for antimicrobial resistance (iAM.AMR)

Manuel PEREZ MALDONADO, Jane PARMLEY, Richard REID-SMITH

University of Guelph, Canada

Background: Antimicrobial resistance occurs when microorganisms evolve mechanisms that allow them to survive exposure to antimicrobials, posing a major threat to human and animal health. Resistant bacteria and resistance genes circulate across interconnected settings, including farms, hospitals, communities, and natural environments. While antimicrobial use is the primary driver of AMR, environmental reservoirs and cross-sector transmission pathways also contribute to its persistence and spread. Integrated modelling approaches can help capture these complex dynamics. This study had two objectives: first, to expand the existing Integrated Assessment Model on Antimicrobial Resistance modelling framework to incorporate environmental and animal antimicrobial resistance data; and second, to use this framework to evaluate the impact of reducing tetracycline-resistant bacteria at different sources on human exposure.

Methods: Phenotypic antimicrobial resistance data were obtained from the Canadian Integrated Program for Antimicrobial Resistance Surveillance, and genotypic data from the Antimicrobial Resistance Genes in Bioaerosols Project, using samples collected in Québec, Canada, from 2020 to 2023. Data included isolates or samples from livestock farms, environmental sources (e.g., wastewater treatment plants, air filters, hospitals), and broiler chicken farms. A group model-building process involving epidemiologists and risk modellers from the Public Health Agency of Canada and the University of Guelph was used to integrate these data into the Integrated Assessment Model on Antimicrobial Resistance framework. Outputs from a source attribution model were used to adjust baseline probabilities of tetracycline-resistant *E. coli* isolatesor samples entering broiler chicken farm and abattoir nodes. The model was implemented in Analytica to simulate intervention scenarios and estimate the number of people potentially exposed to TET-R through chicken consumption in Québec.

Results: Results indicate that reducing tetracycline resistance at broiler chicken farms alone decreased weekly exposure by approximately 134,000 individuals in Québec, while similar reductions across all farm types decreased exposure by 2.287 million, and across all sources by 2.528 million.

Conclusions: These findings show that interventions targeting a single source may be insufficient, and highlight the need for coordinated, multisectoral mitigation strategies to significantly reduce exposure to antimicrobial resistance. The Integrated Assessment Model on Antimicrobial Resistance modelling framework allows for testing multiple scenario sources across the food chain and provides a helpful tool for designing integrated One Health interventions. Future developments incorporating bidirectional feedback, such as environmental recontamination, would improve the model's ability to capture real-world dynamics of antimicrobial resistance dissemination.

Late Breakers: novel and outstanding discoveries

SCS22 LB · 14:00-15:30 · Auditorium I

Spillover of H5 influenza viruses to vampire bats at the marine-terrestrial interface

I-Ting TU (1,2), Christina LYNGGAARD (3), Lorin ADAMS (4,5), Sarah K WALSH (2), Hanting CHEN (2), Savitha RAVEENDRAN (2), Matthew L TURNBULL (2), Megan E GRIFFITHS (1,2), Rita RIBEIRO (1,2), Jocelyn G PÉREZ (1,2), William Valderrama BAZAN (6,7), Carlos TELLO (7), Carlos ZARIQUIEY (7,12), Kristhie Pillaca RODRIGUEZ (7,13), Marco RISCO (7), Illariy Quintero MAMANI (7), Wendi CHÁVEZ (7), Roselvira Zuniga VILLAFUERTE (7), Joaquin Clavijo MANUTTUPA (7), Jean Pierre CASTRO NAMUCHE (7), Andres MOREIRA-SOTO (8), Jan Felix DREXLER (8), Gustavo DELHON (9), Susana CÁRDENAS-ALAYZA (10,11), Massimo PALMARINI (2,14), Kristine BOHMANN (3), Ruth HARVEY (4), Christina FAUST (1), Ed HUTCHINSON (2), Pablo R MURCIA (2), Daniel G STREICKER (1,2)

1: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow; Glasgow, G12 8QQ, UK; 2: MRC-University of Glasgow Centre for Virus Research; Glasgow, G61 1QH, UK; 3: Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen; Copenhagen, Denmark; 4: Worldwide Influenza Centre, The Francis Crick Institute; London, NW1 1AT, UK; 5: Royal Veterinary College; London, NW1 0TU, UK; 6: Universidad Peruana Cayetano Heredia. Facultad de Medicina Veterinaria y Zootecnia; Lima, Perú; 7: Asociación para el Desarrollo y Conservación de los Recursos Naturales (ILLARIY); Lima, Perú; 8: Charité Universitätsmedizin; Berlin, 10117, Germany; 9: University of Nebraska-Lincoln; NE, 68588 USA; 10: Centro para la Sostenibilidad Ambiental, Universidad Peruana Cayetano Heredia; Lima, Perú; 11: Facultad de Ciencias e Ingeniería, Universidad Peruana Cayetano Heredia; Lima, Perú; 12: Programa de Maestría en Salud Pública y Salud Global. Facultad de Salud Pública y Administración. Universidad Peruana Cayetano Heredia; Lima, Perú; 13: Centro de ornitología y biodiversidad (CORBIDI), División de Mastozoología; Lima, Perú; 14: Department of Viroscience, Erasmus Medical Center; Rotterdam, The Netherlands

Background

In late 2022, H5N1 avian influenza A virus (IAV) caused mass mortality in seabirds and South American sea lions along the Peruvian coast. In these areas, common vampire bats (*Desmodus rotundus*) are suspected to feed on marine wildlife, potentially facilitating pathogen transmission at the marine-terrestrial interface.

Methods

To investigate H5N1 IAV exposure in vampire bats, we collected 861 serum samples from 12 Peruvian sites (2011–2024) representing different foraging ecologies: coastal roosts with marine contact (100 m from seafront, N=431), without marine contact (>5 km, N=373), and inland roosts (N=57). A subset of hair and rectal swab samples was analysed for diet as a proxy for prey contact. Additionally, in-vitro experiments assessed the distribution of IAV receptors in vampire bat tissues and the permissiveness of vampire bat cells to avian influenza viruses.

Results

We detected 14 H5 seropositive vampire bats exclusively from marine-contact sites across multiple years. Stable isotope analysis and dietary metabarcoding identified putative sources of bat exposures including South American sea lions, pelicans and vultures, but also revealed feeding on livestock, indicating that bat feeding may bridge marine and agricultural IAV transmission cycles. Vampire bat-derived kidney, liver and lung cells supported replication of multiple IAVs, including 2.3.4.4b viruses, and bat trachea and lung expressed both α2,3 and α2,6 sialic acid receptors.

Conclusion

Low H5 seroprevalence in marine-contact sites suggests sporadic exposure from infected wildlife or contaminated environments. However, the co-expression of both avian- and human-type receptors in bat respiratory tract, the permissiveness of bat cells to IAVs and recurrent viral exposure provide opportunities for adaptation and reassortment with other IAVs. This marine-terrestrial interface may facilitate pathogen spillover to other prey, particularly where bats feed on both marine and domestic animals. We identify a bat-borne pathway for IAV spread between ecosystems which could promote co-infection and reassortment, the primary mechanism underlying past influenza pandemics.

Advancing One Health Solutions to Antimicrobial Resistance: Outcomes from Canada's Genomics Research and Development Initiative

Rahat ZAHEER (1,3), AMR-One Health Team GRDI (3), Catherine CARRILLO (2,3), Tim MCALLISTER (1,3)

1: Agriculture and Agri-Food Canada; 2: Canadian Food Inspection Agency; 3: Genomics Research and Development Initiative for Antimicrobial Resistance - One Health (GRDI AMR-OH) Government of Canada

Antimicrobial resistance (AMR) is a growing global threat affecting human, animal, and environmental health, requiring coordinated action across sectors. The Canadian Genomics Research and Development Initiative on Antimicrobial Resistance – One Health program (GRDI AMR-OH) was established to address this challenge through an integrated One Health framework that leverages genomic technologies, cross-sector surveillance, risk assessment, and mitigation strategies.

The initiative brings together 33 scientists from seven Canadian federal science-based departments and agencies, including Agriculture and Agri-Food Canada, the Canadian Food Inspection Agency, Fisheries and Oceans Canada, Environment and Climate Change Canada, Health Canada, the National Research Council of Canada, and the Public Health Agency of Canada. Research activities are organized into six interconnected work packages addressing: (i) drivers, reservoirs, and dissemination of AMR in environmental matrices; (ii) AMR in healthcare settings and at-risk communities; (iii) mitigation of AMR development and transmission along the farm-to-fork continuum; (iv) transmission pathways of AMR pathogens across the One Health continuum; (v) application of genomics for risk science; and (vi) real-time detection, data integration, and communication of AMR findings.

Although the program continues through 2027, significant outcomes have already been achieved. These include the identification of AMR hotspots across clinical, agricultural, and environmental settings; characterization of potential transmission pathways linking humans, animals, food, and the environment; development of standardized approaches for genomic data generation, storage, and sharing; incorporation of genomics into policy and regulatory decision-making frameworks; and development of promising antimicrobial alternatives, including plant-derived bioactives and vaccines. The initiative has also strengthened interdepartmental collaboration and enhanced Canada's capacity for integrated AMR surveillance and response.

This presentation will highlight key scientific and translational achievements of the program and demonstrate how a genomics-enabled One Health approach can improve understanding of AMR emergence and transmission while supporting evidence-based interventions to reduce the burden of AMR across interconnected ecosystems.

One Health distribution of clinically relevant antimicrobial-resistant bacteria across humans, animals and the environment in rural Côte d'Ivoire: First results from a One Health cohort

Alexandra BAHR (1), Dennis KARNATZ (1), Phillip LÜBCKE (1), Lena-Sophie SWIATEK (1), Oby WAYORO (2,3,4), Pacôme MONEMO (3,4), Léonce KOUADIO (5,6,7), Anne Mutuo KIMEU (1), Franziska STOEK (2), Moritz JOCHUM (5), Kathrin NOWAK (2), Filipe DIAS (2), Jasmin SCHLOTTERBECK (5), Simon KRÜECKEMEIER (5), Vincent ACHI (3,4), Fabian H. LEENDERTZ (5), Fee ZIMMERMANN (2), Katharina SCHAUFLER (1)

1: Department of Epidemiology and Ecology of Antimicrobial Resistance, Helmholtz Institute for One Health (HIOH), Helmholtz Centre for Infection Research (HZI), Greifswald, Germany; 2: Research Group of One Health Surveillance, Helmholtz Institute for One Health (HIOH), Helmholtz Centre for Infection Research (HZI), Greifswald, Germany; 3: Centre Hospitalier et Universitaire (CHU) de Bouaké, Bouaké, Côte d'Ivoire; 4: Université Alassane Ouattara de Bouaké, Bouaké, Côte d'Ivoire; 5: Department of Ecology and Emergence of Zoonotic Diseases, Helmholtz Institute for One Health (HIOH), Helmholtz Centre for Infection Research (HZI), Greifswald, Germany; 6: Centre Suisse de Recherches Scientifiques (CSRS), Abidjan, Côte d'Ivoire; 7: Université Peleforo GON COULIBALY (UPGC) - Korhogo-Côte d'Ivoire

Background

Antimicrobial resistance (AMR) is a growing global health threat requiring a One Health approach to understand transmission across humans, animals, and the environment. Previous environmental sampling in Bouaké, Côte d'Ivoire, has revealed a high number of carbapenem- and cefiderocol-resistant bacteria in an urban clinical setting. A prospective One Health cohort study was conducted from February to May 2026 in nine rural villages surrounding Taï National Park to investigate the emergence of AMR and zoonotic diseases in a different ecosystem in Cote d'Ivoire (see also Posters by Filipe Dias (ID 474) and Oby Wayoro (ID897)).

Methods

A total of 3,936 samples were collected from humans, livestock, wildlife, and environmental sources. AMR Enterobacterales, Pseudomonadales, *Staphylococcus aureus*, and *Enterococcus* spp. were isolated using an in-house cultivation pipeline with selective chromogenic media. Antimicrobial susceptibility testing (AST) was performed using the VITEK2 system. Susceptibility to cefiderocol was determined by agar diffusion testing.

Results

To date, 974 samples have been processed, yielding 1,457 AMR isolates from 81% of all samples. Human stool samples yielded the highest number of AMR isolates per sample. AMR bacteria were detected across all investigated One Health compartments. Half of the processed wildlife samples were AMR-positive, yielding 45 isolates, including three *Serratia marcescens* isolates. In addition, 33% (n = 42) of environmental water samples were AMR-positive, yielding 119 isolates. *Escherichia coli* (n=590) and *Klebsiella pneumoniae* (n=285) were the most isolated bacteria and were found in all sample types, while *Citrobacter koseri* was detected exclusively in nasal swabs. Among processed human samples, 36.8% of participants carried methicillin-resistant *Staphylococcus aureus* (MRSA) in either nasal or nasopharyngeal swabs. AST has been completed for 138 isolates, identifying 71 third-generation cephalosporin-resistant, four carbapenem-resistant, and eight cefiderocol-resistant isolates. Notably, none of the cefiderocol-resistant isolates were carbapenem-resistant, indicating no overlap between carbapenem and cefiderocol resistance in the isolates tested to date. Human AMR positivity varied between villages (40–73%). Only one village showed a higher number of AMR positive samples in livestock than humans (80% vs. 64%) so far.

Conclusions

The detection of carbapenem- and cefiderocol-resistant bacteria in a remote rural region where neither antibiotic is routinely available suggests that clinically important resistance determinants circulate independently of local antibiotic availability. Together with the unexpectedly high community MRSA carriage, these findings highlight a substantial AMR burden in a rural population. Comparison with previous findings from urban Bouaké will provide insight into differences in AMR ecology between densely populated urban environments and a largely undisturbed ecosystem bordering Taï National Park. The exclusive recovery of *Citrobacter koseri*, an opportunistic pathogen increasingly associated with multidrug-resistant healthcare-associated infections, from nasal swabs warrants further investigation of its colonization ecology. Whole-genome sequencing and household questionnaire analyses are ongoing to identify transmission pathways and behavioral risk factors.

A wide diversity of viruses detected in African mammals involved in the wild meat supply chain

Mare GERAERTS (1,2), Laura N. CUYPERS (1,3), Sophie GOMBEER (3,4), Casimir NEBESSE (5), Fanny KRATZ (6), Douglas AKAIBE (5), Dudu AKAIBE (5), Pascal BAELO (5), Paola BURELLI (3), Anne-Lise CHABERT (7), Léa FOURCHAULT (3), Philippe GAUBERT (8,9), Guy-Crispin GEMBU (5), Léa JOFFRIN (2), Anne LAUDISOIT (2,10), Nicolas LAURENT (3,11), Herwig LEIRS (2), Claude MANDE (5), Joachim MARIËN (1,2), Steve NGOY (5), Brigitte SEGERS (3), Nathalie SMITZ (6), Sanne TERRYN (12), Jana TĚŠÍKOVÁ (2), Samuel VANDEN ABEELE (3), Ann VANDERHEYDEN (3), Rianne VAN VREDENDAAL (2), Erik VERHEYEN (2,3), Sophie GRYSEELS (2,3)

1: Institute of Tropical Medicine, Belgium; 2: Evolutionary Ecology group, Department Biology, University of Antwerp, Wilrijk, Belgium; 3: OD Taxonomy and Phylogeny, Royal Belgian Institute of Natural Sciences, Brussels, Belgium; 4: Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland; 5: Centre de Surveillance de la Biodiversité (CSB), University of Kisangani, Kisangani, Democratic Republic of the Congo; 6: Royal Museum for Central Africa, Tervuren, Belgium; 7: School of Animal and Veterinary Sciences, University of Adelaide, Adelaide SA, Australia; 8: Centre de Recherche sur la Biodiversité et l'Environnement (CRBE), Université de Toulouse, CNRS, IRD, Toulouse INP, Université Toulouse 3 – Paul Sabatier (UT3), Toulouse, France; 9: CIIMAR/CIMAR, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros Do Porto de Leixões, Avenida General Norton de Matos s/n, 4450-208 Matosinhos, Portugal; 10: Nature.Health.Global 321 Route 59, Unit 94, Tallman, NY 10982, USA; 11: Department of Environmental Sciences, Open Universiteit, Heerlen, The Netherlands; 12: Sciencano, Brussels, Belgium

Background: Wild meat acquisition, trade, and consumption are increasingly recognised as hotspots for zoonotic spillover. While several viral outbreaks have been traced back to this supply chain, our understanding of the mammalian virome circulating in the wild meat trade remains fragmentary and biased toward a limited number of mammalian taxa and pathogens. In parallel, the international

movement of animal-derived products highlights the need for integrated surveillance strategies to monitor potential biological risks associated with both legal and illegal wildlife trade activities.

Methods: We performed molecular species identification and metagenomic viral screening on (1) an archived tissue and swab collection of African wild animals traded for meat, sampled in multiple regions of the Democratic Republic of the Congo (N=149) and in Brussels, Belgium (N=16), and (2) recently collected samples of wild and domestic animal meat confiscated from passenger luggage at Brussels Airport, Belgium (N=179). Passenger controls, conducted by customs and local food safety authorities, primarily targeted flights arriving from Central Africa and East Asia.

Results: In samples from the archived tissue and swab collection, we identified 40 wild African species, including several protected and endangered species such as the okapi, pangolin, and chimpanzee. Metagenomic analyses revealed a high diversity of vertebrate viruses, with sixteen strains belonging to the families *Arteriviridae*, *Hepadnaviridae*, *Orthoherpesviridae*, *Picobirnaviridae*, *Picornaviridae*, *Retroviridae*, *Sedoreoviridae*, and *Spinareoviridae*. Of particular interest were strains with likely zoonotic potential, including human picobirnavirus, simian foamy virus, and rotavirus A.Analyses of more recently confiscated meat products, carried by airline passengers, are still ongoing. However, several viruses of human and veterinary health concern have already been identified in meat derived from both wild and domestic animals, including a novel orthohepdnavirid strain, peste-des-petits-ruminants virus, and avian influenza H9N2. Approximately one quarter of the confiscated meat products originated from wild animals, of which roughly one third was derived from protected species, including duikers, pangolins, and primates.

Conclusions: Our findings reveal a substantial diversity of viruses associated with the wild meat trade and highlight the importance of coordinated molecular surveillance efforts to better understand and mitigate the risk of zoonotic transmission linked to human–wildlife interactions and the international movement of animal products.

A functionally extinct SARS-CoV-2 lineage persists and evolves in white-tailed deer, independently generating Omicron-defining mutations with human spillback potential

Santhamani RAMASAMY (1), Yoshitha JALADANKI (1), Jobin KATTOOR (1), Aniket NAIK (1), Ariel ENDLICH-FRAZIER (2), Michael LETKO (2), Lindsey LABELLA (1), Vijayasri HARI (1), Jason BOULANGER (3), Nathan KOTSCHWAR (3), Christopher GRIFFIN (4), Xavier DIDELOT (5), Peter HUDSON (6), Kurt VANDEGRIFT (6), **Suresh KUCHIPUDI** (1)

1: Department of Infectious Diseases and Microbiology, University of Pittsburgh School of Public Health, Pittsburgh, USA; 2: Paul G. Allen School for Global Health, Washington State University, Pullman, USA.; 3: White Buffalo Inc., New York, USA; 4: Applied Research Laboratory, Pennsylvania State University, University Park, USA.; 5: Department of Statistics and School of Life Sciences, University of Warwick, Coventry, UK.; 6: Department of Biology, Eberly College of Science, Pennsylvania State University, University Park, USA

BACKGROUND: While SARS-CoV-2 has been detected in multiple wildlife species, it remains unclear whether wildlife populations sustain long-term independent circulation of the virus. We investigated whether white-tailed deer (WTD) serve as autonomous SARS-CoV-2 reservoirs capable of generating divergent variants with antibody-escape properties.

Methods: We conducted genomic surveillance of WTD in Princeton, New Jersey, in February 2025. We sampled 135 free-ranging WTD via nasal and oral swabs and serum collection. RNA was extracted and analyzed by RT-PCR using the OPTI SARS-CoV-2 assay. Whole-genome sequencing employed ARCTIC V5.3.2 amplicon sequencing. Lineage assignment used UShER, and phylogenomic analysis employed maximum parsimony and time-calibrated methods. Recombination analysis was conducted with RDP5, and selection analysis was performed using BUSTED, MEME, Contrast-FEL, and RELAX in HyPhy v2.5.83. Functional characterization included VSV pseudovirus entry assays and molecular dynamics simulations to calculate binding free energy (MM-GBSA). Predicted neutralization escape was estimated using the Bloom Lab DMS framework.

Results: Among 135 WTD sampled, 77 (57%) tested RT-PCR positive. Sequencing of 70 positive samples identified 38 genomes (54%) belonging to the ancestral B.1 lineage, which disappeared from human circulation in August 2022. Phylogenomic analysis estimated that the most recent common ancestor of Princeton B.1 and any known human sequences occurred approximately 4 years before this sampling. The B.1 lineage accumulated more than 53 amino acid substitutions relative to Wuhan-Hu-1. Notably, WTD B.1

independently acquired eleven Omicron-defining spike mutations despite complete isolation from human Omicron lineages. Recombination analysis revealed exchange between B.1 and BA.2 within the WTD population, with breakpoints absent from Omicron-defining positions, confirming convergent evolution. Selection analysis identified episodic diversifying selection in eight genes, particularly strong in Spike (ω_3=24.73) and ORF1a (ω_3=32.68). Seven amino acid substitutions arose independently in both lineages at identical codons. Two convergent mutations (R346T and K356T) in the class 3 RBD epitope are established antibody escape mutations. WTD-adapted B.1 RBDs bound human ACE2 with affinity comparable to Wuhan-Hu-1, while retaining tropism for human cells. VSV pseudoviruses bearing WTD B.1 RBDs entered human ACE2-expressing cells as efficiently as WTD cells. Predicted neutralization escape scaled with mutational divergence (r=0.835), with divergent variants escaping approximately 60% of the human monoclonal antibody panel. New Jersey wastewater surveillance (November 2023–June 2024) detected WTD-specific spike substitutions absent from contemporaneous human variants.

Conclusions: White-tailed deer sustain autonomous SARS-CoV-2 evolution, maintaining extinct human lineages while acquiring Omicron-defining mutations and substantial antibody escape through convergent evolution. Wildlife reservoirs are active generators of pandemic-relevant variants with potential for human spillback, with urgent implications for pandemic preparedness and wildlife surveillance infrastructure.

From Evidence to Action: A 30-Year Synthesis of CGIAR One Health Implementation Models for Scaling in Low- and Middle-Income Countries

Hung NGUYEN VIET

International Livestock Research Institute, Vietnam

Background

Despite widespread global commitment to One Health for addressing zoonotic diseases, antimicrobial resistance (AMR), and food safety risks, developing and translating national strategies into local implementation remains a persistent challenge in low- and middle-income countries (LMICs). For over three decades, CGIAR centers (ILRI, WorldFish, IFPRI, IWMI and others) and local and national partners have conducted One Health research and interventions across Africa and Asia, contributing directly to global health security, livelihood improvement, and environmental sustainability. Here, we share an actionable implementation framework for decision-makers shaped by a synthesis of these experiences.

Methods

In July 2026, researchers from across CGIAR centres convened a writeshop to synthesize One Health experiences. From the case studies that emerged (governance, AMR, food safety, capacity building, community engagement, service delivery, and surveillance), the team identified implementation models, extracted outcomes, and drew out lessons for more effective One Health operationalization.

Results

Six promising implementation models and outcomes emerged from the exercise: (1) community-governed One Health Units integrating human-animal-environmental service delivery, reaching ~300,000 people and 2.5 million livestock across Ethiopia, Kenya, and Somalia; (2) institutionalized multisectoral platforms (e.g., Vietnam's Food Safety Working Group, Cambodia's six-ministry taskforce) sustaining coordination beyond donor funding; (3) regional education benchmarks and workforce training programs reaching over 700 professionals across 12+ countries in Eastern and Southern Africa; (4) participatory behaviour-change approaches that outperformed top-down communication for gender-sensitive practice change and Antimicrobial use and resistance management; (5) decision-support tools (Rift Valley fever risk maps, revised brucellosis testing protocols) directly informing national policies in Kenya; and (6) the “three-legged stool” food-safety model reducing microbial contamination across five countries. Across domains, encouraging government ownership, embedding efforts within existing systems, and early donor investment emerged as critical success factors for scaling.

Conclusions

Three decades of One Health research-for-development experience demonstrate that the gap between policy and ground-level implementation could be narrowed by testing different models rather than

repeated one-off pilots. Collectively, our reflections illustrate how CGIAR's One Health efforts contributed to strengthening global health security while delivering substantial improvements on the ground. We offer governments, donors, and technical partners a concrete menu of investable One Health implementation options ready for scale-up across LMICs.

From Salmonella Strathcona outbreak traceback investigations to environmental surveillance of agricultural water: integrating epidemiology, genomics and passive sampling

Laura BORTOLAMI (1), Sara PETRIN (1), Stefano DI NOLA (2,3), Eleonora CHELLI (2), Fabrizio LAZZARA (2), Valentina CAMBIOTTI (2), Daniela ZORA (4), Giuseppe SMECCA (5), Carmelo CAMPISI (6), Paolo GERVASO (6), Alessandra STANCANELLI (7), Giuseppe CASCONE (7), Valeria GARGANO (7), Antonina ZIMMARDI (7), Giovanni BARONE (5), Maurizio MEZZASALMA (5), Lisa BARCO (1)

1: Italian National Reference Centre for Salmonellosis, Istituto Zooprofilattico Sperimentale delle Venezie, Padova, Italy; 2: Ministry of Health, Directorate-General for Hygiene and Food Safety, Rome, Italy; 3: Unit of Biostatistics, Epidemiology and Public Health, Department of Cardiac Thoracic Vascular Sciences and Public Health, University of Padova, Padova, Italy; 4: Department for Health Activities and Epidemiological Observatory, Regional Department of Health, Sicilian Region, Palermo, Italy; 5: Department of Prevention, Ragusa Local Health Authority, Ragusa, Italy; 6: Department of Prevention, Caltanissetta Local Health Authority, Caltanissetta, Italy; 7: Istituto Zooprofilattico Sperimentale della Sicilia "A. Mirri", Palermo, Italy

Background

Salmonella remains one of the leading causes of foodborne illness worldwide. Although surveillance has traditionally focused on serovars associated with foods of animal origin, fresh produce-associated salmonellosis has increased in Europe, with Italy frequently involved in Rapid Alert System for Food and Feed (RASFF) notifications concerning 'fruits and vegetables'. Recurrent vegetable-associated outbreaks have highlighted irrigation water as a critical but poorly investigated interface between the environment and primary production. Since 2023, a prolonged multinational outbreak caused by *Salmonella* Strathcona ST2559, likely linked to Sicilian cherry tomatoes, has prompted traceback investigations coordinated within a One Health framework involving the Italian Ministry of Health, the Italian National Reference Centre for Salmonellosis (NRCS) and local competent authorities

Methods

Official traceback investigations were performed in Sicilian farms associated with RASFF notifications related to *S.* Strathcona. A total of 258 samples, including irrigation and well water, cherry tomatoes, basil, soil and organic fertilizers, were analysed according to ISO 6579-1, and all *Salmonella* isolates were serotyped. In parallel, all available Italian non-human *S.* Strathcona isolates collected by the NRCS underwent whole genome sequencing (WGS) and core genome MLST (cgMLST) was applied to investigate their genetic relatedness. These findings supported the design of an ongoing environmental surveillance programme based on passive 'torpedo' samplers in irrigation systems, wells and natural water reservoirs in Sicily.

Results

Seventeen of 258 samples (6.6%) tested positive for *Salmonella*, with 16 (94.1%) recovered from irrigation or well water (Table 1). Nine different serovars were identified (Table 2), demonstrating the broad diversity of *Salmonella* in agricultural water. Repeated sampling over a six months recovered *S.* Toulon on three occasions from the same irrigation system and one from a neighbouring farm. WGS showed that isolates from the first farm belonged to the same genomic cluster, whereas the neighbouring isolate differed 22 alleles, suggesting persistence of a local lineage. National genomic surveillance further demonstrated that *S.* Strathcona is distributed across different Italian regions and environmental and animal matrices, including surface waters, shellfish and livestock farms. Nevertheless, a large proportion of the isolates, including 32 Italian non-human isolates, one Sicilian tomato isolate detected in Austria, eight human genomes from ENA and the outbreak reference sequence, belonged to a single highly homogeneous genomic cluster (Figure 1), supporting the persistence of a widespread clone and highlighting the difficulty of linking human cases to specific food sources.

Conclusions

Traceback investigations identified agricultural water as a priority target for environmental surveillance. The detection of multiple *Salmonella* serovars supports a shift from reactive outbreak investigations

towards proactive environmental and animal surveillance. These findings provide the rationale for implementing innovative passive 'torpedo' sampling to improve early detection of *Salmonella* in agricultural water and strengthen the prevention of fresh produce-associated outbreaks.

Figure 1: cgMLST minimum spanning tree of *S.* Strathcona isolates (32 Italian non-human isolates), together with the outbreak reference strain (2023), one Sicilian tomato isolate detected in Austria (2025), one Danish reference isolate (2011) and eight human genomes from ENA (2025).

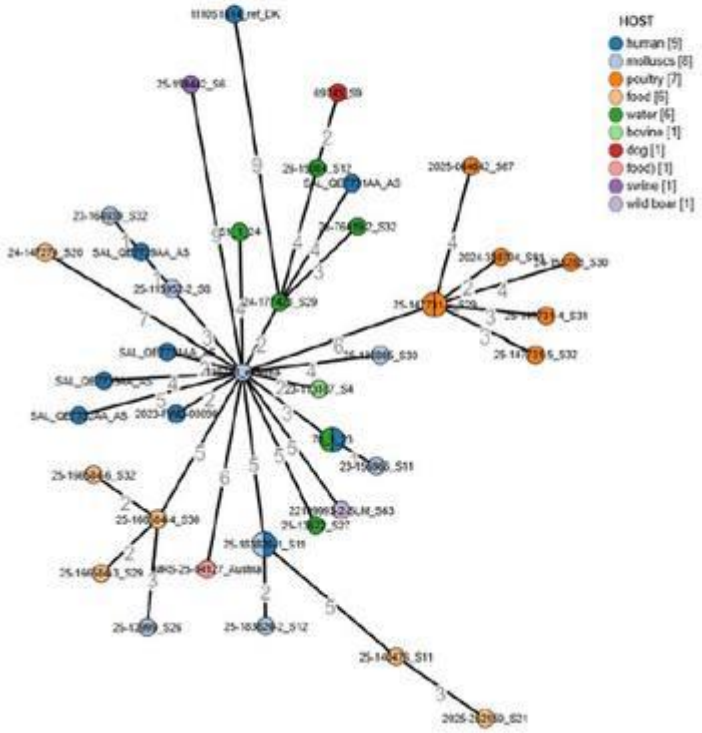


Table 1: Results of official traceback investigations performed in Sicilian farms associated with *S.* Strathcona RASFF notifications (2011-2026).

Sample type	N. of sample	*Salmonella* positive samples
Water	94	16
Tomatoes	51	0
Soil	99	1
Organic fertilizers	8	0
Basil	6	0
Total	258	18

Table 2: *Salmonella* serovars recovered from irrigation and well water samples collected during official traceback investigations in Sicily.

Farm	Sampling date	Serovar
Farm 1	05/12/2024	*S.* Braenderup
Farm 2	22/11/2024	*S.* Strathcona
	22/11/2024	*S.* Cerro
	22/11/2024	*S.* enterica subsp. *salamae* 41:z10:1,2
	15/04/2025	*Salmonella* spp.
	15/04/2025	*Salmonella* spp.
	06/05/2025	*S.* Strathcona
	06/05/2025	*S.* Strathcona
Farm 3	12/12/2025	*S.* Toulon
	23/12/2025	*S.* Kambole
	27/04/2026	*S.* Toulon
	25/05/2026	*S.* Toulon
Farm 4	12/12/2025	*S.* Toulon
Farm 5	11/02/2026	*S. enterica* subsp. *salamae* 42:z:1,5
Farm 6	25/05/2026	*S. enterica* subsp. *enterica* 9:-:e,n,x
	25/05/2026	*S. enterica* subsp. *enterica* 9:-:e,n,x

Late Breakers: novel and outstanding discoveries

SCS23 LB · 14:00-15:30 · Auditorium II

Reemergence of New World Screwworm at the Wildlife–Livestock-Human Interface: Implications for Biodiversity, Wildlife Health Surveillance, and One Health

Lucy KEATTS (1), Luis GUERRA (2), Jeremy RADACHOWSKY (2), Jorge ROJAS (3,4), Rony GARCIA (5), Jonathan PEREZ-FLORES (6), Christian WALZER (1), Diego MONTECINO-LATORRE (1)

1: Wildlife Conservation Society (WCS), Health Program; 2: Wildlife Conservation Society, Mesoamerica and Western Caribbean Regional Program; 3: Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia, USA; 4: TapirVet Project, San José, Costa Rica; 5: Wildlife Conservation Society, Guatemala Country Program, Flores, Guatemala; 6: El Colegio de la Frontera Sur (ECOSUR), Chetumal, Quintana Roo, Mexico

BackgroundFollowing more than three decades of successful regional control, the New World screwworm (Cochliomyia hominivorax) reemerged in Central America in 2023 and rapidly expanded northward, resulting in its re-establishment in the United States in June 2026. While response efforts have focused primarily on livestock production and public health, the implications for wildlife, biodiversity, and protected areas remain poorly understood. We examined the emerging impacts of screwworm on free-ranging wildlife and explored the ecological and anthropogenic drivers influencing parasite spread across wildlife–livestock interfaces.MethodsWe synthesized published literature, official animal health reports, government surveillance data, and field observations from conservation organizations across Mesoamerica. Confirmed wildlife infestations were compiled from diagnostic records, camera trap observations, wildlife rehabilitation centres, and verified field reports. We also evaluated evidence linking parasite spread with livestock movements, wildlife–livestock interactions, protected areas, and landscape change to identify key pathways relevant to biodiversity conservation and One Health.ResultsBy June 2026, the regional outbreak had resulted in more than 185,000 reported animal infestations (livestock, companion animals, and wildlife) and more than 2,100 human cases across Central America and Mexico, culminating in the re-establishment of New World screwworm in the United States after decades of successful eradication. We compiled 39 confirmed wildlife cases involving 13 species across Belize, Costa Rica, Guatemala, Honduras, Mexico, and Panama, including endangered Baird's tapirs (Tapirus bairdii), howler monkeys (Alouatta spp.), Hoffmann's two-toed sloths (Choloepus hoffmanni), black bears (Ursus americanus), porcupines, deer, kinkajous, neotropical otters, opossums, raptors, and other wild birds. These records likely represent only a small fraction of wildlife impacts because surveillance remains fragmented and largely opportunistic. Evidence indicates that illegal cattle trafficking has facilitated long-distance parasite spread by circumventing veterinary controls while simultaneously contributing to deforestation, habitat fragmentation, and increased wildlife–livestock contact. These interacting pressures increase exposure of wildlife populations while complicating regional eradication efforts and highlighting critical gaps in wildlife health surveillance.ConclusionsThe reemergence of New World screwworm represents a transboundary One Health challenge extending well beyond livestock production to biodiversity conservation, wildlife health, and ecosystem resilience. As regional re-eradication efforts expand across North and Central America, wildlife health surveillance should be integrated into preparedness, surveillance, and response systems to detect impacts on biodiversity, identify wildlife hosts and transmission pathways, evaluate control measures, and strengthen sustainable long-term elimination strategies. However, sustainable control will require a coordinated, multisectoral approach that extends beyond surveillance to address the ecological and anthropogenic drivers of parasite spread, including illegal livestock trafficking, protected area management, biodiversity conservation, livestock health, public health, and cross-border collaboration. Failure to incorporate wildlife into regional surveillance and eradication efforts risks overlooking important impacts on biodiversity while missing opportunities for earlier detection, improved control, and more sustainable elimination of this emerging transboundary threat.

Clues from persistent morbillivirus infections in dolphins for the molecular pathogenesis of SSPE in humans

Melvin DANIEL ROJI (1), Laura MARTINO (2), Kristin LAUDELEY (1), Mariano DOMINGO (2), Albert DME OSTERHAUS (1), Martin LUDLOW (1)

1: Research Center for Emerging Infections and Zoonoses, University of Veterinary Medicine, Foundation, Hannover, Germany; 2: Departament de Sanitat i Anatomia Animal, Facultat de Veterniària, Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain

Background:

Measles virus (MeV) can rarely persist after acute systemic infection causing chronic neurological disorders such as invariably fatal sub-acute sclerosing panencephalitis (SSPE). SSPE associated MeV strains accumulate critical mutations in the matrix (M), fusion (F) and polymerase (L) proteins. The rarity of SSPE and its often delayed diagnosis restricts opportunities to study the intra-host evolution of such variant MeV strains. Recently we have shown that animal morbilliviruses also acquire similar mutations in long-term persistent infections of the central nervous system (CNS)1. Although, chronic “brain-only” forms of dolphin morbillivirus (DMV) infection have been observed in dolphins following DMV epizootics, the evolution of these strains remained uncharacterized.

Methods:

Here we explored the prospects of using chronic DMV infections as a natural model for better understanding SSPE pathogenesis. We obtained complete genome sequences of DMV strains causing chronic CNS diseases in dolphins of the Mediterranean Sea, by next generation sequencing of host tissues. The competence of surface glycoproteins to mediate spread in a receptor negative environment was assessed by cell fusion assays. A chronic case (361-19) with limited peripheral infection enabled minor variant analysis on DMV present in peripheral and brain tissues.

Results:

DMV strains from chronic cases were closely related to contemporary DMV strains causing acute infections but presented unique amino acid (aa) changes in the M, F and L proteins. We identified a hyperfusogenic F glycoprotein or defective M protein in DMV23-21 and DMV779-10. The DMV23-21 F glycoprotein also displayed resistance to a small molecule fusion inhibitor previously shown to inhibit MeV induced cell fusion. Furthermore, we identified a case of chronic neurological infection in a striped dolphin (361-19) in which limited peripheral infection was still present. Unique aa changes found in the brain were also observed in the lung and kidney of this animal at varying frequencies. The identification of a hyperfusogenic F variant (T463I) at higher levels in the brain while also being present in the periphery suggests that this chronic case may well represent an early-intermediate stage in the evolution of an animal morbillivirus towards long-term persistence.

Conclusions:

Our study identifies animal analogues to SSPE disease re-iterating that dolphins serve as natural infection models to study persistent morbillivirus infections. Analysis of a chronic case with limited peripheral infection demonstrates for the first time that unique structural protein changes that may contribute to persistence, are present outside the CNS and are progressively enriched in the CNS, providing new insights into the intra-host evolution of morbilliviruses during the establishment of chronic infections of the brain.

Reference:

1. Daniel Roji, M. *et al.* Human and animal morbillivirus strains causing chronic neurological infections share key genotypic and phenotypic traits. *Proc Natl Acad Sci U S A***123**, e2604205123 (2026).

Restoring healthy landscapes to prevent zoonotic and vector-borne diseases: building on evidence to inform restoration policy and practice

Maria Jose LOPEZ JARA (1,2), Raquel CARVALHO (3), Marcelo BOVI (3), Sarah OLSON (4), Skylar HOPKINS (5), Nicole GOTTDENKER (6), Lucinda KILKPATRICK (7), Frauke ECKE (8), Felicia KEESING (9), Christina FAUST (2), Dan SALKELD (10), Nicola WARDROP (11), Samraj SAHAY (1), Samantha DAVALOS SEGURA (12), Natalia ALEKSEEVA (12), Anjana VARMA (13), Lauren HOLIAN (1), Ellie KIRKE (1), Sebastian BOTERO (1), Claudia TAN (1), Jessica FISHER (1), Warren LAVEY (1), Ted LAWRENCE (1), Willow OUTHWAITE (11), Marianela ARAYA QUESADA (14), Regina KIPPER (14), Carina

MUTSCHELE (12), Leandro TAMBOSI (15), Zachary DVORNICKY-RAYMOND (1), Marcela UHART (1,16), Tiggy GRILLO (1,17), Paula PRIST (1)

1: International Union for the Conservation of Nature and Natural Resources (IUCN); 2: The University of Glasgow, United Kingdom; 3: University of São Paulo, Brazil; 4: Wildlife Conservation Society (WCS), United States of America; 5: North Carolina State University, United States of America; 6: Odum School of Ecology, United States of America; 7: Bangor University, United Kingdom; 8: University of Helsinki, Finland; 9: Bard College, United States of America; 10: Colorado State University, United States of America; 11: Foreign, Commonwealth & Development Office (FCDO), United Kingdom; 12: United Nation Environment Program (UNEP); 13: Nature4Health; 14: Convention on Biological Diversity (CBD); 15: Universidade Federal do ABC (UFABC), Brazil; 16: University of California, Davis, United States of America; 17: Wildlife Health Australia (WHA)

Background: Ecological restoration has emerged as a promising Nature-based Solution to promote human health by reversing the environmental drivers of emerging infectious diseases, which cause over one billion illnesses and millions of deaths annually. Yet current restoration initiatives rarely incorporate zoonotic and vector-borne disease risks into their assessments and strategies, a critical oversight given that poorly designed interventions can inadvertently create new interfaces between hosts, vectors, and humans. This gap is particularly consequential in tropical and subtropical regions of low- and middle-income countries, where the global burden of zoonotic disease falls disproportionately and where most ecosystem restoration efforts are concentrated. Operationalising health-focused restoration remains difficult due to a striking lack of empirical evidence and practical guidance to maximise health co-benefits while avoiding unintended consequences.

Methods: We have collated existing empirical evidence on the relationships between ecological restoration and zoonotic and vector-borne disease risk to identify critical considerations for assessing, managing, and monitoring these risks. Between May and August 2026, we conducted a structured expert consultation with 32 specialists in policy and research, including academic researchers based in the UK, USA, Brazil, and Finland, and representatives from intergovernmental bodies and international organisations including the UN, CBD, FCDO, IUCN, WCS, and N4H. Expert input was used to identify evidence-based considerations, policy intersections, integration with existing One Health and restoration frameworks, key knowledge gaps, priority intervention areas, and actionable guidance for integrating disease risk reduction into restoration planning, implementation, and monitoring.

Results: Initial expert consultation revealed wide support for integrating One Health principles into restoration frameworks, while highlighting critical gaps in empirical evidence and practical guidance. Key emerging themes include the need to assess how host and vector community responses, biodiversity responses, landscape configuration, and social factors influence disease risk outcomes. The framework is currently under expert review and is expected to be finalised by August 2026, with its official launch planned at CBD COP17 in Armenia later this year.

Conclusions: Restoration policy and practice must systematically incorporate human health as a core outcome alongside biodiversity recovery. This framework offers structured, evidence-informed guidance to help practitioners and policymakers identify and maximise synergies between biodiversity recovery and zoonotic and vector-borne disease risk mitigation, simultaneously advancing biodiversity and health-related SDGs and building the long-term resilience of socio-ecological systems. The World One Health Congress represents a unique opportunity to gather feedback from the global One Health community ahead of the CBD COP17 launch.

From livestock loss to cultural distress and ecosystem degradation: a gender responsive One Health assessment of an extreme winter disaster (dzud) in Mongolia's Eastern Steppe

Julie GARNIER (1,2), Batkhishig BAIVAL (2), Tsermaa NYAMDAVAA (3), Indra TUMUR (4), Vandandorj SUMIYA (4), Batsaikhan SODNOM (5), Kevin QUEENAN (6), Isobel GABAIN (6), Barbara HÄSLER (6), Richard KOCK (6)

1: Odyssey Conservation Trust, United Kingdom; 2: Resilient Threads project, Mongolia; 3: National University of Mongolia, Mongolia; 4: Sustainable Fibre Alliance, Mongolia; 5: World Organisation for Animal Health, France; 6: Royal Veterinary College, UK

BackgroundDzud is an extreme climate event where severe winter conditions prevent livestock grazing. Often preceded by summer drought, it is projected to intensify and become more frequent. Its impacts are usually assessed within single domains, hiding the systemic drivers of vulnerability. In the context of the Resilient Threads project and following the severe 2023–24 dzud, we conducted the first One Health impact assessment of dzud in Mongolia, in the Eastern Steppe - one of the last temperate grasslands on

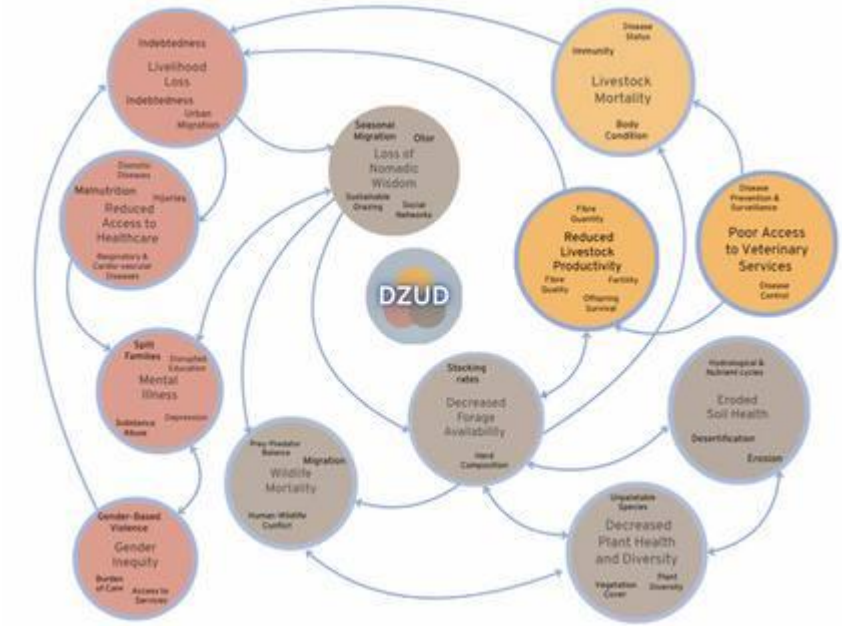
Earth and a stronghold for biodiversity. Our aim was to characterise how dzud cascades across livestock, human, and ecosystem health and to identify leverage points to build resilience.

MethodsBased in Sukhbaatar province, the assessment combined household surveys, key-informant interviews, stakeholder consultations, literature review, official data consultation, and system mapping. A systematic literature review and causal-loop analysis of dzud impacts on public and livestock health is published separately (Kawamoto et al., forthcoming).

ResultsIn Sukhbaatar, 46.8% of all livestock (3,859,471 animals) died during the 2023-24 dzud, with 52.6% and 47.2% mortality rates in sheep and goat populations, respectively; one-third of households lost over 70% of their herds; the endemic Bayandelger Red goat suffered nearly 40% mortality, eroding livestock genetic diversity. Human impacts followed: mental distress surged; incidents of gender-based violence rose; women's burden of care and child malnutrition increased; nearly 60% of households lacked prenatal or postnatal care; two-thirds carried loans; cashmere production fell by 53.9%, with household income losses averaging ~US$1,170, fuelling rural–urban migration and the loss of traditional knowledge and practices.

While pastures can recover shortly after dzud once grazing pressure decreases, post-dzud vegetation often shifts toward grazing-resistant species, reducing plant diversity and forage quality; degraded rangelands deliver fewer ecosystem services, including water retention and disease regulation. Ecosystem impacts are compounded by intensifying degradation cycles: since the 1990s market transition, livestock rose 275% and goats fivefold, driving overgrazing that accelerates erosion and desertification and disrupts nutrient cycling. Rapid post-dzud restocking typically re-initiates degradation before full recovery, risking a shift toward persistent degraded states. Five interconnected leverage points emerged: nomadic wisdom and sustainable rangeland management; biodiversity conservation; integrated One Health service delivery; livelihood diversification and certified value chains; gender equity and social protection, systemically strengthening the resilience of herders, livestock, wildlife and rangelands.

ConclusionsDzud impacts in all domains are reinforced by a systemic climate-ecosystem-sociocultural crisis in which cycles of herd expansion and rangeland degradation, undiversified livelihoods, loss of nomadic wisdom and practices, and eroded biodiversity and ecosystem services heighten vulnerability. Our study shows that interventions must be deployed simultaneously across leverage points to build the adaptive capacity of herding communities and the resilience of the socio-ecological system, thus offering a transferable model for anticipatory adaptation in pastoral systems worldwide.



Compound heat-drought events as datable early-warning signals for arbovirus outbreaks: causal evidence from Northeast Brazi

Mattheus RODRIGUES DA SILVA (1), Tatiane ALMEIDA DE MENEZES (1), Rafaela Camila DA SILVA FERREIRA (1), Celina Maria TURCHI MARTELLI (2), Noêmia TEIXEIRA DE SIQUEIRA-FILHA (3)

1: Universidade Federal de Pernambuco, Brazil; 2: Instituto Aggeu Magalhães, Fundação Oswaldo Cruz (Fiocruz), Brazil; 3: University of York, Reino Unido

Background: Climate change is making the co-occurrence of extreme heat and drought more frequent, yet whether and how this compound exposure worsens the burden of Aedes-borne arboviruses (dengue, chikungunya, Zika) remains unclear. At the population level, the effect of drought is confounded with heat, material deprivation, and seasonality, so the dry side of the water-arbovirus relationship is known only from correlational studies. We ask whether the coincidence of extreme heat and drought causally increases the notified incidence of urban arboviruses, a question at the climate-environment-health interface central to One Health.

Methods: We assembled a monthly panel of all 1,786 municipalities of Northeast Brazil, a semi-arid, high-burden region, from January 2015 to February 2020 (about 110,000 municipality-months). Treating compound heat-drought events as datable, plausibly exogenous shocks, we estimated their dynamic effects with a modern difference-in-differences design robust to staggered adoption and non-absorbing (recurrent) treatment. A municipality enters the treated state when extreme heat (at least three days with maximum temperature above the local 90th percentile) coincides with meteorological drought (one-month SPEI below -1); the regressor is lagged one month. The outcome is the log incidence of notified urban arboviruses. The design absorbs municipality and month fixed effects and non-parametric trends by state and Koppen climate zone, with standard errors clustered by municipality and six pre-shock placebo periods.

Results: Compound shocks significantly increased notified incidence (average total effect 1.32; 95% CI 0.16-2.49), with pre-shock trends jointly indistinguishable from zero. The response was lagged, peaked around the fifth month, and dissipated within a year. Only the composite was identifiable: neither extreme heat nor drought alone produced a discernible effect, despite each being far more frequent and better powered. The effect concentrated in the semi-arid interior and operated on the extensive margin: previously quiescent municipalities began to register cases rather than existing outbreaks being amplified, consistent with a water-scarcity channel that the design does not test directly, plausibly operating through household water storage. Findings were robust to finer regional trends, alternative drought indices, and a spatial permutation placebo (p=0.007).

Conclusions: Compound heat-drought events causally raise the notified incidence of urban arboviruses, providing the first quasi-experimental evidence for the under-studied dry arm of the water-arbovirus relationship. Because the effect is lagged and datable, jointly monitoring heat and drought opens a months-long window for pre-emptive, geographically targeted vector control, and reliable water supply may serve as a complementary preventive margin. More broadly, compound climate extremes can serve as datable, intermittent treatments in One Health causal designs.

Genomic surveillance reveals zoonotic, foodborne, and WHO priority pathogens along the African–European bushmeat trade supply chain

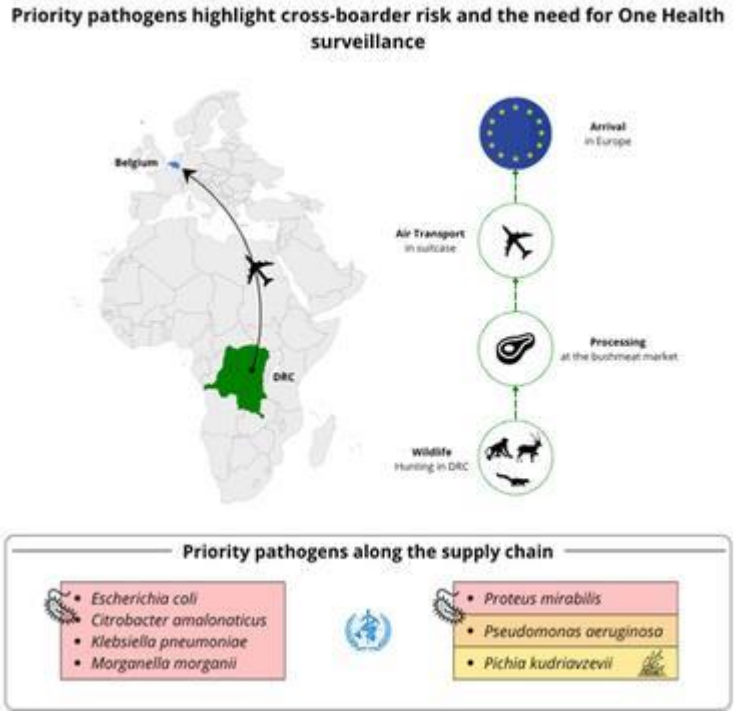
Daniel PIRES (1,2), Emilie LECOMPTE (1), Sophie GOOMBER (3,4), Casimir NEBESSE (5), Douglas AKAIBE (5), Dudu AKAIBE (5), Pascal BAELO (5), Anne-Lise CHABER (6), Guy-Crispin GEMBU (5), Léa JOFFRIN (7), Anne LAUDISOIT (7,8), Nicolas LAURENT (11), Herwig LEIRS (7), Claude MANDE (5,7), Joachim MARIËN (7,9), Steve NGOY (5), Ann VANDERHEYDEN (4), Rianne VAN VREDENDAAL (7), Erik VERHEYEN (4,7), Agostinho ANTUNES (2,10), Sophie GRYSEELS (4,7), Philippe GAUBERT (1,2)

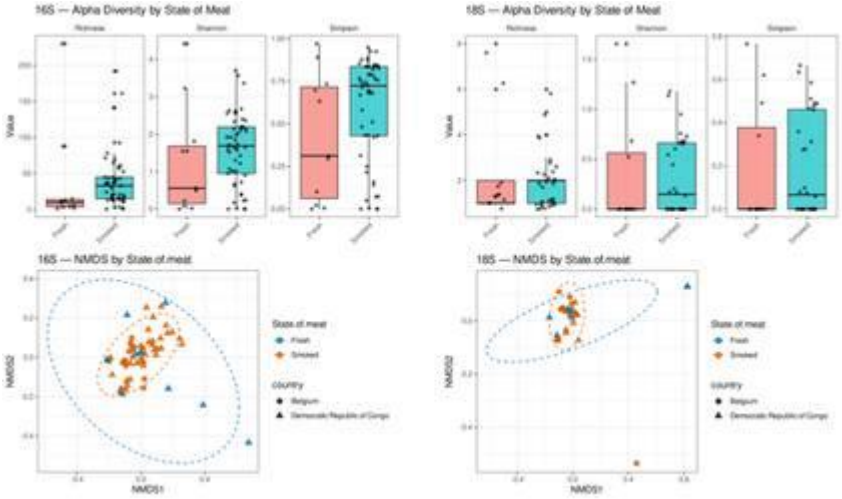
1: Université de Toulouse, Toulouse INP, CNRS, IRD, Centre de Recherche sur la Biodiversité et l'Environnement (CRBE), Bâtiment 4R1, 118 route de Narbonne, 31062 Toulouse Cedex 9, France;; 2: CIIMAR/CIMAR, Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos, s/n, 4450-208 Porto, Portugal;; 3: Biodiversity and Conservation Biology, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland;; 4: OD Taxonomy and Phylogeny (BopCo), Royal Belgian Institute of Natural Sciences, Brussels, Belgium;; 5: Centre de Surveillance de la Biodiversité (CSB), University of Kisangani, Kisangani, Democratic Republic of the Congo;; 6: School of Animal and Veterinary Sciences, University of Adelaide, Adelaide, South Australia, Australia;; 7: Evolutionary Ecology group, Department Biology, University of Antwerp, Wilrijk, Belgium;; 8: Nature Health Global, Tallman, New York, United States of America;; 9: Virus Ecology Unit, Department of Biomedical Sciences, Institute of Tropical Medicine Antwerp, Antwerp, Belgium;; 10: Department of Biology, Faculty of Sciences, University of Porto, 4169-007, Porto, Portugal; 11: Open University of The Netherlands, Environmental Sciences dpt. Heerlen, The Netherlands.

Illegal wildlife trade is a major driver of biodiversity loss and a global public health concern, facilitating the emergence and transboundary spread of infectious diseases. Bushmeat - wild terrestrial vertebrates harvested for human consumption in tropical regions - forms part of wildlife trade networks linking Africa and Europe, and has been identified as a potential pathway for zoonotic pathogen transmission. Using non-targeted genomic surveillance across central Africa and Europe, we investigate the bacterial and eukaryotic pathogen communities associated with the bushmeat trade and assess the diversity of pathogens circulating within Africa and entering Europe through this largely unregulated pathway.

We collected 112 samples from four bushmeat markets in the Democratic Republic of Congo (DRC) and from Zaventem Airport in Brussels, Belgium. DNA metabarcoding targeted bacterial (16S rRNA, V5–V6) and eukaryotic (18S rRNA, V7) communities, enabling untargeted detection of a broad diversity of potential pathogens. Molecular operational taxonomic units (MOTUs) were processed in metabaR using a conservative custom pipeline to maximize confidence in species-level assignments. Pathogens were identified and functionally classified using published reference datasets and authoritative databases. Beta-diversity analyses assessed the effect of carcass processing – typical of bushmeat entering Europe– on microbial community composition. α-diversity did not differ significantly between bushmeat samples from DRC and Belgium, whereas β-diversity analysis revealed that carcass processing had a weak but significant effect on bacterial community composition. We identified 55 microbial pathogens, comprising 43 bacterial species (4.2% of the bacterial community) and 12 eukaryotic taxa (45.5% of the eukaryotic community, excluding vertebrates and plants). Among these, 18 were classified as foodborne pathogens and 11 as zoonotic pathogens, several of which were also associated with meat processing. *Enterococcus faecalis* was the most prevalent pathogen overall (FO = 68.8%), followed by *Proteus mirabilis* (40.6%) and *Escherichia coli* (32.8%) in DRC, and *Bacillus subtilis* (31.2%) in Belgium. The most frequent eukaryotic pathogen was *Meyerozyma guilliermondii* (FO = 31.7%), detected in both countries. Our non-targeted approach detected seven WHO priority pathogens in bushmeat traded in DRC, including two reported for the first time (*): the critical-priority Enterobacterales *Klebsiella pneumoniae*, *Escherichia coli*, *Citrobacter amalonaticus*, *Morganella morganii**, and *Proteus mirabilis*; the high-priority bacterium *Pseudomonas aeruginosa*; and the medium-priority fungus *Pichia kudriavzevii** (= *Candida krusei*). In Belgium, 77.3% of detected pathogens were shared with DRC, while five, mostly opportunistic and foodborne, were unique to the airport.

The detection of zoonotic, foodborne, and WHO priority pathogens along the global supply chain identifies the bushmeat trade as a pathway for the international dissemination of pathogens of public health concern, with major One Health implications. Our findings further suggest that European airports act as entry points for bushmeat-associated pathogens and that carcass processing may further broaden pathogen diversity along the supply chain.




16S — Alpha Diversity by State of Meat
18S — Alpha Diversity by State of Meat
16S — NMDS by State of meat
18S — NMDS by State of meat
NMDS1
NMDS2
State of meat
Fresh
Smoked
COUNTRY
Belgium

Species	Taxonomic Classification	Zoonotic	Foodborne	Opportunistic
Acinetobacter calcoaceticus	Bacteria; Pseudomonadota			✓
Aerococcus viridans	Bacteria; Bacillota			✓
Aeromonas veronii	Bacteria; Pseudomonadota	✓	✓	
Arcobacter cryaerophilus	Bacteria; Campylobacterota	✓	✓	
Bacillus cereus	Bacteria; Bacillota		✓	
Bacillus sphaericus	Bacteria; Bacillota			✓
Bacillus subtilis	Bacteria; Bacillota			✓
Bordetella hinzii	Bacteria; Pseudomonadota	✓		
Brevundimonas diminuta	Bacteria; Pseudomonadota			✓
Citrobacter amalonaticus	Bacteria; Pseudomonadota		✓	✓
Clostridium novyi	Bacteria; Bacillota			
Clostridium perfringens	Bacteria; Bacillota		✓	
Clostridium septicum	Bacteria; Bacillota			
Comamonas testosteroni	Bacteria; Pseudomonadota			✓
Corynebacterium urealyticum	Bacteria; Bacillota			✓
Enterococcus faecalis	Bacteria; Bacillota			✓
Erysipelothrix rhusiopathiae	Bacteria; Bacillota	✓		
Escherichia coli	Bacteria; Pseudomonadota		✓	✓
Fusobacterium periodonticum	Bacteria; Fusobacteriota			✓
Gemella haemolysans	Bacteria; Bacillota			✓
Ignatzschineria indica	Bacteria; Pseudomonadota			✓
Klebsiella pneumoniae	Bacteria; Pseudomonadota		✓	✓
Kluyvera ascorbata	Bacteria; Pseudomonadota			✓
Lactococcus garvieae	Bacteria; Bacillota	✓	✓	✓
Leuconostoc mesenteroides	Bacteria; Bacillota			
Lysinibacillus fusiformis	Bacteria; Bacillota			
Micrococcus luteus	Bacteria; Bacillota			✓
Morganella morganii	Bacteria; Pseudomonadota		✓	✓
Oblitimonas alkaliphila	Bacteria; Pseudomonadota			
Proteus mirabilis	Bacteria; Pseudomonadota		✓	✓
Pseudomonas aeruginosa	Bacteria; Pseudomonadota			✓
Selenomonas noxia	Bacteria; Bacillota			✓
Staphylococcus epidermidis	Bacteria; Bacillota			✓
Staphylococcus simulans	Bacteria; Bacillota			✓
Stenotrophomonas maltophilia	Bacteria; Pseudomonadota			✓
Streptococcus cristatus	Bacteria; Bacillota			✓
Streptococcus equi	Bacteria; Bacillota	✓		
Streptococcus oralis	Bacteria; Bacillota			
Streptococcus salivarius	Bacteria; Bacillota			✓
Streptococcus suis	Bacteria; Bacillota	✓	✓	
Veillonella dispar	Bacteria; Bacillota			✓
Vibrio cholerae	Bacteria; Pseudomonadota	✓	✓	
Wohlfahrtiimonas chitiniclastica	Bacteria; Pseudomonadota			✓
Aedes aegypti	Eukaryota; Arthropoda	✓		
Arthrinium marii	Eukaryota; Ascomycota			
Aspergillus spp.	Eukaryota; Ascomycota		✓	✓
Candida sp.	Eukaryota; Ascomycota			✓
Hepatozoon felis	Eukaryota; Apicomplexa	✓		
Meyerozyma guilliermondii	Eukaryota; Ascomycota		✓	✓
Pichia kudriavzevii	Eukaryota; Ascomycota		✓	✓
Rhizopus sp.	Eukaryota; Mucoromycota		✓	✓
Sarcocystis gruneri	Eukaryota; Apicomplexa	✓		
Trichosporon sp.	Eukaryota; Basidiomycota			✓
Yarrowia sp.	Eukaryota; Ascomycota			✓
Yarrowia lipolytica	Eukaryota; Ascomycota		✓	✓

One Health Implementation in the ECOWAS Region (2023 to 2025): Strong Institutional Commitment, Fragmented Operationalization

Samanta DJALO (1), Céline MBILO (2), Victor FATIMEHIN (1), Babacar FALL (1), Eugene KOFFI (3), Fatima ZANNA (2), Hassane ADAKAL (3), Mamadou DIARRASSOUBA (1)

1: Regional Centre for Surveillance and Disease Control, Economic Community of West African States (ECOWAS); 2: Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ); 3: Regional Animal Health Center, Economic Community of West African States (ECOWAS)

Background: In response to the 2014-2016 West Africa Ebola outbreak, ECOWAS initiated a process to institutionalize the One Health (OH) approach across the region, including the first regional OH Zoonotic Disease Prioritization Workshop conducted by a Regional Economic Community in 2018. These efforts culminated in the development of the ECOWAS Regional OH Strategy (ROHS) 2025-2029 and Governance Manual for the Regional OH Coordination Mechanism. As part of the strategy's monitoring and evaluation framework, this study assessed OH operationalization in the region between 2023 and 2025 to map multisectoral integration, identify operational gaps, and inform annual planning.

Methods: We conducted a cross-sectional study across ECOWAS Member States (MS), with data collected between October 2025 and March 2026 using a structured, piloted questionnaire administered through *Google Forms*. The purposive sample comprised 48 national stakeholders (four per country), including the Heads of the National OH Coordination Mechanisms (NOHCMs) and focal points from the human, animal, and environmental health sectors. The survey covered the thematic areas of the ROHS and assessed implementation of OH-related international frameworks and operational tools. We developed a region-specific indicator-based scoring system to enable harmonized and comparable assessment of OH operationalization across MS. Data were analyzed using descriptive statistics and SWOT analysis.

Results: The survey achieved a 64.6% completion rate (31/48 responses). Institutional commitment to OH is widespread: NOHCMs are established in 10 of 12 MS and are under development in the remaining two. Indicator-based scoring confirmed this commitment but exposed a gap between recognition and function: against the maximum possible score, the region achieved 88% on legal recognition of NOHCMs, compared with 63% for active functionality and 50% for regular coordination meetings. The gap widened at the operational level, with regional scores of 54% for joint surveillance activities, 38% for joint laboratory diagnostic protocols, and only 21% for formal intersectoral data-sharing agreements. Conversely, data sharing among OH sectors (71%) and reporting to ECOWAS (83%) remained robust. Overall, per-country performance scores spanned from 15/18 (Benin) to a low of 6/18 (The Gambia) indicating moderate but uneven operationalization region-wide. Information sharing and data management remain highly fragmented; while DHIS2 dominates human health, the animal and environmental sectors rely on a mixed toolset, hindering digital integration. Financing emerged as a major vulnerability, with 4 out of 12 MS relying exclusively on external funding.

Conclusions: ECOWAS has made significant progress in institutionalizing OH through political commitment, regional coordination and establishment of NOHCMs. However, operationalization remains fragmented and heavily dependent on external funding. Limited functionality of NOHCMs, weak multisectoral integration, and fragmented data systems continue to constrain effective collaboration across sectors. Strengthening sustainable domestic financing, interoperable digital surveillance, and harmonized regional indicators will be critical to translating institutional commitment into resilient operational capacity.

Table 1. One Health Operationalization Scoring Criteria (good=2, moderate=1, poor=0)

Indicator	Good	Moderate	Poor
OHCM sectors	3	2	1
OHCM status	Established	In-Progress	No
OHCM functionality	Functional	Partial	No
Meetings	Quarterly	Occasional	Ad-hoc
Joint surveillance	Regular	Occasional	No
Joint lab protocols	Established	Draft	No
Data agreement	Signed	Draft	No
Data sharing	Yes	On-request	No
ECOWAS reporting	Yes	On-request	No

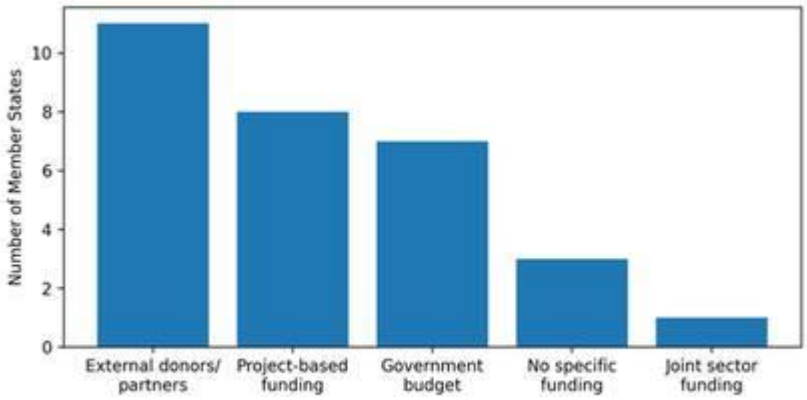


Figure 1. Funding Sources supporting One Health implementation in ECOWAS Member States (n=12), 2025

	STRENGTHS	WEAKNESSES
Internal	• Established coordination mechanisms. • Strong national/regional commitment. • Formal ECOWAS frameworks.	• Missing regional indicators. • Low multi-sectoral collaboration. • Funding dependency. • Fragmented implementation.
	OPPORTUNITIES	**THREATS**
External	• Digital tool advancement. • Global environmental/OH support. • Cross-border partnerships.	• Regional political instability. • Climate change degradation. • Weak health policy enforcement.

Figure 2. SWOT Analysis of OH Approach Implementation in ECOWAS: Internal and External Factors, 2025

Poster Abstracts

Poster zone 1

Olive Tree

109 – Who's working with who? Engagement, collaboration and imbalances in One Health research, 2010 – 2024

Martin SZOMSZOR (5), Mariam KADZAMIRA (1), Hideo ISHII-ADAJAR (1), Tim LEYLAND (6), Urs SCHAFFNER (4), Barbara HÄSLER (7), Abigail WRIGHT (8), Solveig DANIELSEN (3), Dannie ROMNEY (2), **Helen COSKERAN** (1)

1: CABI Ascot, United Kingdom; 2: CABI Africa Centre, Kenya; 3: CABI, The Netherlands; 4: CABI Swiss Centre, Switzerland; 5: Electric Data Solutions LTD; 6: Lifestock Inc. Ltd. New Zealand; 7: Veterinary Epidemiology, Economics and Public Health Group, Department of Pathobiology and Population Sciences, Royal Veterinary College, London; 8: World Health Organisation (WHO), Geneva, Switzerland

Background : Using Social Network Analysis (SNA) this study assesses the trends in research publications self-labelled as One Health and quantifies the scale of collaboration amongst institutions engaged in that research, based on published papers from 2010 to 2024.

Methods: Social Network Mapping was used to meet study objectives. Specifically, 6168 publications (January 2010 – October 2024) were included from a bibliometric analysis applied in the Dimensions database. A full-accounting approach was used to attribute publications to countries or institutions; with Social Network Analysis centrality measures used to quantify the scale and impact of collaboration amongst institutions engaged in One Health research.

Results : Study findings show a rapid growth in number of self-labelled One Health research publications over this time period, with the USA and UK being the largest contributors but with rapid growth in publications by authors in Europe, Asia, and Africa. Furthermore, study findings indicate the existence of international collaboration in self-labelled One Health research published during the study period. In terms of research focus, our study shows that the majority of this research is focused on One Health issues in low- and middle-income countries in Africa and Asia, likely due to historical data pointing to them as global hotspots for emerging infectious diseases (EID) including zoonotic outbreaks. However, this research is led mainly by researchers in countries in the Global North, with North America and Europe having not only the largest volume of research labelled as One Health over the study period, but also the broadest range of collaboration across continents.

Conclusions: These findings demonstrate the growth in adopting the 'One Health' approach globally, however they are also indicative of disparities in One Health-labelled research leadership and influence, as well as institutional silos. Study recommendations provide specific insights for One Health scientific and strategic decision making across the globe to enhance inclusivity and equity in research collaboration.

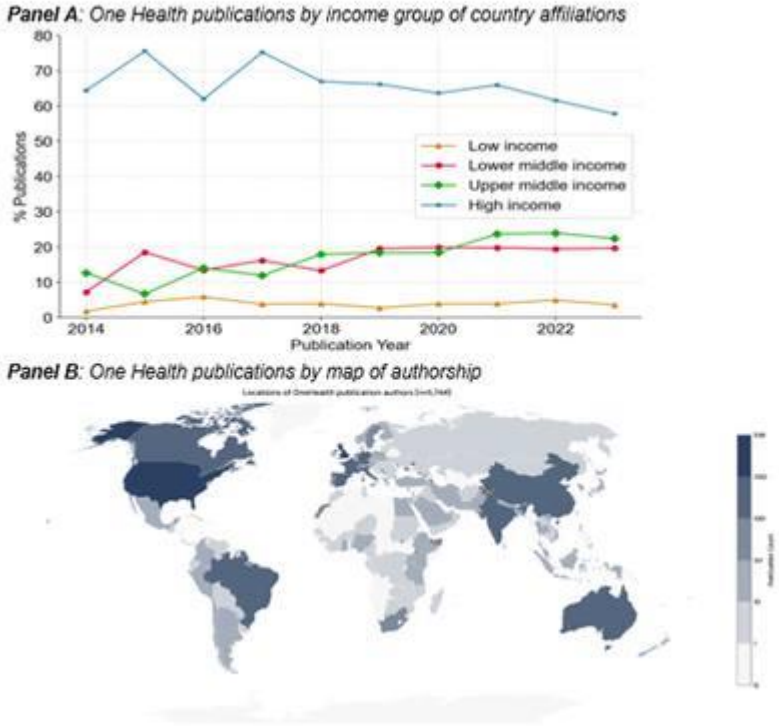


Figure 1: One Health publications by country affiliation of authors and country of focus

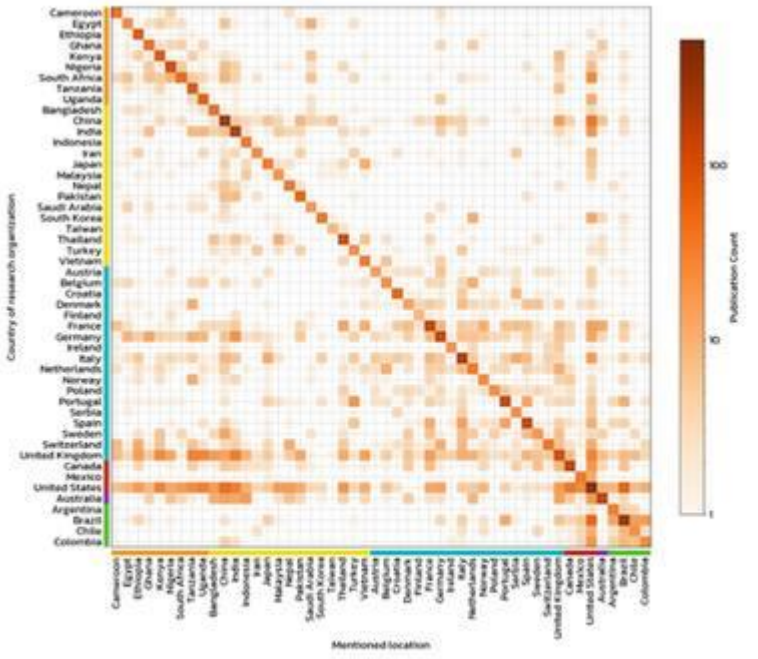


Figure 2 - Heatmap of countries mentioned in OH publications (x-axis), against the author country (y-axis). Countries are grouped by continent (see colour bars) and ordered by country name. The strong diagonal is when authors mention locations in their home country, the most dominant form of location mention.

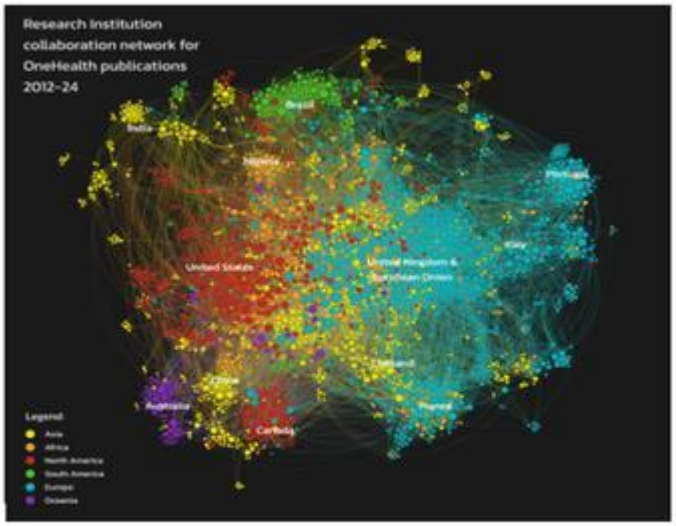


Figure 3: One Health institutional collaboration network (2012 – 2024). Institutions (nodes, with size proportional to the number of publications) are linked by edges based on the number of collaborative outputs, with thicker lines indicating a higher number of papers. Nodes are grouped according to geographic continent (see legend).

147 – Exploring Biofilm Formation, Bacteriocin Traits, and Antimicrobial Resistance in Enterococcus faecalis Isolated from Ready-to-Eat Foods and Water

Helena DELA (1), Helena NGOWI (2), Eric BEHENE (1), Selassie KUMORDJIE (1), Bassirou BONFOH (3), Kennedy Kwasi ADDO (1)

1: Noguchi Memorial Institute for Medical Research, Ghana; 2: Nelson Mandela African Institution of Science and Technology (NM-AIST), Tanzania; 3: Centre Suisse de Recherches Scientifique (CSRS), Côte d'Ivoire

Introduction: Food systems play a critical role in ensuring food safety, public health, and sustainable agricultural development. However, the increasing consumption of ready-to-eat (RTE) foods in urban settings, coupled with inadequate hygiene and water quality, poses significant risks for the transmission of foodborne pathogens and antimicrobial resistance (AMR). This study investigated the occurrence and genomic characteristics of *Enterococcus faecalis* isolated from RTE foods and water samples collected from popular eateries in Accra, Ghana, with implications for food safety within urban food systems.

Methods: In 2021 (January-November), RTE food and water samples were purposively and conveniently sampled from selected eateries and processed using standard microbiological methods for the isolation of foodborne pathogens associated with outbreaks. Fourteen *E. faecalis* isolates were recovered and subjected to phenotypic and genotypic characterization. The isolates were assessed for bacteriocin production, biofilm formation capacity, and antimicrobial susceptibility profiles using established laboratory techniques. Whole-genome sequencing (WGS) was conducted to identify genes associated with antimicrobial resistance, virulence, biofilm formation, and bacteriocin production.

Results: Although 13 of the 14 isolates carried biofilm-associated genes, six lacked phenotypic biofilm expression. Five isolates were multidrug resistant, exhibiting resistance to erythromycin (5/14) and linezolid (3/14). Two isolates were resistant to chloramphenicol, penicillin, and ciprofloxacin, while four were resistant to tetracycline and vancomycin. None of the islolates demonstrated bacteriocin activity phenotypically or harbored bacteriocin genes. Resistance genes *lsa(A), cat, ermB, tet(M),* and *tet(C)* were detected alongside biofilm genes *(ebpA, ebpB, ebpC)* and plasmid replicons *(rep9a, repA(pTW9), rep9b, rep22, rep32, rep9t, repUS43, col3M)*. Clinically relevant sequence types ST16, ST79, ST126, ST81, ST242, and ST376 were identified. Closely related bacterial isolates identified suggest cross-contamination among foods and washing water.

Conclusions: The findings emphasize the importance of integrating food safety surveillance into broader food systems and agricultural health frameworks. Contaminated RTE foods and water not only threaten consumer health but may also contribute to the environmental circulation of AMR, with downstream impacts on agriculture, plant health, and ecosystem integrity. Strengthening hygiene practices, improving

water quality management, and incorporating genomic surveillance into food safety monitoring are essential strategies for mitigating these risks.

Overall, this study highlights the value of a One Health–oriented approach to food systems, recognizing the interconnectedness of human health, agriculture, and the environment. Closely related bacterial isolates highlight the potential contamination pathways and emphasizing the importance of proper hygiene and safe food handling practices dring food preparation and distribution. Addressing foodborne pathogens and AMR in RTE foods is critical to safeguarding public health and promoting resilient and sustainable food systems in rapidly urbanizing settings.

Table 1: Phenotypic and genotypic characteristics of *E. faecalis* isolates

Source	Antibiotype	AMR Genes	Plasmid replicon
RTE food	CIP-TE-VAN-ER-CIP	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	RD	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	RD	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	CHL-TE	*dfrE, efrA, efrB, emeA, lsa(A), tet (L), tet (M)*	rep9a_1_repA, repUS43
RTE food	RD	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	N/A	*dfrE, efrA, efrB emeA, lsa(A)*	repA(pTW9), rep9c
RTE food	RD	*dfrE, efrA, efrB emeA, lsa(A), QnrD1*	-
Water	N/A	-	rep9a_1_repA, rep9b_1_prgW, rep32_2_repB
RTE food	ER-PEN-LZD-RD-VAN	*dfrE, efrA, efrB emeA, lsa(A), tet (L), tet (M)*	repUS43, rep22_1b_repB
RTE food	N/A		-
RTE food	CIP-ER-RD	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	C-CIP-ER-RD	*dfrE, dfrG, efrA, efrB emeA, ErmB, catA8, lsa(A), tet (L)*	rep9a_1_repA, repUS43
Water	TE-ER-PEN-LZD-RD-VAN	*dfrE, efrA, efrB emeA, lsa(A)*	-
RTE food	TE-ER-LZD-RD-VAN	*dfrE, efrA, efrB emeA, lsa(A), tet (L), tet (M)*	repUS43_1_CDS12738

Key: CIP, Ciprofloxacin; PEN, Penicillin; VAN, Vancomycin; ER, Erythromycin; LZD, Linezolid; RD, Rifampicin; TE, Tetracycline; N/A, non-applicable

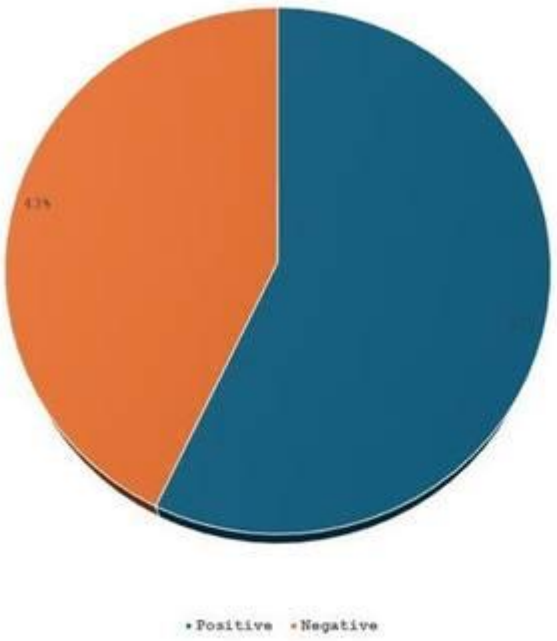
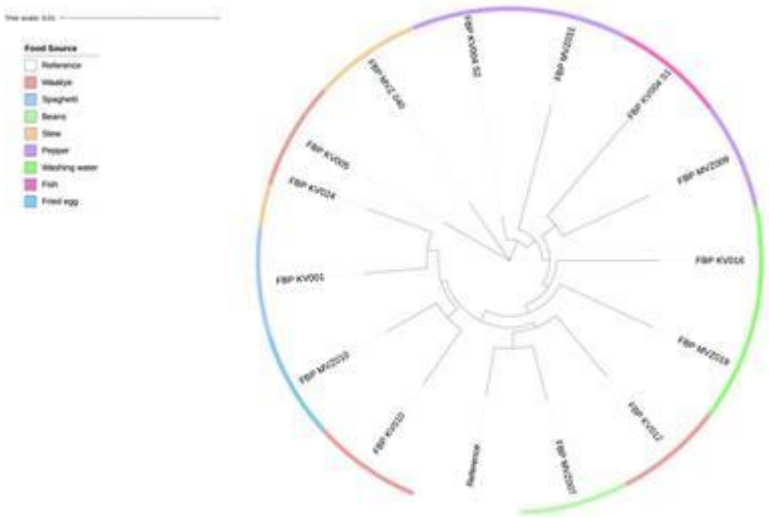


Figure 1: Biofilm analysis



152 – The EU BEACON COST action: developing and implementing one health education curricula EU-wide

Enric Henning GARCIA TORRENTS (1), **María Jesús LIROLA MANZANO** (2), Pinky Haque ANUPOMA (3), Eglantina DERVISHI (4), Pedro ISAIAS (5), Noemia BESSA (6), Elsa LECLERC DUARTE (7), Kwok NG (8), Safieh SHAH (9)

1: Universitat Rovira i Virgili, Spain; 2: Universidad de Almería, Spain; 3: ProRare Austria Alliance for Rare Diseases, Austria; 4: University of Tirana, Albania; 5: IADIS – International Association for the Development of the Information Society – Associação, Portugal; 6: Inštitut pravnih znanosti, raziskave in razvoj na področju prava, Maribor, Slovenia; 7: Universidade de Évora, Portugal; 8: University of Turku, Finland; 9: Institute for Globally Distributed Open Research and Education, Sweden

One Health is widely recognised as an essential framework to address interconnected human, animal, and environmental health challenges. However, despite strong policy endorsement, its effective implementation remains constrained by fragmented education, uneven capacity across regions, and limited integration between disciplines, institutions, and societal actors. COST Action CA24106, EU

BEACON, addresses this structural gap by focusing explicitly on One Health education as enabling infrastructure rather than as an auxiliary activity.

EU BEACON brings together researchers, educators, practitioners, and institutions across the COST area to co develop open, adaptable, and locally contextualised One Health curricula, supported by shared digital infrastructure and transparent governance mechanisms. The Action aims to ensure that One Health competencies can be implemented at scale, across countries and regions, while remaining sensitive to local needs, institutional constraints, and societal priorities.

This presentation introduces the rationale, objectives, and operational model of EU BEACON. It outlines how the Action combines interdisciplinary collaboration, open science principles, and open source digital tools to support curriculum development, training, and sustained collaboration without reliance on resource intensive face to face coordination. Particular emphasis is placed on inclusiveness, capacity building in under resourced contexts, and the role of education in enabling durable One Health practice.

The presentation also discusses how EU BEACON integrates dissemination, exploitation, and governance as core components of its design, ensuring transparency, accountability, and public value. By treating education, infrastructure, and collaboration as shared public goods, the Action seeks to move One Health from declarative consensus to operational reality.

The contribution is relevant to researchers, educators, policy actors, and organisations engaged in One Health implementation, offering a concrete model for building scalable, ethical, and sustainable One Health education systems in Europe and beyond.

187 – A vulnerability case for Upstream One Health

Chris DEGELING (1), Jane JOHNSON (2)

1: University of Wollongong, NSW, Australia; 2: Macquaire University, NSW, Australia

Background

For some time, broad scientific consensus has supported a One Health approach to addressing risks at the human-animal-environment interface. However, it is now apparent that a specific One Health approach (one that focuses 'upstream' rather than 'downstream') might be required for the effective prevention of pandemics of zoonotic origin. Against this background, the World Bank and UN agencies are urging governments to shift to this proactive upstream paradigm. The economic case for more preventative approaches in One Health is being developed. In this paper we support this call by explicitly focusing on the ethical argument that can be made for what we label 'Upstream One Health'. In particular, we want to argue that Upstream One Health offers a means of supporting vulnerable and marginalized human and nonhuman animals.

Methods

We employ casuistry (comparative case-based reasoning using ethical principles) of the key characteristics of upstream and downstream One Health. To elaborate and analyse our cases, we use Rogers, Mackenzie and Dodd's taxonomy of vulnerability concepts because it captures the diverse ways in which vulnerability is produced (inherent, situational and pathogenic) while simultaneously overcoming recognized problems in other accounts.

Results

A downstream One Health approach which prioritizes reacting to pathogen spillovers has clear benefits and efficiencies. However Upstream One Health is better positioned to address the inherent, situational and pathogenic vulnerabilities of humans and animals with respect to risk at the human-animal-environment interface. Although downstream One Health measures are usually effective in the short term, this hinges on appropriate and timely reactions to risks by decision-makers whose choices are shaped and constrained by politics and existing inequitable social and economic power structures. In fact, downstream approaches to risks and threats can thereby actually exacerbate pathogenic vulnerability by reinforcing an unjust status quo. By contrast, upstream approaches challenge and disrupt the status quo, drawing attention to pathogenic vulnerability and facilitating a shift to improve the situation of those who are already vulnerable (including nonhuman animals). Upstream One Health has the potential to contribute to broader change in social practices and institutions and even out disparities

that contribute to vulnerability in and beyond health. However precisely because of the radical nature of the change supported by Upstream One Health, it may be difficult to realize and implement.

Conclusions

The ethical case to prevent (or even to minimise) pandemic and emerging infectious disease risks through structural reforms and ecological countermeasures remains relatively unexplored. Taking One Health upstream is radical and challenging, but warranted given the threats to health and wellbeing we increasingly face. Arguments which take account of vulnerability can provide clear ethical justifications for Upstream One Health as they offer a means of supporting vulnerable and marginalized human and nonhuman animals.

213 – One Health System Strengthening in Zanzibar: A Workshop Series to Identify Implementation Barriers, Workforce Competencies, and Advocacy Strategies.

Hamisi MSAGAMA (1), Carolyn HENRY (2), Gabrielle LAING (2), Shaali AME (3)

1: One Health Society, Tanzania; 2: Unlimit Health, UK; 3: Ministry of Health, Zanzibar

Background: Zanzibar remains a major global tourism destination, presenting opportunities for economic growth while simultaneously increasing public health, animal health, and environmental pressures. These include heightened risks of endemic and emerging diseases, growing demand for animal products, and the need for environmental conservation.

The Zanzibar One Health Strategic Plan 2021–2025 (OHSP) articulates a vision of “a Nation with optimal health for people, animals, and the environment.” Responsibility for implementation rests with the Second Vice President’s Office; however, persistent institutional, workforce, and resource-related challenges continue to constrain effective delivery of the plan.

Methods: Key One Health stakeholders from across government sectors in Zanzibar were convened through a series of three 2-day workshops conducted between April 2025 and January 2026. The workshops aimed to support One Health Systems Strengthening (OHSS) by identifying implementation barriers and developing practical solutions.

The first workshop focused on identifying major challenges affecting implementation of One Health approaches and the OHSP. The second and third workshops addressed two priority barriers identified during the initial convening. Participatory methods were employed throughout, including rapid knowledge exchanges, individual learning journals, facilitated group work, and plenary discussions.

Results: Barriers identified during the first workshop were analyzed to determine their underlying root causes. A logic model was developed to map pathways for overcoming these barriers and informed the design of workshops two and three.

Workshop two focused on workforce knowledge and skills required for effective One Health implementation among in-service, health-associated professionals. Competencies were adapted from the Network for Evaluation of One Health (NEOH) core competencies and contextualized for Zanzibar. They were organized using the One Health High-Level Expert Panel (OHHLEP) 4Cs framework: Communication, Coordination, Collaboration, and Capacity Building. Competencies were structured as progressive tiers, with communication as the foundational level, followed by coordination and collaboration for staff with expanded One Health functions, and a final tier for those responsible for training and capacity development.

Workshop three focused on advocacy, resulting in the development of targeted advocacy skills and messages. These were subsequently applied during engagement with a high-level, cross-ministerial government panel.

Conclusion: Participants developed sustained professional relationships across the workshop series, forming the Zanzibar One Health Network. The agreed competencies have been institutionalized through a newly established knowledge platform hosted by the One Health Office under the Second Vice President’s Office. The platform will deliver hybrid learning opportunities, Zanzibar-specific modules, and continuous professional development credits recognized by relevant professional associations, strengthening long-term One Health implementation capacity in Zanzibar.

219 – Electricity-Free, Smartphone-Assisted On-Site Colorimetric Molecular Detection of Poultry Respiratory Viruses: A One Health Approach

Mohamed EL-THOLOTH (1,2), Rabiha SEBOUSSI (3), Mahmoud HUSSEIN (3), Salameh RAHMDEL (1), Alanoud ALALAWI (1), Haim H BAU (4)

1: Health Sciences Division, Al Ain Zakhir Campus, Higher Colleges of Technology, Abu Dhabi 17155, United Arab Emirates.; 2: Department of Virology, Faculty of Veterinary Medicine, Mansoura University, Mansoura 35516, Egypt.; 3: College of Veterinary Medicine, University of Al Dhaid, Sharjah, United Arab Emirates.; 4: Department of Mechanical Engineering and Applied Mechanics, University of Pennsylvania, Philadelphia, PA 19104, USA.

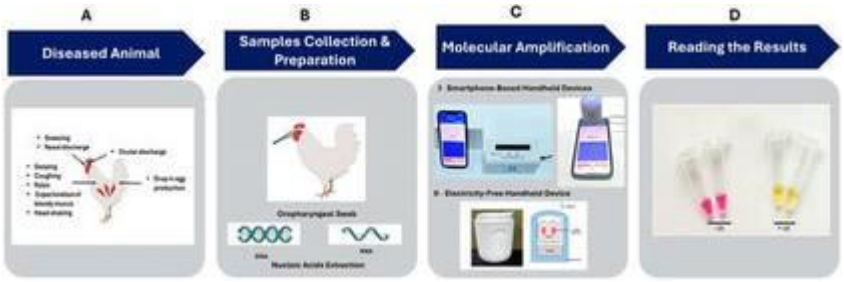
Background: Efficient control measures for respiratory diseases in humans and farm animals require accurate, specific, and rapid diagnostics. Traditional PCR-based molecular diagnostics are restricted to centralized laboratories, which results in significant, potentially catastrophic delays in test results. A case in point is the recent avian flu outbreak, which has culled more than 280 million poultry birds worldwide (over 157 million in the USA alone) since 2022; has spread to other farm animals, such as cattle; has further heightened the risk of a human pandemic; and threatens food security.

Methods: To enable molecular diagnosis of bird respiratory diseases at the point of need, we employ loop-mediated isothermal amplification (LAMP) in two platforms: (A) portable devices linked to a smartphone and (B) an inexpensive, disposable, electricity-free, instrument-free device with closed-tube, colorimetric detection that can be produced with minimal resources. Smartphone integration offers an

unexplored opportunity for spatiotemporal disease mapping, equipping policymakers with critical data for outbreak control.

Results: Our assays demonstrated 100% sensitivity and specificity compared to the gold standard, lab-based, quantitative PCR (qPCR). We tested contrived samples of the avian flu H5N1 virus, laryngotracheitis virus (ILTV), and infectious bronchitis virus (IBV) spiked into clinical samples, achieving a detection sensitivity adequate for early infection diagnosis in under 45 min.

Conclusions: The test is simple, requires minimal training, and can be performed without refrigeration, making it well-suited for resource-limited settings.



227 – Bridging Silos: One Health Antimicrobial Resistance Dynamics and Policy Integration to Contain the AMR Crisis

Chunlei SHI

Shanghai Jiao Tong University, China, People's Republic of

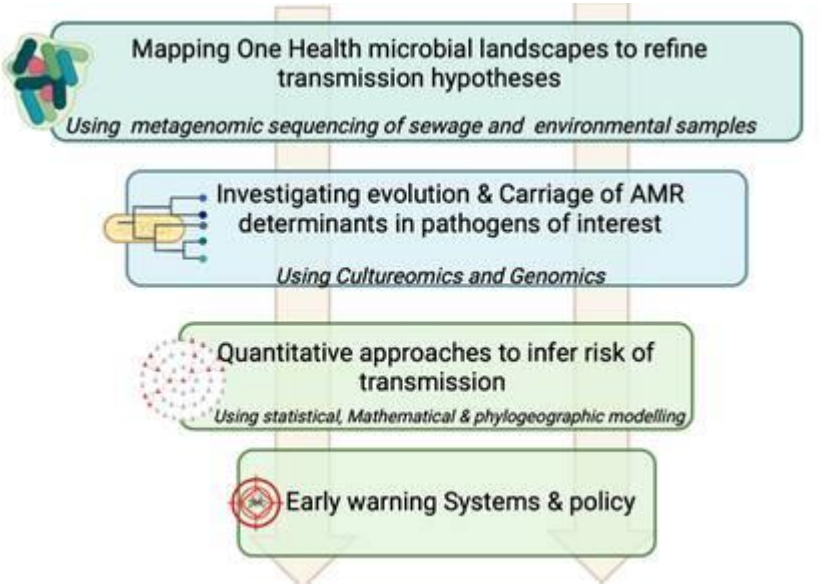
Antimicrobial resistance (AMR) is a quintessential One Health challenge, with its drivers and impacts spanning human, animal, and environmental ecosystems. Despite recognition of this interconnectedness, actionable policies and surveillance systems often remain siloed, hindering effective containment.

This session will move beyond describing the problem to focus on integrated, implementable solutions for AMR. It will highlight cutting-edge, cross-sectoral surveillance technologies that reveal the dynamics of resistance across the One Health spectrum. It will also present successful models of policy integration from varied global contexts, and explore economic incentives for sustainable practice change. The session's impact lies in its direct relevance to policymakers, researchers, and practitioners seeking concrete frameworks to translate the One Health paradigm into tangible AMR mitigation actions.

Audience members will benefit by gaining a clear understanding of effective interdisciplinary collaboration mechanisms. They will learn about novel tools for integrated surveillance, evidence-based policy models that have worked in different settings, and strategies to overcome sector-specific barriers to implementation. The outcome will be a toolkit of ideas and contacts to advance comprehensive AMR National Action Plans.

Proposed Talks and Speakers:

Proposed Session Chairs:



265 – Governing Integrated Risks through Siloed Policies: How Have Countries Incorporated One Health into Policy and Regulatory Frameworks?

Carmen BULLON CARO (1,2), **Marion SELOSSE** (1), **Fairouz LARFAOUI** (1), **William GARTHWAITE** (1), **Junxia SONG** (1)
1: FAO, Italy; 2: Universidade da Coruña (Spain)

Background One Health addresses interconnected risks at the human, animal and plant and environment interface. Yet, legal and policy frameworks governing these risks have traditionally been organized through sector-specific and often disconnected instruments. While this fragmentation is well recognized, limited analysis has been conducted on how national authorities and regional institutions integrate One Health into their governance systems. This study analyses how countries and regional organizations operationalize One Health across policies and legislation, identifying emerging governance patterns.

Methods The analysis draws on an empirical review of approximately 480 policy documents and 100 legal instruments at national and regional levels that explicitly reference One Health. These instruments were identified through the One Health Dashboard, a FAO-hosted dataset fueled by FAOLEX compiling national and regional policies and legislation that explicitly incorporate or refer to One Health. The corpus was analyzed by sector (including human health, animal health, food safety and environmental protection) and by geographic origin, using a combined quantitative and qualitative comparative approach to assess how One Health considerations are reflected within governance frameworks.

Results Among the instruments collected, 43 instruments (representing 8.8 percent of the total) focus explicitly and primarily on One Health. Their review shows several governance patterns, including differences in scope, institutional roles, coordination mechanisms and stakeholder involvement.

Africa and Europe account for the largest number of instruments, followed by Asia and Latin America.

Nearly half of the policy documents focus on antimicrobial resistance (AMR), confirming AMR as the dominant entry point for One Health operationalization to date. Beyond AMR, One Health is reflected across a range of sectoral and cross-sectoral instruments, particularly in environmental policy, agriculture and livestock development, human health and food systems.

Conclusion

The findings suggest that One Health is most frequently operationalized through sector specific instruments incorporating coordination requirements, rather than comprehensive One Health instruments. At the same time, a growing number of integrated One Health policies and strategies establish dedicated coordination mechanisms to support implementation. These instruments vary in scope, ranging from general One Health strategies to sector-specific policy domains, such as biosecurity, zoonoses management or emergency preparedness. The results indicate that effective One Health implementation does not depend on system-wide legal reform, but on carefully designed policy and

legislative choices capable of translating integrated risk awareness into coordinated responses. These findings offer practical guidance for lawmakers and policymakers seeking to operationalize One Health.

274 – Development and characterization of anti-polystyrene mouse monoclonal antibodies

Liu CAO (1,2), William DAVIS (3), Ivelin GEORGIEV (4), Perry WASDIN (4), Ximin ZENG (1), **Jun LIN** (1)

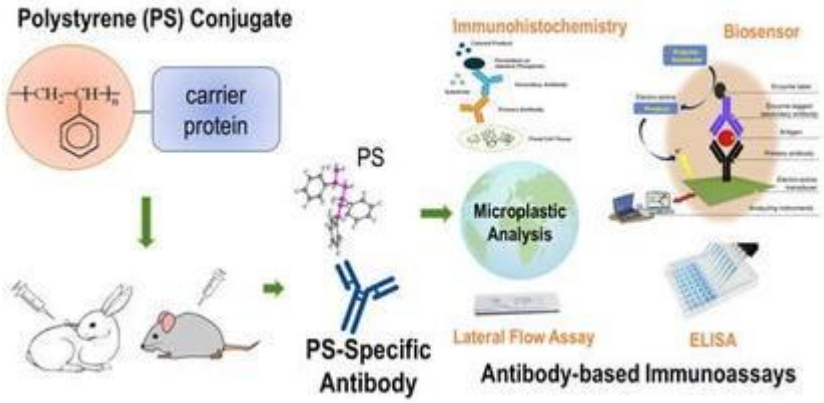
1: University of Tennessee, United States of America; 2: Gannon University, Erie, PA, USA; 3: Washington State University, Pullman, WA, USA; 4: Vanderbilt Institute for Infection, Immunology and Inflammation, Nashville, TN, USA

Background: Micro- and nano-plastic (**MNP**) pollution is a pressing global health and environmental concern. Growing evidence from animal studies suggests that exposure to ubiquitous MNP may contribute to various human health issues. However, our understanding of the health effects of MNPs is still in its infancy, primarily due to a significant technical bottleneck: lack of a cost-effective, user-friendly, sensitive, and reliable analytical tool. Antibody-based immunoassays have been widely recognized as an efficient approach for qualitative and quantitative analysis; generation of specific antibodies is crucial. Recently, we successfully produced polyclonal antibodies directed against polystyrene (**PS**) and demonstrated feasibility of PS antibody-based immunoassays for MNP analysis. The objective of this study is to develop and characterize PS-specific mouse monoclonal antibodies (**mAbs**).

Methods: Mice were immunized with PS-KLH conjugate for mAb development using standard protocol. The anti-PS mAbs from purified hybridoma cell lines were subjected to isotype and titer analyses using ELISA. Reactivity and specificity of the mAbs to oxidized PS and other plastics (polyethylene and polypropylene) were examined using immunostaining and ELISA. The representative mAb 35 was affinity purified for enzyme digestion, LC-MS/MS, and *de novo* peptide sequencing. The mAb 3B sequence was compared to human and mouse antibody sequence databases.

Results: We obtained five hybridoma cell lines producing anti-PS mAbs that are all IgM isotype. The anti-PS mAbs showed vivid reactions to standard pristine PS particles as well as oxidized PS; however, the mAbs displayed weak or no reactions to polyethylene and polypropylene, respectively, indicating that the mAbs are highly specific for PS. Complete amino acid sequences of both light chain and heavy chains of the mAb 3B were obtained. Strikingly, the mAb 3B is basically unmutated germline with only a few mutations in the CDRH3. Comparison of mAb 3B to mouse (n = 31,642) and human (n > 1.7 million) antibody sequences revealed rare features of mAb 3B with respect to both gene pairing and CDRH3. Revisit of the rabbit serum samples from previous anti-PS polyclonal antibody development further confirmed that anti-PS IgM level was elevated and persistent upon immunization with PS-KLH conjugate.

Conclusion: The PS-specific mAbs were successfully obtained for developing efficient immunoassays to detect, track, and quantify MNPs in the future. Our findings also suggest that PS antigen behave in a T cell-independent manner and the anti-PS mAbs come from early B-cell response with little somatic hypermutation.



278 – Combating Antimicrobial Resistance and Reducing Chemical Misuse through a Territorial One Health Approach: Experience from the THIELLAL Project in Senegal

Credo HOUNDODJADE, **Sophie OUVRARD**, **Serge BREYSSE**, Clemence DOUMENC-AÏDARA, Karel NANA, Patrick KARUME, Christian SAMBOU
SOLTHIS

Background: Antimicrobial resistance (AMR) constitutes a major global threat to public health. In Vélingara department, Senegal, diagnostics revealed widespread self-medication (55%), excessive anti-infectious prescriptions (70% of consultations, notably amoxicillin), massive antibiotic use in animal health (70% of veterinary medicines), improper pesticide handling, and poor perception of antibiotic resistance as a health risk. The THIELLAL project ("one health" in Pulaar) tested whether a participatory territorial One Health approach, integrating human health, animal health, and environmental sectors, could reduce antibiotic and pesticide misuse, thereby limiting AMR emergence while promoting agroecological transition.

Methods: The intervention occurred in 4 communes of Vélingara department (Linkéring, Paroumba, Pakour, Wassadou) between 2021-2024, targeting 15 villages. The AVSF-SOLTHIS-CASADES consortium, funded by AFD, implemented a multi-phase methodology. Diagnostic phase: 12 participatory studies documented medicine distribution circuits, prescription practices, and AMR perception. Structuring phase: establishment of 64 DIMITRA clubs, 4 communal consultation frameworks, and revitalization of the departmental Multi-sectoral Instance. Capacity building: multi-stakeholder training on One Health, AMR, and rational medicine use (277 community actors, 668 people on 4 priority themes). Awareness phase: pedagogical AMR scenario in 4 themes (microorganisms, infection pathways, treatments, resistance mechanism), community discussions, home visits (13,936 people sensitized), radio broadcasts. Agroecological phase: 4 Agroecological Field Schools promoting pesticide alternatives. Evaluation used qualitative approaches with 17 focus groups and individual interviews.

Results: Results demonstrate territorial One Health effectiveness against AMR. Awareness reached 13,936 people (48% women, 16% youth). Human health outcomes: significant self-medication decrease, increased antibiotic dosage compliance, reduced street medicine sales, increased medical consultations before treatment. Animal health: 154 producers and professionals adopted good antimicrobial practices, rational veterinary antibiotic use, limited fraudulent medicines, increased professional diagnostic services. Agroecology: 108 trained farmers adopted pesticide alternatives (biopesticides), notable pesticide reduction in market gardening and cotton crops, improved chemical handling and storage. Three specific objectives achieved: collective AMR awareness evolution (level 1 to 3), effective One Health territorial governance with 64 dynamic DIMITRA clubs (64% women), production of 2 capitalization documents as reference tools and 3 AMR policy briefs.

Conclusions: THIELLAL demonstrates that territorial participatory One Health effectively combats antimicrobial resistance in resource-limited contexts. Integration of human health, animal health, agriculture, and environment enabled holistic AMR understanding and sustainable local solutions. Key success factors include contextual pedagogical AMR scenarios, local languages, DIMITRA club engagement, technical service involvement, and permanent field facilitation. Documented behavioral changes significantly impact AMR containment and health protection. A second phase is recommended to consolidate governance, expand coverage, and strengthen national antibiotic resistance advocacy.

281 – The imperative of aligning pandemic prevention and preparedness with evidence on spillover risk

David BELL, Blagovesta TACHEVA, **Jean VON AGRIS**, Garrett BROWN
University of Leeds, United Kingdom

Background

The global pandemic prevention, preparedness and response (PPPR) agenda is heavily premised on a rising risk of ‘spillover’ of pathogens from zoonotic hosts, underpinning the importance of One Health approaches. A consequent rapidly rising pandemic risk underpins major proposed investments in PPPR centred around the recently revised International Health Regulations and proposed Pandemic Agreement of the World Health Organization (WHO). As WHO and the World Bank claim:

"Epidemics *and pandemics … are occurring more often, and spreading faster and further…*", "every year, zoonotic diseases sicken billions…, killing millions…", and "…the potential for diseases to emerge has increased exponentially".

With $20 billion in new annual spending in PPPR and One Health proposed by WHO and the World Bank, potential gains and opportunity costs have huge implications for international public health. Financing and policy must be based on a deep understanding of underlying complexity to ensure net gain rather than harm.

Methods

To determine how reliably the cited evidence base supported funding and policy recommendations, we assessed major reports from WHO, World Bank and G20 from 2020 to 2025, with their primary and secondary sources, regarding spillover risk and consequent risk of pandemics.

Results

While a major increase in reported outbreaks has occurred over 60 years, no analyses took the development and roll-out of diagnostic and communications technologies into account. The long history of humans in forest fringe agriculture and in hunter-gathering and the ecological complexity of ecotone interactions were also poorly addressed.

While various sources used by WHO, the World Bank and G20 recognize the complexity of interactions between outbreak frequency and climate, forest and agricultural changes, selective quotations and misrepresentation of these sources have led to claims supporting policy that are at odds with the cited literature. Circular referencing between agencies, and with panels set up by the agencies, or with the agencies' support, compounds this problem. A reduction in new virus identification and outbreak frequency over the last 15 years, repeated in their cited sources, is poorly reflected or contradicted.

Conclusion

Poor support for claims of rapidly rising outbreak frequency driven by zoonotic spillovers, based on their own citations, raises concerns regarding proportionality and risks of net harm in pandemic policy. A failure to consider advances in diagnostic and communications technologies, and simplification of highly complex ecological interactions, weakens current finance requests.

While ecological change resulting from human population growth is accelerating in many areas, its relationship with spillover risk and consequent outbreaks is complex and underdeveloped. To justify the investment and opportunity costs of current PPPR proposals, it is imperative that the One Health community develop a firmer evidence base and ensure good policy outcomes.

---

289 – Adapting the One Health zoonotic disease prioritization tool for subnational One Health implementation through comparative analysis of disease severity and governance-driven approaches

Soawapak HINJOY (1), Kittichai UNJIT (2), Anyarat THIPTARA (2), Wansane TOANAN (3), Ariya BUNNGAMCHAIRAT (4), Pusana RODSOM (1), Sukunlaya SIRISUKKARN (5), Sudarat DAMRONGWATANAPOKIN (1), Serge MORAND (6,7,8)

1: Department of Disease Control, Ministry of Public Health, Thailand; 2: Department of Livestock Development, Ministry of Agriculture and Cooperatives, Thailand; 3: Department of National Parks, Wildlife and Plant Conservation, Ministry of Natural Resources and Environment, Thailand; 4: Faculty of Public Health, Mahidol University, Thailand; 5: Department of Disease Control Foundation, Thailand; 6: IRL HealthDEEP CNRS; 7: Faculty of Veterinary Technology, Kasetsart University, Thailand; 8: Faculty of Tropical Medicine, Mahidol University, Thailand

Background: Zoonotic and environmentally driven health threats increasingly emerge at the human–animal–environment interface, highlighting the need for prevention-oriented and community-centered One Health approaches. This study adapted the OHZDP tool developed by the United States Centers for Disease Control and Prevention (U.S. CDC) for subnational use in Thailand, integrating environmental and social science perspectives and expanding community participation to ensure context-specific and operationally relevant prioritization.

Methods: A comparative mixed-methods case study was conducted in two Thai provinces—Ubon Ratchathani and Nan—using multisectoral, four-day participatory workshops in 2025. Approximately seventy participants per province represented human, animal, environmental health, local governance,

and civil society sectors. Health hazards were identified using an all-hazards approach. Six decision criteria were weighted through multisectoral consensus, and hazards were scored using a structured multi-criteria framework, complemented by qualitative deliberation to generate consensus-based prioritization.

Results: Prioritization outcomes differed between provinces due to variations in criteria weighting. Ubon Ratchathani emphasized biomedical severity and cross-sectoral impact, prioritizing emerging infectious diseases, rabies, non-communicable diseases, and other high-mortality infections, reflecting a catastrophic risk preparedness profile. In contrast, Nan prioritized governance capacity and policy feasibility, resulting in rankings dominated by environmental and governance-dependent hazards, including PM2.5 air pollution, open waste burning, stray dog management, agricultural chemical exposure, and climate-related disasters in Table 1.

Conclusions: Community-led adaptation of prioritization tools strengthens subnational One Health action. Integrating governance, environmental, and social determinants into biomedical frameworks enhances multisectoral engagement, supports prevention-focused implementation, strengthens early warning systems, and builds community resilience against zoonotic disease emergence.

Table 1: Comparative Top Hazards: Ubon Ratchathani vs. Nan

Rank	Ubon Ratchathani (Severity Focus)	Nan Province (Governance Focus)	Primary Strategic Driver
1	Emerging Infectious Diseases (Disease X)	PM 2.5	Preparedness vs. Environmental Governance
2	Rabies	Severe Acute Respiratory Diseases	Severity vs. Governance Enforcement
3	All Cancers (aggregate)	Stray dogs & rabies	Chronic NCD Burden vs. Municipal Governance
4	Diabetes	Agricultural chemical hazards	Chronic NCD Burden vs. Agricultural Policy
5	Impacts from Armed Forces/Conflict	Tuberculosis + XDR-TB	Geopolitics vs. Severity
6	Road Traffic Accidents	Floods/landslides	Societal Impact vs. Disaster Command
7	Hypertension	Waste management and burning	Chronic NCD Burden vs. Municipal Governance
8	Flooding	Streptococcus suis	Environmental vs. Zoonotic Interface

298 – Sustainability in the context of One Health: definitions, concepts and a framework for analysis

Osman Ahmed DAR

UK Health Security Agency, United Kingdom

Background: This research addresses the conceptual and operational ambiguity surrounding sustainability in One Health and global health security. Despite widespread rhetorical endorsement and a growing policy emphasis, sustainability remains poorly defined and inconsistently applied across sectors. The central aim of this research was to develop and empirically validate a cross-sectoral conceptual framework and definition of sustainability for application in One Health initiatives. The specific objectives were to synthesise existing definitions across disciplines develop an integrated framework; explore expert understandings of sustainability; and assess how existing global health security tools, namely the WHO Joint External Evaluation (JEE) and the WOAH Performance of Veterinary Services (PVS) tool, reflect sustainability concepts and are perceived by policymakers.

Methods: A multi-method design was employed, grounded in interpretivist and social constructionist epistemologies. First, an umbrella systematic review was conducted to identify sustainability definitions and frameworks across disciplines. The resulting synthesis informed the development of an integrated definition and meta conceptual framework. This was followed by a document analysis of the JEE and PVS tools and two rounds of semi-structured qualitative interviews with global One Health and health security experts.

Results: Based on the research findings, the proposed definition conceptualises sustainability as: *"A quality-assured system, strategy, service, programme, project, intervention or initiative, which is equitably and justly delivered while being socially, economically and environmentally viable, that continues to be implemented while effective and adapts as needed over a defined period of time, to produce a state of optimised health benefits across humans, animals and ecosystems without compromising the ability of future generations to meet their health and well-being needs."*

The corresponding framework incorporates both process dimensions (e.g., governance, financing, institutional capacity, adaptability, systemic integration) and outcome dimensions (e.g., ecological resilience, sustained health improvements, equity). Interview and document analysis findings independently affirmed the framework dimensions' relevance across sectors and scales and highlighted the limited and fragmented integration of sustainability in global health security tools. They also illuminated that the meaning and determinants of sustainability not only vary across sectors, but are also deeply shaped by epistemic tradition, disciplinary background, power relations, and socioeconomic and political context.

Discussion and Conclusion: The deterioration of multilateral development financing, increased geopolitical polarisation and weakening of public trust in institutions all challenge the sustainability of health systems and their capacity to address complex, cross-sectoral threats. The research offers a theoretically grounded and practically applicable framework for embedding sustainability into One Health programme design, evaluation, and governance. It also highlights the inadequacy of current health security assessments in addressing long-term resilience and multisectoral integration. This research contributes to bridging conceptual gaps and advancing a shared understanding of sustainability in global health at a time of funding contractions and mounting ecological and institutional fragility.

317 – Intra-host convergent evolution of persistent morbilliviruses associated with fatal CNS disease in humans and other mammalian species

Melvin DANIEL ROJI (1), Franziska GEISELHARDT (1,2), Georg BEYTHIEN (2), Kristin LAUDELEY (1), Monica MIROLO (1), Wendy K. JO (1), Laura MARTINO (3), Andreas BEINEKE (2), Wolfgang BAUMGÄRTNER (2), Martin PETERS (4), Judith M.A. VAN DEN BRAND (5), Trine H. JENSEN (6), Thijs KUIKEN (7), Johannes P. M. LANGEDIJK (8), Mariano DOMINGO (3), Albert DME OSTERHAUS (1,6,7,9), Martin LUDLOW (1)

1: Research Center for Emerging Infections and Zoonoses, University of Veterinary Medicine, Foundation, Hannover, Germany; 2: Department of Pathology, University of Veterinary Medicine, Foundation, Hannover, Germany; 3: Departament de Sanitat i Anatomia Animal, Facultat de Veterniària, Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain; 4: Chemisches und Veterinäruntersuchungsamt (CVUA) Westfalen, Arnsberg, Germany; 5: Dutch Wildlife Health Centre, Utrecht University, The Netherlands; 6: Sealcentre Pieterburen, Pieterburen, The Netherlands; 7: Erasmus Medical Center Rotterdam, The Netherlands; 8: ForgeBio BV, Amsterdam, The Netherlands; 9: Leibniz Institute of Virology, Hamburg, Germany

Background:

Chronic morbillivirus infections of the central nervous system (CNS) present as late sequalae associated with high mortality levels that occur in humans and animals following resolution of the acute infection. The decline in measles vaccination rates in recent years is expected to result in a parallel increase in cases of invariably fatal subacute sclerosing panencephalitis (SSPE), due to persistent measles virus (MeV) infection of the CNS. Similarly, SSPE-like chronic neurological infections have been observed in adult dogs, dolphins and seals caused by canine distemper virus (CDV), dolphin morbillivirus (DMV) and phocine distemper virus (PDV) respectively. However, characterization of animal morbillivirus strains associated with such chronic infections are lacking, especially with respect to genotypic and phenotypic similarities to SSPE associated MeV.

Methods:

The complete genome sequence of animal morbillivirus strains, CDVlynx (from a Eurasian Lynx), PDV2001, PDV2014 (both from harbor seals) and DMV232-18 (from a striped dolphin) that persisted in the CNS of their respective host species for several years following the initial acute infection was obtained by next generation sequencing from brain tissue samples. Sequence analysis showed unique amino acid (aa) changes in all viral proteins, with the Matrix (M) and Fusion (F) proteins particularly affected. The competence of the surface glycoproteins to mediate virus entry and cell-to-cell spread in a receptor negative environment was assessed by fusion assays and the use of pseudotyped viruses. The impact of

amino acid changes in individual viral proteins on virus replication kinetics was studied with recombinant CDVs generated for this study.

Results:

Here we show that the immune privileged environment of the CNS promotes intra-host convergent evolutionary signatures in different animal morbilliviruses associated with chronic CNS disease manifestations. Persistent animal morbillivirus strains accumulate mutations in multiple genes with amino acid changes in the M and F proteins, resulting in impaired M protein function and hyperfusogenic F proteins. These are both hallmark features of SSPE-associated MeV strains. Recombinant viruses encoding a hyperfusogenic CDV F protein display increased cell-cell fusion but reduced replication kinetics, consistent with evolutionary constraints favouring viral persistence in the CNS. Mutational patterns in PDV2014 support the precedence of functionally impaired M protein to the subsequent F protein changes during chronic CNS infection.

Conclusions:

Our findings show that similar evolutionary pathways across different mammalian species drive morbilliviruses to evolve analogous mechanisms that favour virus persistence in the CNS and the development of fatal chronic neurological disease. Such naturally occurring chronic animal morbillivirus infections of the CNS provide natural analogues for studying the evolutionary trajectory and molecular basis of the pathogenesis of SSPE in humans. This may pave the way for developing early diagnostics and intervention strategies for SSPE.

---

325 – Co-designing an antimicrobial resistance intervention with poultry farmers and animal health professionals in Nigeria

Alice B. J. E. JACOBSEN (1,2), Jane OGDEN (2), Aliyu WAKAWA (3), Abel B. EKIRI (1)

1: Department of Comparative Biomedical Sciences, School of Veterinary Medicine, University of Surrey, United Kingdom; 2: School of Psychology, University of Surrey, United Kingdom; 3: Faculty of Veterinary Medicine, Ahmadu Bello University, Nigeria.

Farmers and animal health professionals play a crucial role in the use of antibiotics in the animal sector. Therefore, it is essential to understand ways to work with these stakeholders to mitigate the growing crisis of antimicrobial resistance (AMR). Our study aims to identify a plausible AMR intervention through co-production with poultry farmers and animal health professionals in Nigeria.

The study consists of three pathways: 1) Establishing a theoretical framework, 2) Identifying plausible interventions, and 3) Refining and justifying interventions and selecting the most feasible intervention. Pathway one involved reviewing the literature and theoretical frameworks. Pathway 2 involved interviewing poultry farmers, veterinarians, and other key stakeholders, as well as conducting surveys among poultry farmers. The interviews and survey aimed to establish current knowledge, opinions, and practices, as well as gather deductive questions on specific interventions. Pathway 3 was centred around stakeholder discussions with farmers and veterinarians about plausible interventions established in the earlier pathways.

The interviews (n = 22) and the survey (n = 25) established six plausible interventions: 1) withdrawal period adherence, 2) probiotic use, 3) education around highest priority critically important antimicrobials, 4) education around antimicrobial use (AMU), AMR and biosecurity, 5) reduction of routine AMU prior to vaccines, 6) and education of veterinary students. Education about AMU, AMR, and biosecurity, along with the use of probiotics, were most selected. Of the survey respondents, 56% expressed a desire for change but were limited by a lack of time, money, and knowledge. They also highlighted a mismatch between farmers' opinions and practices and AHPs' beliefs about farmers' opinions and practices. The discussions with stakeholders (n = 7) revealed that all interventions had some positive attributes; however, as with the interviews and survey, education was most favourably received.

In conclusion, this study highlights the strengths of co-production and the development of an intervention with the community for the community. General education about AMU, AMR, and biosecurity was selected as the most feasible intervention for implementation in the Nigerian poultry sector.

362 – One Health as the Institutionalized Delivery Architecture for Planetary Health: The Green One Health Imperative

Noel MIRANDA (1), Oliver AGONCILLO (2), Alice HUGHES (3), Liz WILLETTS (4), Christina PETTAN-BREWER (5), Serge MORAND (6), Nai Rui CHNG (7), Gyanendra GONGAL (8), Mafalda VIANA (9), Remi GALAY (10), Mike TEE (11), Ron LAW (12), Percival Ethan LAO (13), Mary Elizabeth MIRANDA (14), Gemimn Louis C APOSTOL (15), **Katie WOOLASTON** (16)

1: Independent; 2: ASEAN Centre for Biodiversity; 3: University of Melbourne; 4: Independent; 5: University of Washington; 6: University of Montpellier; 7: University of Glasgow; 8: World Health Organization; 9: University of Glasgow; 10: University of the Philippines; 11: University of the Philippines; 12: Department of Health, Philippines; 13: Ateneo Center for Research and Innovation; 14: Field Epidemiology Training Program Foundation Inc; 15: Ateneo Center for Research and Innovation; 16: Green Governance Solutions

Background Planetary Health defines the health of human civilization as inseparable from the state of the natural systems on which it depends (Whitmee et al., 2015). Evidence increasingly demonstrates that the Triple Planetary Crisis—climate change, biodiversity loss, ecosystem degradation and pollution, alongside widening socio-economic inequities—operates as a tightly coupled determinant of health risk within interconnected socio-ecological systems (IPBES, 2019; IPCC, 2023; Myers, 2020). While Planetary Health provides a powerful normative and diagnostic framework, it does not itself constitute an institutionalized, multisector delivery system embedded within routine governance. This creates a governance asymmetry: what must be protected is clear, but how to operationalize coordinated prevention at scale remains insufficiently specified. Recent Quadripartite deliberations have identified the Triple Planetary Crisis as a health security risk requiring One Health approaches. One Health is already widely institutionalized across human–animal–environment interfaces, particularly in relation to zoonoses and emergency response.

Methods This paper advances a conceptual governance analysis of One Health as an operational delivery architecture for Planetary Health objectives. Drawing on governance theory, institutional analysis, and recent regional policy processes, it develops the concept of Green One Health (GOH) as the upstream mandate completion of the existing One Health architecture. The analysis examines the institutional implications of extending One Health beyond its prevailing downstream focus and builds on previously articulated GOH principles (Miranda et al., 2026).

Results Three arguments are advanced. First, One Health represents the most institutionalized multisector governance architecture currently available to operationalize Planetary Health objectives at scale. Second, its prevailing implementation remains predominantly downstream, focused on zoonotic diseases and emergency preparedness and response. Third, Green One Health constitutes the upstream completion of this architecture by extending legal mandate, operational scope, and formal cross-sector inclusion into ecological integrity, sustainable land and resource governance, climate adaptation, and community livelihood resilience. GOH does not propose parallel institutional structures; rather, it deepens and fully authorizes existing coordination, surveillance, risk assessment, planning, financing, and accountability functions across upstream socio-ecological domains. The principal constraint to such extension is not technical feasibility but political authorization, institutional alignment, and sustained financing.

Conclusions The central governance challenge is incomplete authorization of an existing delivery architecture. Green One Health re-scopes One Health upstream to embed prevention at source as a routine function of governance, guided by equity and transformative justice. Institutionalizing this shift requires formal mandate extension, multisector coordination across governance levels, aligned public and private incentives, and embedded policy-oriented research and evidence generation. The question for decision-makers is not whether an integrated system is needed, but whether the existing One Health architecture will be fully embedded across the planetary risk continuum to deliver sustained multisector prevention at scale.

371 – Strengthening Integrated Bite Case Management in Uganda through the REACT app: Early Lessons from Implementation Science approach

Rabina GHIMIRE (1,2), Frederic LOHR (3), Terence ODOCH (4), Samuel OKECH (4), Flavia NAKANJAKO (5), Francesca BAKER (3), Dickson AKANKWATSA (6), Salome DÜRR (7), Sonja HARTNACK (1,2)

1: Centre for Veterinary Public Health and One Health, Clinical Department for Farm Animals and Food System Transformation, University of Veterinary Medicine Vienna, Vienna, Austria; 2: Section of Epidemiology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland; 3: Mission Rabies, Worldwide Veterinary Services, Cranborne, UK; 4: College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala, Uganda; 5: Ministry of Agriculture, Animal Industry and Fisheries, Entebbe, Uganda; 6: Infectious Diseases Institute, Makerere University, Kampala, Uganda; 7: Veterinary Public Health Institute, University of Bern, Bern, Switzerland

Background: Rabies is endemic in Uganda, where underreporting due to weak surveillance obscures the true burden. Effective rabies surveillance requires a One Health approach, and Integrated Bite Case Management (IBCM) provides such framework for timely reporting, risk assessment, and coordinated follow-up of bite cases. To strengthen IBCM, the Rabies Exposure Assessment and Contact Tracing (REACT) app was piloted in Uganda to digitalize case reporting and improve coordination between human and animal health sectors.

Methods: Four districts in Uganda were selected for the pilot: Arua, Kyegegwa, Masaka, and Soroti. Implementation began in May 2024 with training workshops for animal and human health officers, followed by operationalization of the app. Two REACT users, one from each sector (human health and animal health), were identified per district. Monitoring activities included regular online follow-ups and district visits. This was complemented by training in animal rabies sample collection and testing. Evaluation of feasibility, adoption and sustainability of REACT use is guided by the Consolidated Framework for Implementation Research (CFIR) and Reach, Effectiveness, Adoption, Implementation, and Monitoring (RE-AIM) framework, using in-app analytics, case records, user feedback, workshop outputs, and qualitative interviews with REACT app users and stakeholders.

Results: By mid-February 2026, 214 bite cases have been reported through REACT app across the four districts. Among these, 39 cases remain under follow-up. Additionally, 19 animal samples have undergone rabies rapid testing in the field and were subsequently submitted to the national laboratory for confirmatory analysis using the indirect Fluorescent Antibody Test (iFAT). REACTapp has been reported to improve timeliness and completeness of bite investigations, record-keeping and cross-sectoral collaboration, with regular communication between stakeholders supported by phone exchanges and WhatsApp groups. Users reported benefits such as improved rabies case investigation, better record-keeping, and enhanced community engagement through follow-up calls and information sharing on post-exposure prophylaxis.

Adoption varied across districts, influenced by local resources, user motivation, and health system priorities. Offline functionality and structured training materials supported the uptake. Challenges identified included community practices of killing and hiding suspected animals, shortage of vaccines, testing and animal-handling equipment, and inconsistent outbreak management strategies such as culling roaming dogs, contrary to WHO recommendations.

Conclusion: Preliminary findings suggest REACT app is a feasible and adaptable tool in both rural and urban settings, providing more structured rabies surveillance and strengthening One Health collaboration. By August 2026, a comprehensive evaluation will be presented providing lessons for integrating digital tools within IBCM in Uganda and offering transferrable insights applicable to other rabies endemic settings.

382 – Zoonotic and Infectious Disease Prevalence in Community Cats

Jim FERRARA
The Ohio State University, United States of America

Background

Highly pathogenic avian influenza (HPAI) H5N1 is an emerging zoonotic threat with expanding host and geographic range. Recent epizootics have been affecting poultry facilities all over the globe and dairy farms in the United States, with confirmed spillover into cats resulting in a high mortality rate. Free-roaming community cats are at risk of exposure through contact with infected birds, wildlife, and contaminated environments raising concerns for both feline and public health. Yet global data on HPAI exposure in community cats is extremely limited. Most feline cases are identified post-mortem in rabies-negative cats, and it remains unclear whether some cats survive HPAI infection. Community cats may also act as bridge vectors, transmitting zoonotic diseases between species—including to humans, making this an important One Health issue.

This study aims to address a critical gap in understanding HPAI H5 epidemiology in cats and determine the current seroprevalence of other infectious diseases: FIV, FeLV, Panleukopenia, and Toxoplasmosis. While prevalence has been reported sporadically in regions of the United States and globally, few studies focus on community cats and the risk factors for these pathogens. Results from this study will inform strategies to reduce zoonotic and infectious disease risks from community cats, ultimately improving the health and welfare of both cats and humans.

Methods

Blood samples were collected from anesthetized cats undergoing routine sterilization as part of established community cat TNR programs. Blood samples were tested for FIV/FeLV utilizing a point-of-core ELISA test and, if submitted prospectively and the test returned a positive result for either disease, these samples were then submitted for confirmatory testing via RealPCR. Serum samples were tested using validated serologic assays for HPAI: Nucleoprotein-based (NP) ELISA to detect Influenza A antibodies and Hemagglutination Inhibition (HI) for H5 subtyping on NP positive samples. Serum samples were submitted for Indirect Fluorescent Antibody (IFA) testing of toxoplasmosis and panleukopenia. Risk factor analysis incorporated cat-level variables (e.g., age, sex, body condition, health status, geographic location).

Results

Seroprevalence of influenza A and H5N1 in community cats are reported as well as relevant risk factors for exposure. Prevalence of FIV, FeLV, toxoplasma, and panleukopenia are reported and compared to regionally relevant data.

Conclusions

The results of this study can inform veterinary decision making when working with community cats, especially with respect to establishing biosecurity and biosafety protocols as part of a One Health Approach. They will also help quantify the potential risk that community cats may present to pet cats, which veterinarians in private practice can share with their clients. For HPAI, this can help determine if cats are at risk from current strains carried by wild birds, helping to determine if they might play a future role in spreading this virus to humans.

394 – (How much) Do humans transmit AMR risk to agricultural enterprises? Case study: Clostridioides difficile cross-sectoral transmission dynamics

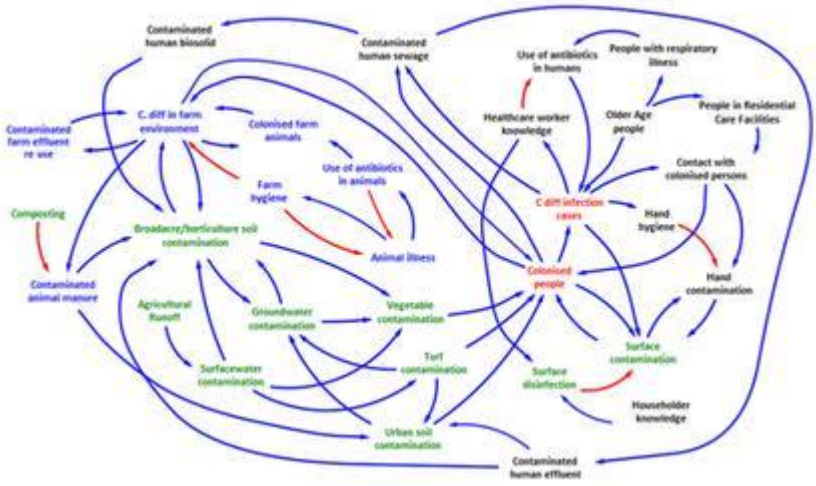
Simon REID (1), Angela WILLEMSEN (1), Russell RICHARDS (1), Tom RILEY (2,3,4), Su Chen LIM (2), Linda SELVEY (1), Oz SAHIN (1)
1: The University of Queensland, Australia; 2: The University of Western Australia; 3: Edith Cowan University; 4: PathWest Laboratory Medicine

Background:*Clostridioides difficile* infection (CDI) is a major public health challenge with complex transmission dynamics spanning human, animal, and environmental systems. While traditionally considered a healthcare-associated infection, the significant rise in community-associated cases suggests critical roles for non-clinical reservoirs and environmental persistence. The goal of this study was to map these complex "One Health" dynamics and to identify new multi-sectoral intervention strategies. The specific objectives were to develop an integrated System Dynamics Model (SDM) to quantify feedback loops and identify high-leverage points for sustainable, population-level infection control.

Method: A participatory Systems Thinking approach was employed, involving stakeholders from healthcare, agriculture, and waste management to develop a Causal Loop Diagram (CLD). This qualitative structure informed the development of a mathematical SDM that stratified the human population by age and antibiotic exposure. The model explicitly integrated human, animal and environmental sources of *C. difficile* and the pathways for movement of spores between them. Four policy levers: Antibiotic Stewardship, Human Transmission Control, Animal Source Control, and Environmental Biosolids Management were evaluated by simulating system behaviour over a 20 year period.

Results: The qualitative model shows the presence of two independent transmission cycles between humans and animals, and their respective environments. Importantly, it also demonstrates the nature of the bidirectional connections that link these two cycles into a single large system that is governed by delays associated with the persistence of spores in the environment. Simulations reveal that a small demographic—antibiotic users over 65—accounts for nearly half of the symptomatic CDI burden, functioning as the primary system amplifier. Environmental reservoirs are the dominant drivers of long-term endemic stability and reinfection potential. Environmental Biosolids Management emerged as the most influential long-term lever, with enhanced spore decay rates halving equilibrium concentrations. Combined strategies demonstrated that synergistic responses are possible with leverage points in different subsystems. High-intensity implementation of the most effective combined strategy reduces the cumulative incidence by 73% across 20 years. Importantly, early implementation of environmental controls was significantly more effective than delayed action in preventing irreversible spore accumulation.

Conclusions/implications: Sustainable CDI control requires a coordinated One Health strategy that addresses human, animal, and environmental reservoirs simultaneously. The findings highlight that environmental infrastructure, such as advanced wastewater treatment, is a critical public health priority for disrupting long-term transmission cycles. This is relevant because it provides a quantitative methodology for translating the One Health paradigm into operational strategies for managing environmentally persistent antimicrobial-resistant pathogens.



409 – Biochemical and Immunological Signature of tertiary care center: Implication for One Health

Dr. Shivam TIWARI (1), Ajay YADAV (2), Ashish ASHISH (3)

1: Department of Biochemistry, All India Institute of Medical Sciences, India; 2: Department of Gastrology,Institute of Medical Sciences,Banaras Hindu University India; 3: Department of Anatomy Institute of Medical sciences, Banaras Hindu University

Background: The All India Institute of Medical Sciences (AIIMS) Guwahati, established in 2021, serves as a premier tertiary care institution in North East India—a recognized hotspot for zoonotic disease transmission and emerging infectious threats. The Department of Biochemistry has developed comprehensive infrastructure spanning clinical chemistry, molecular biology, immunology, and proteomics, positioning it as a potential hub for One Health integration. However, the biochemical and immunological signature of the patient population served, and its implications for cross-sectoral health surveillance at the human-animal-environment interface, remain uncharacterized. This study aimed to establish the baseline biochemical and immunological profile of patients presenting to AIIMS Guwahati, identify region-specific biomarker patterns indicative of zoonotic disease burden, and evaluate the feasibility of leveraging this institutional laboratory capacity for One Health biosurveillance.

Methods: A cross-sectional study was conducted at AIIMS Guwahati Department of Biochemistry between January 2024 and May 2025. The study population comprised 2,850 patients presenting with undifferentiated febrile illness, suspected zoonotic infections, and healthy individuals undergoing routine screening. Biochemical parameters were analyzed using automated clinical chemistry analyzers. Immunological profiling included cytokine quantification (IL-6, TNF-α, IFN-γ) and pathogen-specific antibody detection against six priority zoonotic pathogens. A parallel pilot component collected 450 animal samples and 200 environmental water samples from the same catchment areas.

Results: Complete profiling was achieved in 2,640 cases (92.6%). Hepatic analysis revealed elevated ALT in 34.2% of febrile patients, with distinct transaminitis in 18.6% of scrub typhus cases. Renal biomarkers demonstrated elevated creatinine in 22.4% of leptospirosis patients, correlating with severity. CRP >50 mg/L was observed in 68.4% of confirmed zoonotic infections. Immunological profiling identified seropositivity for at least one zoonotic pathogen in 40.2% of suspected cases: scrub typhus (18.2%), leptospirosis (12.4%), Japanese encephalitis (4.8%), brucellosis (3.2%), Q fever (1.8%), and hantavirus (0.6%). Cytokine analysis revealed significantly elevated IL-6 and TNF-α in acute zoonotic infections versus healthy controls (p0.001). A distinct signature of elevated IFN-γ characterized 64% of scrub typhus patients (sensitivity 82%, specificity 76%). Reference interval estimation demonstrated regional variations: ALT upper limit 45 U/L vs. 40 U/L nationally; CRP upper limit 8 mg/L vs. 5 mg/L. Animal sampling identified pathogen carriage in 27.6% of livestock: leptospirosis in cattle (15.2%), scrub typhus in rodents (8.4%), Japanese encephalitis in pigs (4.2%). Environmental sampling revealed Leptospira contamination in 9.0% of sites. Spatial analysis identified six clusters where human, animal, and environmental positivity overlapped within 5-kilometer radii. Comparative analysis revealed shared antibody profiles in 42% of concordant clusters, supporting cross-species transmission.

Conclusions: This study establishes the first comprehensive biochemical and immunological signature of patients at AIIMS Guwahati, revealing region-specific biomarker patterns with significant One Health implications. Distinct hepatic/renal profiles enable improved diagnostics for specific zoonotic pathogens. A cytokine-based signature differentiates scrub typhus from other febrile illnesses.

416 – Antimicrobial resistance (AMR) and sustainable development goals (SDGs): An integrated approach in livestock systems in Northeast Brazil

Glenda Lídice Cortez Marinho SILVA, Thiago Vinicius Costa NASCIMENTO, Victor Fernando Santana LIMA, Paula Regina Barros de LIMA, José Eduardo Marque da SILVA, Maria Josineide Nascimento de ALMEIDA, Riany Claire Silva Dantas de ARAÚJO, Pedro Andrade CALDERARO, Adrianne Camily Menezes BOMFIM, Izaquiel dos Santos SIBALDO, Jean Alves de ARAUJO, Gileno Francisco da HORA JÚNIOR

Universidade Federal de Sergipe, Brazil

Context: Livestock production in semi-arid regions plays a key role in food security and the socio-economic development of populations. However, diseases such as bovine mastitis and enzootic pneumonia in pigs are often associated with the use of antimicrobials, contributing to antimicrobial resistance (AMR) and posing risks to public health. This study aimed to assess how the Sustainable Development Goals (SDGs), associated with two independent studies in the field of animal health, act as an integrative framework for promoting sustainability, health, and the prevention of antimicrobial resistance in the semiarid region of the state of Sergipe, Northeast Brazil. **Methods:** Two independent

studies related to enzootic swine pneumonia and bovine mastitis were analysed. The dimensions of sustainability were assessed using the Sepúlveda Biogram (2008), with an emphasis on social indicators related to sanitary conditions, technical training, and territorial impact. Empirical alignment with the SDGs and contribution to AMR mitigation were assessed using the SDG Mapping Framework (Körfgen et al., 2018). Epidemiological data, health management practices, and diagnostic protocols were considered as indicators of antimicrobial use and disease control. **Results:** The study on bovine mastitis identified risk factors related to hygiene practices, animal management, and therapeutic protocols. Farms that adopted microbiological diagnosis and targeted treatment showed greater rationality in the use of antimicrobials, while standardised antibiotic treatments indicated a greater potential for antimicrobial resistance selection. The study on enzootic swine pneumonia provided epidemiological evidence reinforcing the importance of epidemiological surveillance and early detection of the disease, reducing the need for indiscriminate use of antimicrobials. According to the Sepúlveda Biogram, the research showed positive performance in the social dimension of sustainability, evidenced by improved herd health conditions, strengthened health awareness, and promotion of technical training. The analysis by the SDG Mapping Framework demonstrated direct contributions to SDG 3 (Good Health and Well-being) and SDG 12 (Responsible Consumption and Production), as well as indirect contributions to SDG 2 (Zero Hunger and Sustainable Agriculture), SDG 4 (Quality Education), SDG 8 (Decent Work and Economic Growth), and SDG 9 (Industry, Innovation and Infrastructure). **Conclusions:** The integration of the SDGs as a guiding framework for animal health research allows for a systemic approach to the prevention of AMR in livestock systems in the Semiarid region. The combined use of sustainability assessment and SDG mapping demonstrated that research effectively contributes to the rational use of antimicrobials and the implementation of One Health principles in Northeast Brazil.

420 – Baseline field evidence establishing the ectoparasite layer at a human–wildlife interface, explicitly intended to guide future One Health surveillance

Syamsuar MANYULLEI, Anwar MALLONGI, Erniwati IBRAHIM, Apik Indarty MOEJIONO, Erwan ARIFIN
Hasanuddin University, Indonesia

Background

Human–wildlife interfaces represent critical settings for the emergence of zoonotic diseases, where interactions among wildlife hosts, associated arthropods, and human activities may facilitate pathogen circulation. Bats are increasingly recognized as important reservoir hosts, yet the ectoparasite layer associated with bats remains under-documented in many tropical settings, despite its potential relevance in One Health surveillance frameworks. This study aimed to generate baseline field evidence on the occurrence and burden of bat ectoparasites in an interface-relevant setting in Indonesia, as an initial step to inform future integrated One Health surveillance. The study was exploratory in nature and did not test causal hypotheses, but rather addressed the problem of limited empirical baseline data on bat ectoparasite infestation in rural human–wildlife interface contexts.

Methods

A cross-sectional exploratory field survey was conducted in selected locations in Soppeng Regency, South Sulawesi, Indonesia. A total of ten bats (n = 10) were captured using active hand-net techniques at roosting or low-flight sites. Each bat underwent systematic external examination and combing of fur and wing membranes to collect ectoparasites. Specimens were preserved in 70% ethanol and examined using stereomicroscopy for morphological characterization. Ectoparasite identification was conducted conservatively based on diagnostic morphological features consistent with bat flies (family Nycteribiidae), and reported as *Eucampsipoda cf. sundaica*. Primary outcomes included ectoparasite presence/absence per bat and ectoparasite counts per individual. Data were analyzed descriptively to summarize infestation prevalence and burden, consistent with baseline surveillance objectives.

Results

Ectoparasites were detected in all examined bats, yielding an infestation prevalence of 100% (10/10). A total of 34 ectoparasites were collected, with individual burdens ranging from 2 to 6 ectoparasites per bat (mean 3.4). Ectoparasites were consistently observed on fur and wing membranes, indicating close host–parasite association. Morphological examination supported assignment to bat-associated flies

(Nycteribiidae), suggesting a stable and obligate ectoparasite presence within the sampled bat population. No statistical testing, diversity indices, or pathogen screening were conducted, in accordance with the exploratory baseline design.

Conclusions

This study provides baseline field evidence demonstrating a consistently high ectoparasite burden among bats at a human–wildlife interface in Soppeng Regency. While limited by small sample size and descriptive scope, the findings establish the presence and intensity of the ectoparasite layer as a biologically plausible component of One Health zoonotic risk pathways. These results justify expanded sampling, seasonal comparisons, and targeted pathogen screening of bat ectoparasites in future One Health surveillance efforts.

---

429 – Risk Assessment and Risk-Based Mitigation of Transboundary Rabies in Nan Province, Thailand: A Multi-Sectoral One Health Approach

Anyarat THIPTARA (1), Soawapak HINJOY (2), Nantaporn WANDEE (3), Wannawat DANGKAPAO (4), Charung MUANGCHANA (5), Serge MORAND (6,7,8)

1: Veterinary Research and Development Center (Upper Southern Region), Department of Livestock Development, Nakhon Si Thammarat, Thailand; 2: Department of Disease Control, Nonthaburi, Thailand; 3: National Institute of Animal Health, Department of Livestock Development, Bangkok, Thailand; 4: Division of Communicable Diseases, Department of Disease Control, Nonthaburi, Thailand; 5: Department of Disease Control Foundation, Nonthaburi, Thailand; 6: International Research Laboratory HealthDEEP CNRS; 7: Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand,; 8: Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Background: Under the PREZODE-ASAMCO framework, stray dogs and rabies transmission were identified as priority risks in Nan Province due to high likelihood and significant cross-sectoral impacts. Despite Nan Province maintaining human rabies-free status for three decades, persistent animal cases in districts bordering Lao PDR—Chaloem Phra Kiat—indicate active transboundary circulation. A critical knowledge gap remains regarding definitive sources and mechanisms of these outbreaks. While cross-border movement of infected dogs is suspected, it remains unconfirmed through formal evidence. This study conducted the first provincial cross-border Joint Risk Assessment (JRA) of rabies using a multi-sectoral One Health approach, engaging stakeholders from policy leaders to community representatives to develop targeted mitigation strategies and safeguard public health in high-risk border corridors.

Methods: A systematic risk analysis followed the World Organization for Animal Health (WOAH) framework. The assessment was performed by a multi-sectoral panel from animal, human, and environmental health sectors. The methodology combined technical analysis with participatory One Health dialogue to co-design solutions across four stages: 1) Hazard identification; 2) Entry assessment using scenario trees to analyze biological pathways from transboundary sources; 3) Exposure assessment to estimate contact likelihood between infected animals and susceptible populations; and 4) Consequence assessment using consensus-based criteria across human, animal, and socio-economic dimensions. Uncertainty was recorded for each node to account for data gaps. Finally, risk estimation integrated likelihood and consequences via a standardized matrix to prioritize mitigation efforts.

Results: Hazard identification confirmed transboundary stray dogs as the primary threat, with wildlife as a minor source. Entry assessment identified four critical pathways: official checkpoints, road-based routes, natural forest channels, and human-mediated animal movement. Exposure assessment pinpointed humans in border areas as the primary high-risk group, with villages and waste disposal sites identified as critical convergence points. Road-based routes and forest channels were marked as high-likelihood pathways due to absent screening protocols. Regarding consequences, 67% of human health and 40% of animal health impacts were classified as severe, driven by 100% clinical mortality and heavy operational burdens. Integration revealed 75% of evaluated pathways carry high-risk levels. The participatory process enabled stakeholders to identify underlying drivers, including weak dog registration, informal movement, and limited surveillance coordination.

Conclusion: To mitigate these risks, the study recommends a One Health approach focusing on enhanced transboundary surveillance and joint forest patrols utilizing the "Detect-Report-Act" protocol. Priority must be given to mandatory dog registration, identification collars, and increasing vaccination coverage through mobile clinics. Strengthening multi-sectoral coordination, ensuring pre-exposure prophylaxis

(PrEP) for high-risk personnel, and conducting joint after-action reviews (JAAR) are essential to maintain Nan Province's rabies-free status. This methodology provides an innovative and scalable model for addressing complex zoonotic risks through evidence-based, collaborative decision-making focused on high-risk transboundary pathways.

Table 1. Risk Estimation of Transboundary Rabies Pathways

Pathway Description	Likelihood	Consequence	Risk Level
Natural forest channels to villages	High	Severe	**High**
Road-based routes to border markets	High	Severe	**High**
Illegal animal transport pathways	High	Severe	**High**
Official checkpoints with screening	Low	Severe	**Moderate**

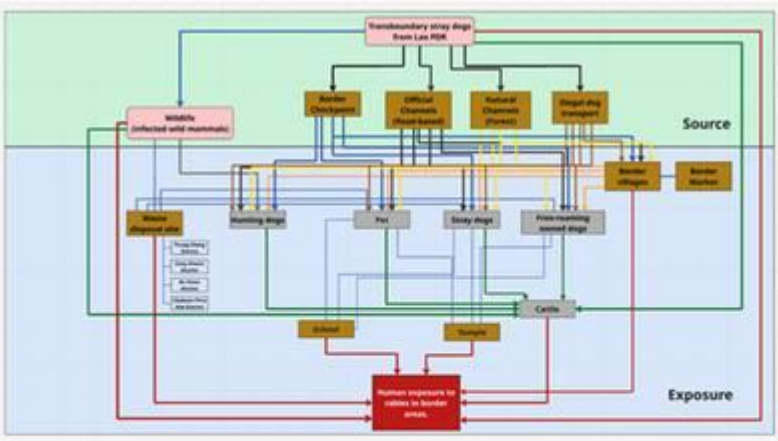


Figure 1: Multi-sectoral One Health framework for rabies risk assessment in Nan Province. This figure depicts the integrated One Health approach used in the study, highlighting the collaborative process between animal, human, and environmental health sectors to identify, assess, and prioritize transboundary rabies risks through the WOAH risk analysis framework.

Figure 2: Multi-sectoral One Health stakeholder engagement in the rabies risk assessment workshop. Representatives from human, animal, and environmental health sectors collaborating during a structured risk assessment workshop. The session utilized participatory methods and expert brainstorming to identify transboundary rabies pathways and establish consensus-based criteria for consequence assessment.

448 – Earth observation as a scalable public health sensor for climate–environment–ecosystem risks: fusing Copernicus EO with in-situ health and population data

Sylvie TEYSSEYRE
Aerospace Valley, France

Background

Climate change is increasing health risks linked to heat extremes, floods, wildfires smoke, changing vector habitats, water contamination, and coastal ecosystem disturbances. Public health actors often lack timely, spatially explicit, and comparable intelligence to anticipate impacts, target prevention/response, and coordinate across jurisdictions. Earth Observation (EO) provides continuous spatio-temporal monitoring of environmental determinants (e.g., land surface temperature, soil moisture, vegetation stress, flood extent, air composition) that can be translated into actionable health risk intelligence when combined with in-situ data.

Methods

We propose a system fuses open Copernicus products (temperature, wetness, surface water, vegetation, air quality, coastal conditions) with in-situ and administrative data streams (human and animal health activities, entomology data, water quality, population structure). This system produces weekly–monthly indicators: exposure (urban heat islands, smoke/pollutant proxies, flood extent and standing-water likelihood, drought/water stress) directly convertible in actionable information One health. We can know where is the risk, who could be impacted and when it will appear. Data can be disseminated via dashboards/maps and aligned with operational triggers (e.g., heatwave staffing reinforcement, flood-response routing and facility protection, targeted risk communication, and enhanced vector surveillance). We will demonstrate an example of application to predict Aedes mosquito population densities on a spatial scale suited to the organization of surveillance and control actions based on the fusions of local entomological, meteorological and remote sensing data at high and very high spatial resolution.

Results

EO-in-situ fusion enables replicable outputs that strengthen climate-resilient public health operations:

Conclusions Earth observation acts as a "health sensor" for the climate-environment-ecosystem nexus when translated into actionable indicators and integrated into practitioners' work. It proves useful in numerous areas, including vector-borne diseases, waterborne diseases, zoonoses, respiratory illnesses, certain allergies, malnutrition, some mental health conditions (stress, depression), and the effects of heat waves on our systems. Key success factors include co-design with end users, transparent methodologies and quality assurance, communication of uncertainties, and governance frameworks that guarantee ethical use and interoperability with health information systems (including the constantly evolving European data-sharing frameworks).

450 – A novel use for the evaluation of the BIOFIRE®FILMARRAY® Antimicrobial Resistance Research Use Only Panel on wastewater sewer shed in a hospital setting

Cody FIRMAGE (1), Franck CHATIGNY (2), **Claude MABILAT** (2)
1: bioMerieux, United States of America; 2: bioMerieux, France

Antimicrobial resistant (AMR) bacteria are a rising concern in health care and are associated with an up to five-fold increase in mortality for infected patients. Current identification methods require antibiotic susceptibility testing in a laboratory setting. Sample collections can often be invasive and require directed action. Wastewater-based epidemiology (WBE) is the practice of estimating infection rates in a large population by testing wastewater for the presence of infectious disease biomarkers commonly shed in feces.

To assess performance of the BIOFIRE®FILMARRAY® RT-qPCR system in wastewater a unique research use only AMR panel previously developed consisting of 28 assays for 23 genes and 5 species-IDs. This panel can detect genetic markers associated with AMR including carbapenems, cephalosporins, fluoroquinolones, and aminoglycosides that may be present in multi-drug-resistant Gram-negative

bacteria *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter cloacae*.

Wastewater samples were obtianed bi-monthly from a sewer shed access point connected to the Nielson Rehabilitation Hospital at the University of Utah. Samples were collected from December 2024 – December 2025. Analysis was performed using crossing point (Cp) data obtained through the FIREWORKS™ software to trend both frequency and quantity of detections.

Results showed a high consitancy of detection for 18/23 of the target assays. However, little or no detections were observed for NDM, armA, aac(6')-Ib-cr, OXA 23, and OXA 24/40. Many assays showed simular Cp trending with respective organisms, such as CTX-M with *E. coli.* This study demonstrates a novel approach to wastewater epidemiology and non-invasive surveillance of antimocrobial gene markers.

We would like to acknowledge our study partners at the Nielson Rehabilitation Hospital and the University of Utah

458 – 'Disease takes away our right to be joyful, to live': Residents' perceptions of factors affecting health in disadvantaged urban communities in Salvador, Brazil

Anna DURRANCE-BAGALE (1,2), Fabiana Almerinda Gonçalves PALMA (3,4), Yeimi Alexandra Alzate LOPEZ (3), Cainã QUEIROZ (3), Mirella RIBEIRO (3), Diogo César de C. SANTIAGO (5), Ana Maria BARRETO (3), Ariane Sousa DO CARMO (6), Antonia DOS REIS (3), Gislane de Jesus DO CARMO (3), Andrea Maria LIMA (3), Renata Santos ALMEIDA (3), Lucineide OLIVA (3), Adedayo Michael AWONIYI (3), Fabio Neves SOUZA (3,4), Max T. EYRE (1), Cleber CREMONESE (3), Federico COSTA (3,4)

1: London School of Hygiene & Tropical Medicine, Department of Global Health & Development, London, WC1H 9SH, UK; 2: Nature.Health.Global, Tallman, NY 10982, USA; 3: Instituto de Saúde Coletiva, Universidade Federal da Bahia, Salvador, BA, Brazil; 4: Instituto Gonçalo Moniz, Fundação Oswaldo Cruz, Salvador, BA, Brazil; 5: Departamento de Medicina Preventiva e Social, Faculdade de Medicina da Bahia, Universidade Federal da Bahia, Salvador, BA, Brazil; 6: Universidade Salvador, Salvador, BA, Brazil

Background: We present preliminary findings from focus groups conducted as part of the community engagement component of a broader cluster non-randomised controlled trial evaluating a simplified sewerage intervention in two disadvantaged urban communities in Salvador, Brazil. While the larger study examined reductions in exposure to water-borne pathogens, this qualitative component focused on understanding how residents themselves perceive health, disease, and the factors shaping ill-health in their everyday lives. Guided within a context of engagement activities based on popular health education, the study aimed to explore community-based interpretations of health within interconnected social, environmental, and structural contexts, contributing to a One Health perspective grounded in lived experience.

Methods: Thirty adult residents (15 women and 15 men) from two disadvantaged urban communities participated in gender-stratified focus groups embedded within community engagement activities. Discussions explored perceptions of health and disease, environmental conditions, sanitation, and the relationships between these dimensions. All sessions were audio-recorded, transcribed verbatim, and analysed using NVivo v15. Reflexive thematic analysis combining deductive and inductive approaches was employed, allowing both theoretically informed categories and community-generated meanings to emerge.

Results Preliminary deductive analysis identified themes related to definitions of health, disease, and sanitation; perceived relationships between health and the environment; and changes in local living conditions over time. Inductive analysis revealed additional themes around health education and awareness, responsibility for health-related behaviours, community cohesion, and perceived causes of illness. Together, these themes informed a community-derived explanatory framework of ill-health. Participants described ill-health as shaped by interconnected spiritual (faith and reliance on God), psychological (stress, lack of respect), biological (viruses and bacteria), cultural (erosion of community bonds), socio-economic (poverty and food insecurity), environmental (poor sanitation, waste accumulation, presence of animals, noise), and structural factors (limited access to healthcare, unemployment, lack of public services). These dimensions were understood as overlapping and mutually

reinforcing rather than as isolated causes. No substantial differences in perceptions were observed between men and women or between the two communities.

Conclusions: Participants emphasised that health is central to a meaningful life, stating that "*disease takes away our right to be joyful, to live*." Their perspectives reflect an expanded understanding of health as physical, mental, social, and spiritual wellbeing, closely aligned with One Health principles that foreground human–environment relationships and structural determinants. Clean and hygienic environments, dignified work, social cohesion, self-worth, and access to healthcare were identified as essential to health preservation. These findings highlight the importance of community-engaged qualitative approaches and popular education in informing One Health research and interventions that are socially grounded, context-sensitive, and attentive to health as a fundamental human right.

464 – Differential survival of Campylobacter jejuni on broiler meat strips under conventional versus high oxygen modified atmosphere packaging

Rauni KIVISTÖ (1), Donna GRANROTH (1), Anniina JAAKKONEN (2), Johanna BJÖRKROTH (1)
1: University of Helsinki, Finland; 2: Finnish Food Authority, Finland

Background:*Campylobacter jejuni* is the leading cause of bacterial gastroenteritis worldwide and raw or undercooked chicken is a major source of human infections. Since campylobacters are highly sensitive to high oxygen concentrations, the purpose of this study was to compare the survival of different *C. jejuni* strains on broiler chicken meat strips under conventional (30 % CO_2 + 70 % N_2) or high oxygen (80 % O_2, 20 % CO_2) modified atmosphere packaging (MAP). Our hypothesis was that *C. jejuni* would survive better under conventional compared to high oxygen MAP, and we expected to find differential survival between *C. jejuni* strains.

Methods: Fresh broiler chicken meat strips were divided into 25 g aliquots and stored frozen at -70°C. The meat was artificially contaminated, aiming at 103–104 CFU/g, with one of three different *C. jejuni* strains: NCTC 11168 (A), FIAR-618 (B) or FIAR-645 (C), representing a well-known reference strain (A) and two clones (B and C) commonly circulating among poultry and human infections in Finland. The strains were grown over-night in Mueller-Hinton broth at 41.5°C under microaerobic conditions. Separate meat packages were defrosted for each combination of *C. jejuni* strain (A, B or C), gas composition (conventional or high oxygen MAP) and time point (day 0, 1, 2, 5 or 7) studied. The gas composition of each package was analyzed prior to *C. jejuni* enumeration on mCCDA using standard methods. The 1:10 dilutions of the meat strips in peptone-saline were used to measure the pH of the homogenate. The experiment was repeated three times.

Results: We found better survival of *C. jejuni* under conventional compared to high oxygen MAP (p0.002) confirming our hypothesis. Under conventional MAP no significant *C. jejuni* reduction was observed in 7 days, compared to an average D-value of 7 days for the high oxygen MAP, corresponding to a 1-log reduction in 7 days. Contrary to our prior expectations, no significant differences were observed between the survival of different *C. jejuni* strains. Instead, their survival was comparable, however the growth of strain B was inferior in Mueller-Hinton broth under static culture compared to strains A and C. The pH of the meat strip homogenates reduced only slightly (approximately 0.1 pH unit) in 7 days, and no difference was observed between the two different MAP or between different strains suggesting only limited spoiling of the meat during storage.

Conclusions: High oxygen MAP led to reduced survival of *C. jejuni* in broiler meat strips compared to conventional MAP suggesting improved consumer safety for high oxygen MAP products. However, further studies are needed to evaluate the effects of the different packaging atmospheres on the sensory quality and shelf-life of broiler meat products in more detail.

471 – A participatory approach to the design and implementation of a One Health cohort study in Côte d'Ivoire

Filipe DIAS (1), Oby WAYORO (1,2), Léonce KOUADIO (1,3), Ahou Véronique KOFFI (3), Dominic BLÄSING (1), Markus ULRICH (1), Valère KOUAKOU (4), Arsène MOSSOUN (5), Lydiah KISOO (6), Yaw AWUKU-LARBI (6), Hadassa Abi

YOBOU (3), Carolina KLETT-TAMMEN (6), Franziska STOEK (1), Kathrin NOWAK (1), Berit LANGE (6), Gilbert FOKOU (3), Fabian LEENDERTZ (1), Fee ZIMMERMANN (1)

1: Helmholtz Institute for One Health, Greifswald, Germany; 2: Centre Hospitalier Universitaire de Bouaké, Bouaké, Côte d'Ivoire; 3: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, Côte d'Ivoire; 4: Université Jean Lorougnon Guede, Daloa, Côte d'Ivoire; 5: Université Alassane Ouattara, Bouaké, Côte d'Ivoire; 6: Helmholtz Center for Infection Research, Braunschweig, Germany

Sub-Saharan Africa remains highly affected by emerging and re-emerging infectious diseases, particularly in regions characterized by high biodiversity, rapid ecological change and intense human-animal-environment interactions. One Health cohort studies can generate critical long-term data to improve early detection and management of infectious diseases. However, their success depends on meaningful engagement of local stakeholders. Local communities are often undervalued in study design despite their contextual knowledge and central role in disease dynamics. Here we present a participatory approach to the design and early implementation of a One Health cohort study in Côte d'Ivoire.

We implemented a participatory and transdisciplinary approach involving national stakeholders, local authorities and community members. The process was conducted in two phases: (i) project presentation and stakeholder engagement, and (ii) participatory co-design of the study protocol. In November and December 2024, data were collected through stakeholder workshops (national and local levels), focus group discussions, meetings with traditional leadership, and analysis of demographic and health system data. Engagement activities were conducted in nine villages, ensuring inclusiveness across gender, age groups and community sub-groups. As a subsequent operational step preceding the cohort implementation, a household identification and mapping was conducted in November 2025. Using a randomized, proportional sampling strategy informed by satellite imagery and official health data, 443 households were invited to participate in the cohort study across the nine villages. Household heads were informed about the project using infographics, completed a short questionnaire on household composition and animal ownership, and households were geolocated using ODK-based data collection tools.

A total of approximately 314 persons were engaged in the participatory design of the study. The participatory process generated detailed insights into community priorities, concerns and expectations, as well as social and cultural norms, gaps in knowledge, rumors and misinformation relevant to health and disease surveillance. In the cohort preparation phase, 443 households, randomly distributed across nine villages proportionally to village size, were invited to participate in the cohort study. Baseline data collected in those households included household composition by age and sex and animal ownership by species, providing a baseline characterization of human and animal populations. These activities presented the foundation for the recruitment of approximately 1500 cohort participants.

Early and inclusive engagement of communities and authorities at different levels, enabled the establishment of a context-sensitive One Health cohort protocol and facilitated the transition from conceptual design to practical implementation. This participatory approach strengthens trust and ownership while enhancing the scientific robustness and sustainability of the study. The resulting One Health cohort will support early detection of infectious diseases, and improved understanding of disease determinants at the human–animal–environment interface, offering transferable lessons for similar settings globally.

476 – Closing the Biosurveillance Gap: Portable Sequence Typing for Endemic Zoonotic Pathogens

Ashton CREASY-MARRAZZO (1,2), Melissa L. ADAMS (1,3), Nora CLEARY (4,5,6), Alejandro MENA SANCHEZ (4,5,6), Boldbaatar BAZARTSEREN (7), Julianne MEISNER (8,9,10), Michael VON FRICKEN (4,5,6), Jeffrey KOEHLER (1)

1: Diagnostic Systems Division, United States Army Medical Research Institute of Infectious Diseases, Fort Detrick, USA; 2: Oak Ridge Institute for Science and Education, US Army Medical Research Institute of Infectious Diseases, Diagnostic Systems Division, Frederick, MD, USA; 3: Chenega Professional and Technical Service, Chesapeake, VA, USA; 4: Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; 5: Department of Environmental and Global Health, College of Public Health and Health Professions, University of Florida, Gainesville, FL, USA; 6: One Health Center for Excellence, University of Florida, Gainesville, FL, USA; 7: School of Veterinary Medicine, Mongolia University of Life Sciences, Ulaanbaatar, Mongolia; 8: Department of Global Health, University of Washington, Seattle, WA, USA; 9: Department of Epidemiology, University of Washington, Seattle, WA, USA; 10: Center for One Health Research, University of Washington, Seattle, WA, USA

Introduction: *Brucella spp.* and *Coxiella burnetii* are high-consequence zoonotic pathogens with a global reach. To enhance biosurveillance and outbreak response, there is a need for a simple, field-deployable sequence typing protocol for use in remote, high-prevalence regions. Our objective was to develop and validate a robust sequence typing assay designed for field deployment in austere environments, enabling rapid data generation for epidemiological tracking and network analysis.

Methods: We selected 21 established oligonucleotide sequences for *Brucella spp.* and 9 for *C. burnetii* from the pubMLST database, targeting conserved genes. Sequence alignments were verified in Geneious Prime v2025.2. The assay was developed with previously extracted reference strain genomic DNA from *B. abortus*, *B. ovis*, *B. suis*, *B. melitensis*, and C. *burnetii*. Targets were first validated individually in triplicate using singleplex PCR with Phusion polymerase. The PCR protocol involved a 2-min denaturation at 98°C, followed by 38 cycles of 98°C for 10s, 60°C for 10s, and 72°C for 1 min. Positive amplification was confirmed in triplicate via gel electrophoresis (3% gel; 50V for 1h, 75V for 2h) using the self-contained miniPCR® Gelato® system. Validated oligonucleotides were then organized into three multiplex panels for *Brucellaspp.* and two for *C. burnetii.* Multiplex panels were assessed *B. ovis* and *C. burnetii* gDNA.

Results: Our analysis identified an optimal set of twelve gene targets for *Brucellaspp.* and eight for *Coxiellaburnetii* that balanced ease-of-use with the generation of high-value surveillance data (Table 1). Furthermore, we determined that a 10-fold dilution of the amplification product significantly improved band clarity and resolution during gel electrophoresis for both *Brucella spp.* (Fig. 1) and *Coxiellaburnetii* (Fig. 2) amplicons.

Conclusions: In conclusion, we developed a simplified, multiplexed sequence typing assay for *Brucella spp*. and *C. burnetii*. This assay is optimized for clarity and designed around a field-deployable system, providing a valuable new tool for enabling rapid biosurveillance. Next steps will be generating preliminary data from human and livestock study participants in rural Mongolia and targeted sequencing for precise epidemiological data.

Table 1: MLST multiplex panel targets and amplicon lengths for *Brucella spp.* and *Coxiella burnetii*

organism	panel	target	length (bp)
Brucella spp.			
	1	*cobQ*	459
		gyrB	506
		putA	561
	2	*gap*	624
		calA	486
		omp25	524
		cdsB	568
	3	*mutL*	610
		int-hyp	495
		dnaK	507
		trpE	534
Coxiella burnetii			
	1	*aroA*	601
		cox2	396
		cox37	462
		cox18	556
		cox61	611
		cox51	674
	2	*cox3*	395
		cox58	477
		cox57	606
		cox20	631

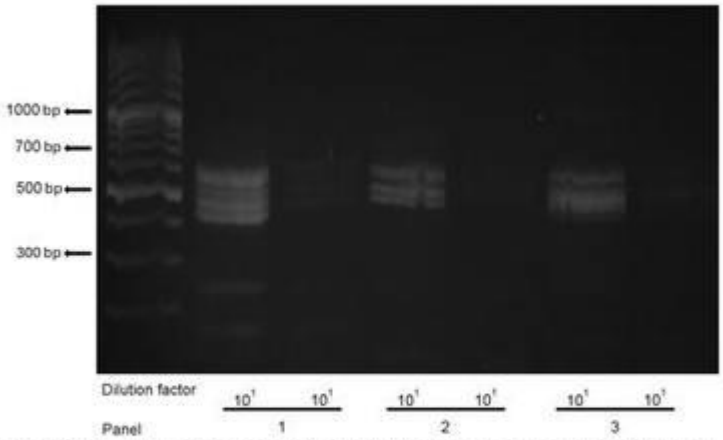


Fig 1. High resolution separation of *Brucella* MLST amplicons using miniPCR® Gelato® system. Multiplex PCR was performed targeting *Brucella ovis* gDNA (1 ng). Amplification products from each multiplex panel were diluted 1:10 and 1:100. A total of 10 µl was loaded onto a 3% agarose gel for electrophoresis.

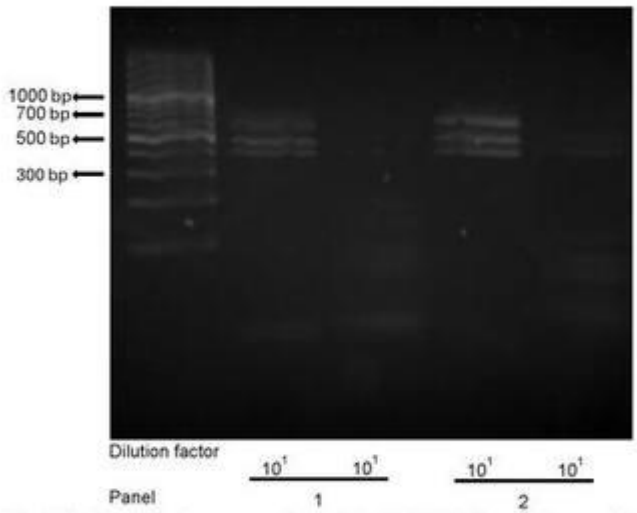


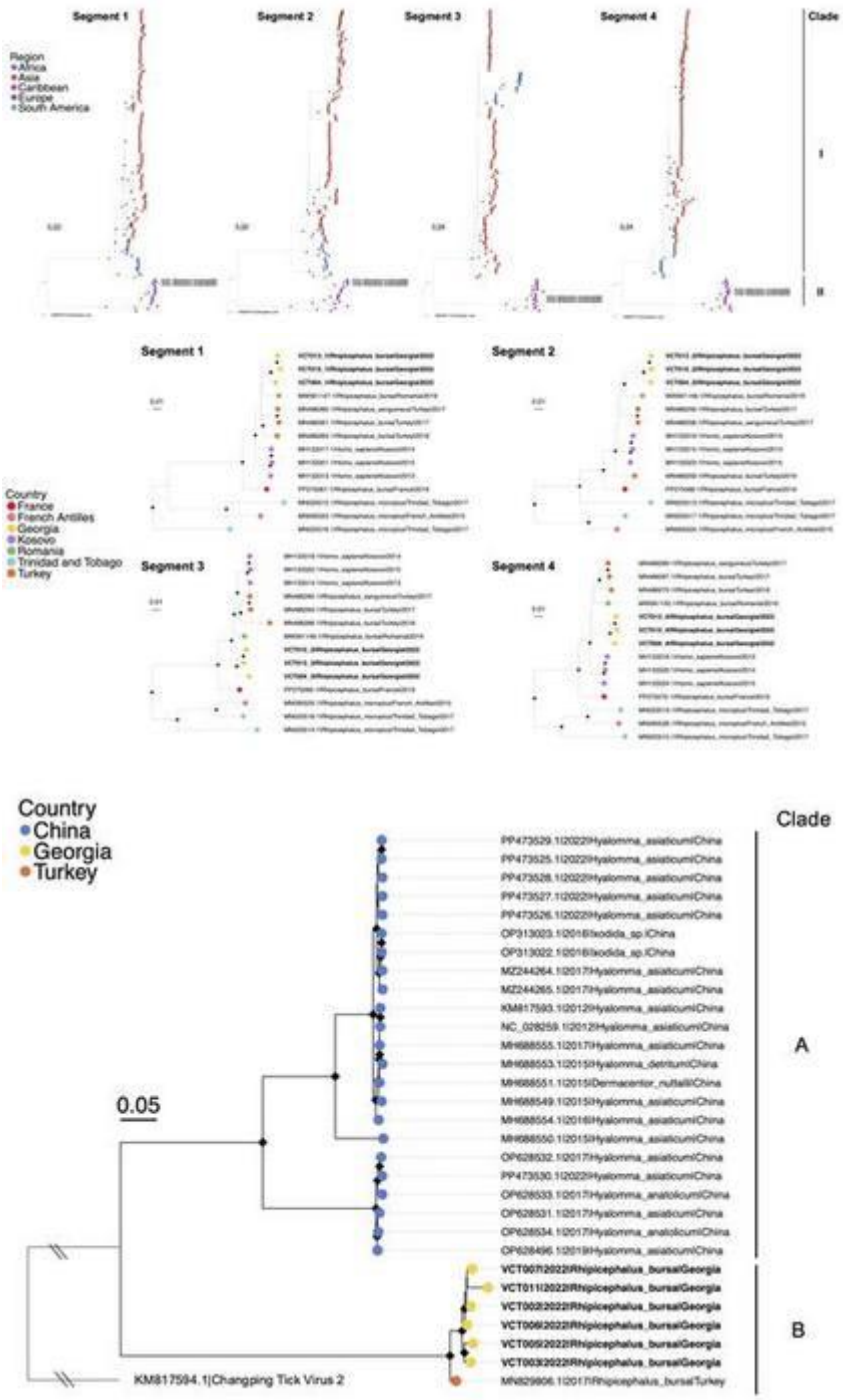
Fig 2. High resolution separation of *Coxiella* MLST amplicons using miniPCR® Gelato® system. Multiplex PCR was performed targeting *Coxiella burnetii* gDNA (1 ng). Amplification products from each multiplex panel were diluted 1:10 and 1:100. A total of 10 µl was loaded onto a 3% agarose gel for electrophoresis.

482 – JMTV detection for the first time in Rhipicephalus bursa ticks collected from the Country of Georgia

Julia PAOLI (1), Adam KOTORASHVILI (2), Samantha ANDRITSCH (1), Carla MAVIAN (1), Nato KOTARIA (2), Gocha GOLUBIANI (2), Giorgi KIRKITADZE (2), Tamar CHUNASHVILI (2), Anano SHUBASHISHVILI (2), Nicholas DI PAOLA (3), Jeffery KUGELMAN (3), Christine HULSEBERG (2), Brian WALKER (2), Thomas MUSICH (2), Drew REINBOLD-WASSON (2), David DENLINGER (2), **Michael VON FRICKEN** (1)

1: Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; 2: Walter Reed Army Institute of Research (WRAIR) Europe – Middle East (WRAIR-EME), Tbilisi, Georgia; 3: US Army Medical Research Institute of Infectious Diseases (USAMRIID), Fort Detrick, MD

Ticks harbor several emerging viruses, several of which are pathogenic to humans. The country of Georgia (hereafter “Georgia”), located in the Black Sea region at the crossroads of Europe and Asia, is a geographically important transit hub with ecological conditions suitable for multiple tick species. To characterize the tick-virome in Georgia, we conducted environmental sampling of ticks in seven provinces from 2021 to 2022. Ticks were morphologically identified, pooled, and subjected to Sequence-Independent, Single-Primer Amplification (SISPA) followed by Illumina sequencing. Sampling efforts yielded 1,396 ticks from nine species across five genera. We report the first detection of Jingmen Tick Virus (JMTV) in *Rhipicephalus bursa* in Georgia, identified in three tick superpools collected in Samtskhe-Javakheti. We recovered three partial JMTV genomes which phylogenetic analysis revealed to cluster with other JMTV sequences of European origin. In addition, partial Bole Tick Virus 3 (BTV3) genomes were detected in six *R. bursa* superpools also collected in Samtskhe-Javakheti. The BTV3 study sequences clustered tightly with a BTV3 sequence from *R. bursa* in Turkey. These findings expand the known geographic distribution of JMTV and BTV3 and underscore the need for continued tick-borne virus surveillance in Georgia. The detection of JMTV in Samtskhe-Javakheti is public health relevant, as this virus has been associated with human disease which highlights the importance of integrated vector and syndromic surveillance in the region.



488 – Strengthening the One Health Approach in Morocco: Outcomes of a National Multisectoral Consultation Workshop

Dahbi ZAHRA (1), Hammou JAOUAD (1), El Bouchtaoui HAYAT (2), Belbachir KHADIJA (1), Youbi MOHAMMED (1), Aouane ELMAHJOUB (3)

1: Ministry of Health, Directorate of Epidemiology and Diseases control, Morocco; 2: National Office for Food Safety; 3: Ibn Tofail University, Morocco

Background:

Public health risks linked to the human–animal–environment interface are increasing, highlighting the need to operationalize the One Health (OH) approach. In Morocco, despite the existence of intersectoral

coordination mechanisms for some public health issues, the Joint External Evaluation of IHR capacities (JEE) conducted in 2016 identified several gaps in integrating actions across sectors, including the absence of formalized governance framework. A national workshop was organized in December 2024 to update the One Health roadmap, established during the National Bridging Workshop (NBW), and propose a governance body adapted to the national context.

Methods:

A four-day consultation workshop brought together representatives from the human health, animal health, and environmental sectors, as well as international technical partners. Workshop was structured around four strategic pillars considered essential for the operationalization of the One Health approach: (1) governance and multisectoral coordination, (2) integrated surveillance and laboratory systems, (3) joint response and outbreak investigation, and (4) risk communication and information sharing. Participants were divided into four working groups corresponding to these pillars. Each group conducted a structured SWOT (Strengths, Weaknesses, Opportunities, and Threats) analysis to assess the current situation, identify key challenges, and propose priority actions for strengthening multisectoral collaboration. Findings and recommendations from each group were subsequently presented, discussed, and refined during plenary sessions in order to reach consensus on priority for action.

Results:

The workshop highlighted several important achievements that provide a strong foundation for strengthening the One Health approach in Morocco. These include the existence of a national regulatory framework supporting disease control and food safety, progressive development of laboratory diagnostic capacities across sectors, and substantial experience in managing major health crises through coordinated national responses. Despite these advances, participants identified a number of structural and operational gaps. These include the absence of an institutionalized and structured One Health coordination mechanism, fragmented surveillance systems that limit systematic data sharing between sectors, insufficiently formalized procedures for joint outbreak investigation and response, and limited institutionalization of intersectoral risk communication. Based on these findings, several priority recommendations were formulated. These include the establishment of a National and Regional One Health Committees, the development of an integrated and digitalized multisectoral surveillance system, the formalization of a national laboratory network to facilitate data exchange and standardize diagnostic's methods , the operationalization of multisectoral rapid response teams, and the creation of an intersectoral risk communication committee.

Conclusion:

This national consultation workshop represents an important step toward the development and operationalization of a comprehensive One Health strategy in Morocco. By bringing together key stakeholders from multiple sectors, the workshop enabled a shared assessment of current capacities and challenges while fostering consensus on priority actions.

---

492 – One Health intervention for elimination of anthrax (animal to human disease transmission) in an endemic district of Odisha

Debdutta BHATTACHARYA, Hariram CHOUDHARY, Matrujyoti PATTNAIK, Rachita` PRADHAN, Tanveer REHMAN, Srikanta KANUNGO, Subrata K PALO, Sanghamitra PATI

ICMR-REGIONAL MEDICAL RESEARCH CENTRE, Bhubaneswar, India

IntroductionAnthrax is a rare but serious infectious disease of public health importance caused by the bacteria Bacillus anthracis. Anthrax cases have been documented in various states of India, including Odisha. In Odisha, Koraput district stands out with more than 300 reported human cases and over 10 confirmed deaths due to Anthrax infection in the past six years. The present study is a baseline and endline survey to assess the knowledge, attitude and practices with regards to the anthrax disease among the communities of indigenous population residing in the region pre and post of the tailored made One Health intervention for elimination of human Anthrax in this endemic district. Methodology:This is a repeated cross-sectional survey conducted both as a baseline survey in mid of 2020 among 2670 respondents and again as endline survey during end of 2022 among 2511 respondents using a structured 85 item questionnaire by multi-stage sampling method. Descriptive statistics were

reported and logistic regression was performed to estimate the relationship between the variables and knowledge of anthrax. One Health intervention package was developed with the help of various multistakeholders from the Koraput district which include establishing an active surveillance, developing a dedicated anthrax diagnostic facility in the state for the early diagnosis, sensitization and capacity-building training for all the stakeholders, behavioral Change Communication (BCC) and Information Education Communication (IEC) activities at the community and free livestock vaccination drive across the district with the help of district veterinary department and coordination or support from the other stakeholders for smooth execution of the vaccination drive.ResultOut of the total participants in the study, males were about 76.25% in baseline and 72.08% in endline and about half of the total respondents were illiterate. Majority of the respondents had reported agriculture as their main occupation during both surveys. More than 50% of the respondents had livestock in their houses and farming was the main purpose for keeping them in both surveys. Around 20.26% of respondents knew about anthrax in baseline which raised to 53.64% after One Health intervention. Almost 21.29% of livestock owners had vaccinated their animals against anthrax disease throughout baseline, which increased to 66.5% during the endline survey.ConclusionThis study highlights a significant surge in both knowledge and practices related to anthrax within the community after the implementation of intervention packages based on the One Health approach. The outcome of our study signified the importance of One Health interventions to address the health challenges related to zoonotic diseases in tribal communities. The data could be useful for local Governments to incorporate such an approach in their health policy to eliminate human anthrax.

497 – Understanding Mongolian herders' knowledge, attitudes, and practices about ticks, tick-borne diseases, insecticide use, and climate change

Nora CLEARY (1,2), Otgonbayar DAARIIMAA (3), Enkhbaatar LKHAGVADULAM (4), Riley WARD (1,2), Doniddemberel ALTANTOGTOKH (3,5), Gansukh GANBILEG (3), Alejandro MENA-SANCHEZ (1,2), Chimedtseren LKHAGVAJAV (6), Gotovdorj GANTSETSEG (7), Sandagsuren TSENDDULAM (4), Bazartseren BOLDBAATAR (5), Sarah MCKUNE (1), Sadie RYAN (2,8), Julianne MEISNER (9,10,11), Caroline WADDELL (1,2), Michael VON FRICKEN (1,2)

1: Department of Environmental and Global Health, University of Florida, Gainesville, FL, USA; 2: Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; 3: National Center for Zoonotic Diseases, Ulaanbaatar, Mongolia; 4: Center for Zoonotic Disease, Uvurkhangai, Mongolia; 5: Mongolian University of Life Sciences, Ulaanbaatar, Mongolia; 6: Center for Zoonotic Disease, Zavkhan, Mongolia; 7: Center for Zoonotic Disease, Khentii, Mongolia; 8: Department of Geography, University of Florida, Gainesville, FL, USA; 9: Department of Global Health, University of Washington, Seattle, WA, USA; 10: Department of Epidemiology, University of Washington, Seattle, WA, USA; 11: Center for One Health Research, Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA, USA

Background

Ticks and tick-borne diseases (TBDs) pose significant risks to human and livestock health in Mongolia. Livestock control strategies by the General Authority for Veterinary Services rely on insecticide use to reduce tick infestation. Meanwhile, these control measures are increasingly threatened by environmental changes that influence tick and host distributions and associated pathogen dynamics. However, limited data exists on how these ecological patterns are shifting and the impact on knowledge, attitudes, and practices of Mongolian pastoralists about tick control and TBD prevention.

Methods

In three Mongolian aimags (provinces), 372 surveys were conducted from March to June 2025. The survey instrument included five sections: demographics, knowledge, attitudes, practices, and climate for a total of 50 questions. Quantitative data was analyzed using chi-square tests or Fisher's exact tests to compare responses by aimag, age, and years as a herder. Multiple logistic regression was used to assess the associations between demographics, tick encounters, and TBD knowledge and attitudes towards pesticide effectiveness and pesticide use practices among pastoralists. Qualitative responses were analyzed using thematic analysis with two independent coders and a third coder who resolved discrepancies. Identified themes were subsequently developed into tree maps.

Results

After adjusting for age, sex, and years spent as a herder, knowledge and perception were significantly associated with the use of TBD prevention measures. Participants who had knowledge about TBD

prevention had a higher odds of taking measures against tick bites (OR: 7.81; 95% CI: 4.72, 19.72; p-value: 0.001). Those who perceived TBDs to be a critical issue were more likely to use preventative measures (OR: 3.96; 95% CI: 1.74, 12.26; p-value: 0.002). Additionally, those who knew about TBD prevention in livestock were more likely to regularly wash their animals with pesticide (OR: 3.64; 95% CI: 2.25, 11.98; p-value: 0.001).

Pastoralists reported limited knowledge and awareness regarding choosing a tick control method and challenges in keeping their livestock healthy. Most participants viewed animal protection measures as the most important way to prevent ticks including washing, spraying, and injections followed by a lack of knowledge. The majority used animal protection measures followed by vaccination. Pastoralists reported a wide range of observed climate changes during their lifetime including *dzud* (severe winter disaster), weather changes, environmental degradation, as well as associated animal impacts and economic loss.

Conclusion

Knowledge and perception about TBDs was significantly associated with the adoption of tick prevention practices by pastoralists. The most common prevention measures included washing and spraying livestock with insecticides. However, significant gaps in knowledge regarding TBDs were identified. This highlights the need for targeted education in Mongolia especially as many pastoralists have observed climate changes in their lifetime that will impact livestock health, tick distribution, pathogen dynamics, and ultimately TBDs.

---

503 – Quantifying antibiotic-resistant E. coli, Pseudomonas aeruginosa, and Enterococcus in wastewater effluent and receiving river waters in Northeast Tennessee

Walid ALALI, Phillip SCHEUERMAN

East Tennessee State University, United States of America

Background

Treated wastewater effluent can act as a continuous point source of antibiotic-resistant bacteria (ARB) to receiving waters. We quantified resistance patterns across fecal indicator and opportunistic “sentinel” organisms in effluent and adjacent river water to evaluate potential downstream impacts over repeated monthly sampling.

Methods

From March–November 2025, grab samples were collected from a wastewater treatment plant final effluent and two points at a river water (i.e., upstream [UW] and downstream [DW] of the effluent [EF] outfall) in Northeast Tennessee. Samples were membrane-filtered and cultured on selective media with and without antibiotics (cefotaxime, ceftazidime, imipenem, erythromycin, and vancomycin) to enumerate colony-forming units (CFU/100 mL). For each organism–antibiotic combination, antibiotic-selected colony counts were analyzed using negative binomial regression (log link) to compare sites while adjusting for month, with offsets for no-antibiotic counts and volume plated. Models yielded rate ratios (RRs) with 95% confidence intervals; analyses were conducted in Stata statistical software.

Results

Across sites, no-antibiotic mean counts were highest at DW for *E. coli* (120.4±124.8) and Enterococcus (107.95±142.8), whereas *P. aeruginosa* no-antibiotic mean counts were low overall (DW 6.98±13.3; EF 0.17±0.3; UW 2.53±4.8). Means of antibiotic-resistant counts were generally low for cefotaxime *E. coli*: DW 0.67±1.0; EF 0.13±0.3; UW 0.79±1.8, Enterococcus–vancomycin: DW 0.07±0.20; EF 0.06±0.20; UW 0.21±0.34, and ceftazidime- *P. aeruginosa*: DW 0.43±0.8; EF 0.06±0.1; UW 0.31±0.7), but higher for imipenem- *P. aeruginosa* (DW 4.33±9.9; EF 0.36±0.5; UW 2.22±4.3) and erythromycin-Enterococcus (DW 2.10±3.7; EF 0.08±0.2; UW 1.19±2.1). Cefotaxime-resistant *E. coli* counts (adjusted by month and no-antibiotic counts) differed by site, with significantly higher counts at UW vs. DW (RR 1.89, 95% CI: 1.24–2.88) but no difference between EF and DW (RR 0.63, 95% CI: 0.24–1.65). For Enterococcus, erythromycin-resistant counts showed no site differences, whereas vancomycin-resistant counts differed by site, with higher counts at E (RR 7.41, 95% CI: 1.51–36.44) and UW (RR 30.75, 95% CI: 1.56–605.95) relative to DW. For. *P. aeruginosa,* imipenem-resistant counts did not differ by site, whereas ceftazidime-*P. aeruginosa* counts were sparse, and the negative binomial model did not converge.

Conclusions

Overall, antibiotic-selected colony counts were often low and highly variable, and site patterns differed by organism and antibiotic rather than showing a uniform effluent-driven increase downstream. These findings suggest that background/upstream inputs and temporal variability may be as important as effluent discharge for ARB levels in receiving waters.

---

505 – Advancing National One Health Coordination through the United States One Health Coordination Unit, 2024-2026

Casey BARTON BEHRAVESH (1,4), Lisa BRANUM (2,4), Michael NEAFSEY (3,4), Natalie WENDLING (1,4), Elizabeth RUSSELL (2,4), Steven REKANT (3,4), On behalf of U.S. ONE HEALTH COORDINATION UNIT (4)

1: U.S. Centers for Disease Control and Prevention, United States of America; 2: U.S. Department of the Interior; 3: U.S. Department of Agriculture; 4: United States One Health Coordination Unit

Background

In 2017, multisectoral efforts in the United States identified a critical need to formalize One Health coordination across the federal government to better address zoonoses and related One Health threats. In 2021, Congress directed the Centers for Disease Control and Prevention (CDC) to lead interagency coordination and development of a national One Health framework (NOHF) and collaborate with the U.S. Department of Agriculture (USDA) and the Department of the Interior (DOI) to formalize federal-level One Health coordination.

Methods

In 2021, designated One Health leaders from CDC, DOI, and USDA formed an interagency core leadership team (ICLT) to implement the congressional mandate. This team jointly developed a Terms of Reference and established the United States One Health Coordination Unit (U.S. OHCU). In parallel, a coordinated interagency process was used to develop the NOHF. Federal One Health experts participated in developing the NOHF through a consensus-building process that also incorporated public feedback.

Results

The U.S. OHCU, established in January 2024, serves as a congressionally mandated governance structure to advance One Health collaboration across the federal government. Built on shared interagency leadership from CDC, DOI, and USDA (Figure 1), the U.S. OHCU unites 27 agencies from eight departments. The U.S. OHCU operates under a formal governance structure with the ICLT meeting regularly to guide strategic direction and oversee technical working groups addressing priority One Health topics.

Key outcomes include strengthened interagency communication, improved coordination of One Health-related investigations, and release of the first *National One Health Framework to Address Zoonotic Diseases and Advance Public Health Preparedness (2025–2029)* (NOHF-Zoonoses). The NOHF-Zoonoses establishes a national structure for federal One Health coordination, collaboration, and communication and outlines strategic goals to protect people, animals, and the environment from zoonoses while advancing public health preparedness, national security, food safety/security, biodiversity, and conservation outcomes while complementing existing U.S. initiatives.

The U.S. OHCU also coordinates several communication platforms to coordinate with federal, state, tribal, local, and territorial partners, as well as non-governmental stakeholders including industry, academia, communities, and non-profit organizations. Ongoing challenges include improving data interoperability, strengthening coordinated surveillance systems, and ensuring adequate resources to support long-term implementation.

Conclusions

The U.S. OHCU launch represents a major milestone for One Health in the United States, marking the first formalized federal coordination mechanism spanning all relevant sectors. From 2024-2026, this effort demonstrated that institutionalized national-level governance structures with clearly defined roles and ongoing coordination are essential for effective One Health implementation. Through the U.S. OHCU and the NOHF-Zoonoses, federal agencies have strengthened their collective capacity to prevent, detect, and respond to zoonoses and related One Health threats improving efficiency, optimizing resource use, and

enhancing collaboration to protect the health, safety, and security of people, animals, plants, and the environment.

Figure 1. United States One Health Coordination Unit (U.S. OHCU) Organizational Structure Highlighting Shared Interagency Leadership Across Sectors

*Rotating U.S. OHCU Chair: One agency representative from the U.S. OHCU Interagency Core Leadership Team serves as chair to the U.S. OHCU on a rotating biennial calendar year basis, alternating between a representative from CDC, USDA, and DOI.

†As of January 30, 2026, 27 agencies from eight federal departments are represented on the U.S. OHCU.

517 – Structural Drivers of Veterinary Antimicrobial Use: Governance, Markets, and Livelihood Pressures in Malawi and Kenya

Amos Lucky MHONE (1,2), Dishon MULOI (1,3), Simon MBUGUA (1,4), Alexina MORANG'A (1,4), Pater GATHURA (4), Joshua ONONO (4), Eugine IBAYI (1), Karoline KOCH (2), Marika WENEMARK (5), Ian DOHOO (6), Kristina ROESEL (7), Arshnee MOODLEY (1,2)

1: Health Program, International Livestock Research Institute, Nairobi, Kenya; 2: Department of Veterinary and Animal Sciences, Faculty of Health and Medical Science, University of Copenhagen, Frederiksberg C, Denmark; 3: Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, United Kingdom; 4: Department of Public Health, Pharmacology and Toxicology, Faculty of Veterinary Medicine, University of Nairobi, Nairobi, Kenya; 5: Department of Medicine and Health Sciences, Division of Community Medicine, Linköping University, Sweden; 6: Centre for Veterinary Epidemiological Research, University of Prince Edward Island, Charlottetown, Canada; 7: Department of Animal Breeding and Husbandry in the Tropics and Subtropics, Faculty of Agricultural Sciences, University of Hohenheim, Stuttgart, Germany

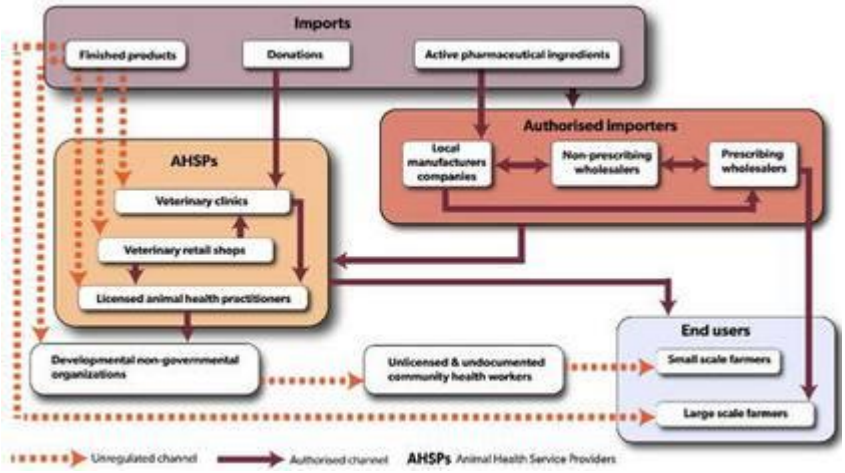
Background Antimicrobial resistance (AMR) is partly driven by antimicrobial use (AMU) in livestock systems. In many low- and middle-income countries, inappropriate veterinary AMU is often attributed narrowly to knowledge deficits among animal health practitioners and farmers. This study examines an alternative hypothesis that veterinary AMU is largely shaped by governance arrangements, market structures, and livelihood pressures. Focusing on Malawi and Kenya, with comparative insights from Denmark, we analysed how antimicrobial access, regulation, and use are structured across livestock production systems.

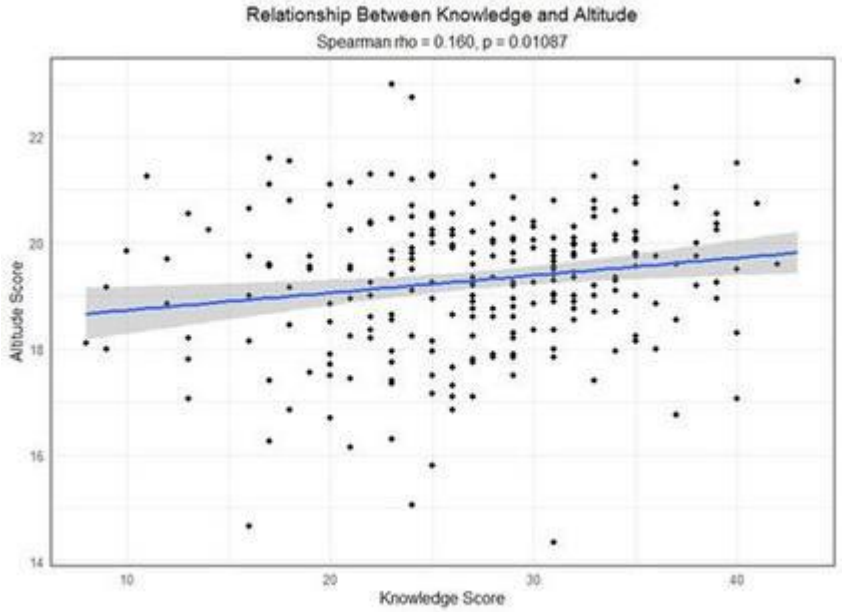
Methods: A mixed-methods, multi-level study design was employed. In Malawi, veterinary antibiotic value chains and governance arrangements were examined using focus group discussions (n = 15), key informant interviews (n = 6), and individual interviews (n = 189). A qualitative legal review of 522 AMU-relevant laws and policies using the FAO legal assessment framework, while Institutional coordination was explored through One Health governance mapping and social network analysis. In Kenya, a comparative legislative review identified 547 instruments regulating veterinary AMU, contrasted with 206 in Denmark. Practitioner-level evidence was generated through a cross-sectional survey of 252 animal health practitioners across six dairy-producing counties, complemented by cognitive interviews with nine practitioners. Quantitative data were analyzed using regression and correlation analysis, while qualitative data analyzed thematically.

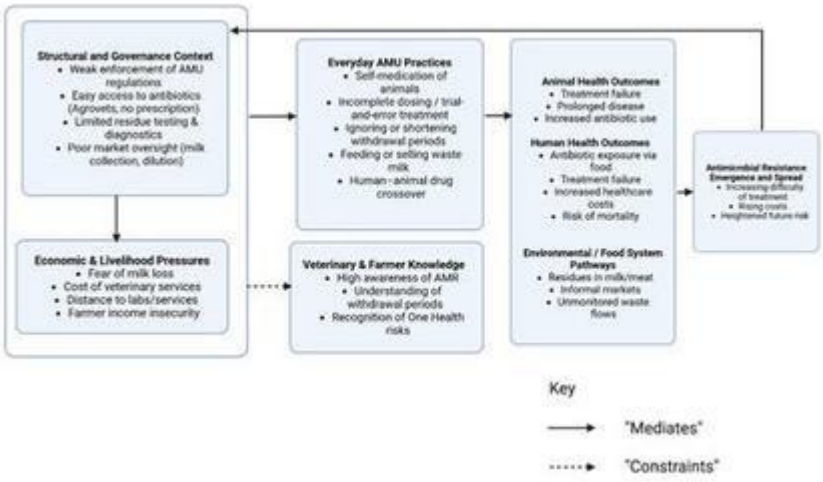
Results: Across both countries, veterinary antibiotic systems were characterized by fragmented governance, weak regulatory enforcement, and parallel formal and informal distribution pathways (Figure1). In Malawi, major regulatory gaps included the absence of national veterinary treatment guidelines, limited restrictions on critically important antimicrobials, weak disposal systems, and the lack

of integrated AMU/AMR surveillance. In Kenya, practitioner knowledge of antimicrobial stewardship was generally high, yet knowledge showed only a weak association with stewardship-supportive attitudes and reported practices (Figure 2). Qualitative findings revealed that structural pressures including dependence on daily milk income, easy over-the-counter antibiotic access, limited residue testing, and weak market oversight, regularly undermined adherence to withdrawal periods (Figure 3). Comparatively, Denmark's regulatory framework demonstrates how integrated legislation, surveillance systems, and enforcement mechanisms can align institutional incentives and support sustained reductions in veterinary AMU.

Conclusions: Inappropriate veterinary AMU is not primarily a consequence of insufficient knowledge, but a structurally produced outcome shaped by governance fragmentation, economic vulnerability, and misaligned institutional incentives. Effective AMR mitigation therefore requires governance-centered interventions, including coherent regulatory frameworks, integrated One Health coordination, and stewardship strategies that account for the livelihood realities of livestock-dependent communities







530 – PLANET4HEALTH Case Study: Data-Driven Early Warning System for Canine Leishmaniasis in the Iberian Peninsula

Carla MAIA (1), Sergio NATAL (2), Filipe GONÇALVES (3), Manuel MAGALHÃES SANT'ANA (3,4), Lisa MESTRINHO (3,5), Felisbina QUEIROGA (3,6), Emir CHAHER (3), Zeynep N. ULGEZEN (7), Ehsan MODIRI (8), Daniel SAN-MARTÍN (2), Suzana BLESIC (9)

1: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisboa, Portugal; 2: Predictia Intelligent Data Solutions, Santander, Spain; 3: Associação Portuguesa de Médicos Veterinários Especialistas em Animais de Companhia (APMVEAC), Lisboa, Portugal; 4: Faculdade de Medicina Veterinária, Animal Production Department, Universidade de Lisboa, Lisboa, Portugal; 5: Faculdade de Medicina Veterinária, Clinical Department, Universidade de Lisboa, Lisboa, Portugal; 6: Departamento de Ciências Veterinárias, Universidade de Trás-os-Montes e Alto Douro, Vila Real, Portugal; 7: Wildlife Ecology & Conservation Group, Department of Environmental Sciences, Wageningen University & Research, Wageningen, The Netherlands; 8: Helmholtz Centre for Environmental Research – UFZ, Department of Computational Hydrosystems, Leipzig, Germany; 9: Faculty of Physics, University of Belgrade, Belgrade, Serbia

Background: The PLANET4HEALTH project investigates how environmental degradation and climate change affect planetary health by examining interconnected human, animal, and ecosystem dynamics through a One Health perspective.

Zoonotic leishmaniasis, caused by *Leishmania infantum* and transmitted by phlebotomine sand flies, remains endemic across the Mediterranean basin. Dogs serve as the principal domestic reservoirs for human infection, and the seroprevalence of canine leishmaniasis (CanL) varies geographically, reflecting local ecological and epidemiological conditions. Ongoing climate and environmental changes, together with increasing mobility of people and animals, are contributing to the expansion of competent vector populations and increasing transmission risk.

Within the Horizon Europe project PLANET4HEALTH, this case study focuses on CanL across the Iberian Peninsula. It integrates environmental, climatic, and epidemiological data into a co-designed Early Warning System (EWS) aimed at improving early detection and prevention of CanL, thereby mitigating adverse impacts on both animal and human health.

Methods: Using a transdisciplinary One Health framework, an EWS is being co-created in collaboration with veterinarians, public health authorities, and other stakeholders integrating high-resolution hydrometeorological indicators (temperature, humidity, rainfall, soil moisture) with environmental, entomological, and CanL surveillance data. Statistical and machine learning approaches characterize sand fly seasonality and transmission dynamics, generating spatial risk maps, short-term forecasts, and projections (Figure 1). Model performance and usability are being assessed through stakeholder validation and iterative refinement.

Results: The initial prototype integrates near real-time climatic and epidemiological datasets to produce dynamic spatiotemporal risk assessments for CanL across the Iberian Peninsula. The system identifies seasonal and geographic hotspots, enhances understanding of environmental drivers of transmission, and supports targeted proactive responses. Stakeholder validation is ongoing to refine the system,

assess predictive performance, and optimize usability as part of a scalable data infrastructure for One health.

Conclusions: This PLANET4HEALTH case study demonstrates how integrated environmental and animal health data can support proactive surveillance and prevention of leishmaniasis under a One Health approach. By linking climate, ecosystem, and epidemiological data, the EWS contributes to improved prediction, preparedness, and mitigation of climate- and environment-related one health threats, with potential replication in other endemic regions.

Funding: European Commission grant 101136652. The five Horizon Europe projects, GO GREEN NEXT, MOSAIC, PLANET4HEALTH, SPRINGS, and TULIP form the Planetary Health Cluster.

Figure 1: Climate Suitability Component of the Early Warning System for Canine Leishmanaisis Risk in the Iberian Peninsula

536 – Assessing Acceptability, Willingness to Pay, and Market Readiness of Oxfendazole for Porcine Cysticercosis Control in Southern Rwanda

Simplice Umuhoza NSABIMANA

UGHE, Rwanda

Background: Transmission of *Taenia solium* continues in Rwanda despite control efforts targeting humans. In southern Rwanda, porcine cysticercosis prevalence in slaughtered pigs has been reported between 25–43%, and about 21.8% of epilepsy cases have been associated with cysticercosis, indicating continued animal–human transmission. Oxfendazole (30 mg/kg) has been shown to effectively eliminate viable muscular cysticerci in pigs in several studies in sub-Saharan Africa. However, the drug is not commercially available in Rwanda, and there is limited information on farmer acceptance, willingness to pay, and the feasibility of introducing it into the local veterinary market. This study aims to assess acceptability, willingness to pay, and market readiness for oxfendazole among pig-keeping households in southern Rwanda.

Methods: This study uses a mixed-methods design, with a household survey conducted concurrently with Focus Group Discussions (FGDs) and Key Informant Interviews (KIIs). The study is being carried out in Nyamagabe District, Southern Province, Rwanda. A total of 420 pig-keeping households are included: 210 households previously exposed to oxfendazole through the Community One Health Empowerment in Rwanda and Senegal (COHERS) project, and 210 households without prior exposure. Structured questionnaires are used to collect information on treatment acceptability, intention to use the drug, willingness to pay, and awareness of dosing and withdrawal periods. FGDs with pig farmers and KIIs with district veterinarians, paraveterinarians, and agro-veterinary drug distributors explore perceptions of the drug, potential barriers to its use, and factors affecting its availability in the veterinary drug supply chain.

Preliminary Results: Data collection is ongoing. Early responses suggest strong interest in the use of oxfendazole among pig farmers, particularly among those who have previously used the drug. Willingness to pay appears to vary by herd size and previous experience with treatment. Interviews with veterinary

stakeholders indicate that regulatory approval processes, farmer awareness of withdrawal periods, and reliable drug distribution systems will be important considerations for future introduction.

Conclusions: This study will provide evidence on farmer demand and the potential market for oxfendazole in southern Rwanda. The findings will help inform decisions on regulatory approval, pricing, and distribution strategies for integrating pig treatment into broader One Health efforts to control *Taenia solium* transmission.

539 – Mapping Progress and Setting Priorities for a More Inclusive One Health Antimicrobial Resistance Action Plan in Pakistan

Muhammad Farooq TAHIR (1), Riasat WASEE ULLAH (2), Hamid IRSHAD (3), Muhammad ABUBAKAR (4)

1: Integral Global, Pakistan; 2: Food and Agriculture Organization, Pakistan; 3: Animal Sciences Institute, National Agriculture Research Center, Islamabad, Pakistan; 4: National Veterinary Laboratories, Islamabad, Pakistan

Pakistan's first Antimicrobial Resistance (AMR) National Action Plan (NAP) was developed in 2017 to guide interventions to tackle AMR from 2017–2022. The NAP 1.0 predominantly focused the human health sector and several evaluations identified the need to better integrate agriculture, livestock and environment sectors. The National Institute of Health (NIH), Pakistan initiated the process of its revision in 2024.

To support this revision we conducted a two-day consultative workshop of selected stakeholders from agriculture and livestock sectors in August 2024. We divided the participants into five sub-groups based, and assigned one of the five objective of AMR to each group. We used activities outlined in AMR NAP 1.0 and recorded the response of participants to assess the implementation status. Similarly, we used the recommended agro-livestock activities from FAO's AMR Global Action Plan (GAP) to deliberate priority agri-livestock activities for AMR NAP 2.0. The result from the consultative workshop were compiled and presented to the NIH Pakistan as recommendations from the agri-livestock sectors

We identified lack of integration of agri-livestock activities, as only 59% of the recommended activities from FAO's AMR GAP were part of Pakistan's AMR NAP 1.0. Implementation status of activities ranged from 12-27% with AMR surveillance being the highest and governance being the lowest. Significant gaps were identified in areas related to multisectoral coordination, regulatory framework and financial sustainability. About 27 new agri-livestock related activities were recommended for inclusion in AMR NAP 2.0.

Agri-livestock related activities were included in the first AMR NAP on a limited scale however; their implementation status is significantly low. Even after seven years of implementation quite a few of the activities did not even start. This broader consultation provided a platform for agri-livestock stakeholders to incorporate their sectoral priorities in the next NAP iteration. This will lead to improved ownership of AMR NAP by the agri-livestock stakeholders and ultimately better implementation of NAP 2.0 activities.

543 – A mixed methods approach to exploring biosecurity implementation and perceptions on small ruminant farms in Ontario, Canada

Juliet GERMANN (1), Charlotte WINDER (1), Lauren GRANT (1), Delma KENNEDY (2), Angela WILSON (2), Kelsey SPENCE (1)

1: Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada; 2: Ontario Ministry of Agriculture, Food and Agribusiness

Background: Biosecurity practices are essential for ensuring animal welfare, supporting industry sustainability, and reducing the risk of disease transmission. However, current levels of adoption of biosecurity practices on Ontario sheep and goat farms are unknown. The objectives of this study were to describe biosecurity practices used on Ontario sheep and goat farms and to explore factors influencing implementation of different biosecurity practices using a mixed methods approach.

Methods: An online cross-sectional questionnaire of sheep and goat producers was conducted between April 2024 and February 2025. Descriptive statistics were collected, and multivariable logistic regression models were used to explore associations between flock/herd characteristics and use of biosecurity

practices. Questionnaire respondents were invited to participate in semi-structured interviews to explore their responses in depth. Interviews were transcribed and analyzed using reflexive thematic analysis.

Results: A total of 153 questionnaire responses and 25 interviews were included in our analysis. Of the questionnaire responses, 78 (51%) were from sheep producers, 57 (37%) were from goat producers, and 18 (12%) producers had both species. While 58% of respondents (89/153) did not maintain a closed herd, 79% (116/153) reported quarantining newly acquired sheep or goats. Forty-three respondents (31%) expressed concerns about acquiring diseases themselves from their herd or flock, and 24 (15.7%) reported both being concerned with, and presently having, zoonotic diseases within their flock or herd. These included Q-fever (Coxiellosis), Listeriosis, and Campylobacteriosis. Respondents who referred to educational websites for disease prevention questions had higher odds of keeping a closed herd compared to those who did not (OR=2.58, 95% CI:1.05-6.32, p-value=0.039). Similarly, respondents who referred to other producers for questions had higher odds of isolating sheep or goats suspected to have disease (OR=2.61, 95% CI: 1.05-6.51, p-value=0.040). In contrast, respondents who utilized online resources for disease prevention questions had lower odds of having protocols for staff/on-farm advisors entering the farm compared to those who did not (OR=0.14, 95% CI: 0.04-0.47, p-value=0.002). Interview findings suggested that producers viewed conducting their own research and being self-sufficient as important aspects of sheep and goat ownership. Many emphasized the importance of learning and implementing good management practices, including biosecurity, before an outbreak occurs. Mentorship from experienced producers was also frequently described as a valuable learning method. Several participants highlighted the importance of being proactive by starting with a clean herd or flock to prevent future outbreaks, noting that some had learned the consequences of not doing so.

Conclusion: This study provides an overview of biosecurity practices and perspectives on Ontario sheep and goat farms. Information sources appear to play an important role in biosecurity uptake, and producers value proactive learning to prevent outbreaks. Future research should explore how producers engage with different educational resources to help inform targeted interventions.

546 – Integrating One Health concepts with longitudinal malaria research in northern Zambia

Shelby M CAGLE (1), Margaret V BECKER (1), Renee LMN ALI (1), Mbanga MULEBA (2), Westone HAMWATA (2), James S LUPIYA (2), Hunter CHILUSU (2), Douglas E NORRIS (1)

1: Johns Hopkins Bloomberg School of Public Health & Johns Hopkins Malaria Research Institute, United States of America; 2: National Health Research and Training Institute, Zambia

Background: Nchelenge District in northern Zambia experiences high, sustained, year-round malaria transmission. Control and elimination of malaria is challenged by factors including, but not limited to: ecosystem complexity, human behaviors, insecticide resistance, diagnostic gaps, and access to medical care. While previous studies have considered human behavioral characteristics, such as bed net usage, our study seeks implement a One Health framework to further investigate how anthropogenic and ecological complexities may facilitate the continual exposure to malaria mosquitoes in this region and to identify household-level characteristics that contribute to transmission risk.

Previous studies show *Anopheles gambiae* and *Anopheles funestus* are predominant vectors in Nchelenge. These malaria mosquitoes facilitate year-round transmission; however, the breeding sites of these mosquitoes and the relative abundance of culicine arbovirus vectors are unknown. Ground-truthing has been performed to identify mosquito breeding potential. Streams, ponds, agricultural canals, swamps, and seasonal rains are hypothesized to be driving mosquito abundance near community members and their livestock.

Anthropogenic characteristics are currently being investigated to develop efficacious community-based health interventions. These characteristics include, but are not limited to house design, outdoor cooking and sleeping, community gatherings, agricultural and fishing practices, and bed net usage. We hypothesize community characteristics are reducing the efficacy of currently employed insecticide and mosquito reduction strategies, which exclusively target indoor spaces. The success of mosquito interventions is contingent upon the cooperation of individuals at the household levels. Therefore, efficacious interventions should be designed to integrate into community livelihoods and practices, rather than disrupt these community structures.

Methods: Adult mosquito trapping inside and outside of households, and larval collections at identified breeding sites will be conducted monthly to determine mosquito species abundance and diversity. Concordantly, household members complete monthly surveys to capture self-reported disease incidence, herd health, agricultural and fishing practices, household structure composition (i.e. roofing materials, windows, location), and community interactions. Data will be qualitatively and quantitively analyzed to determine ecological changes, impacts on fishing and agriculture, mosquito bite risk behaviors, house construction, and community practices contributing to sustained malaria rates in Nchelenge.

Results: Longitudinal, regional malaria data from Zambia will be reported, alongside ongoing surveillance in Nchelenge. Results from in-depth enrollment surveys will be presented. Data regarding house construction and proximity to aquatic ecological features (pond, lagoon, stream, water pumps) may reveal factors contributing to malaria transmission via anophelinesand arbovirus potential from culicines contributing under-diagnosed febrile illness in these populations.

Conclusions: This study seeks to identify mosquito breeding sites, relative mosquito abundance, and to characterize anthropogenic behaviors that contribute to malaria risk. These data can be used to guide efficacious, community-based vector control strategies. Science communication and education strategies and malaria reduction will be developed accordingly and alongside community partners.

557 – Brucellosis Prevention Practices, Risk Perceptions, and Trust in Veterinary Advice Among Livestock Keepers and Service Actors in the Bedouin Community in the Southern West Bank: A Cross-Sectional Study

Akram AMRO (1), **Julianne MEISNER** (2), **Alhareth AMRO** (1), **Raghda AMRO** (1), **Hazem AGHA** (1), **Amira ROESS** (2), **Nadav DAVIDOVITCH** (3)

1: Green Land Society for Health Development, Palestinian Territories; 2: University of Washington, United States; 3: Ben Gurion University of the Negev, Isreal

Background

Brucellosis is a priority zoonosis in pastoral and agropastoral systems, and control depends on sustained livestock vaccination, disease surveillance, and coordinated One Health action. Border-adjacent communities may experience context specific exposure pathways shaped by constrained service access, informal trade networks, and mobility. Bedouin communities in the West Bank are traditionally semi-nomadic pastoral groups whose livelihoods rely heavily on small ruminant livestock production, making them a key population in understanding brucellosis transmission and control dynamics in the region. This study assessed brucellosis related practices and risk perception; trust in veterinary advice; and cross border livestock exchange.

Methods

A cross-sectional survey was conducted from September to November 2025 in rural and peri urban communities of the Hebron Governorate in the southern West Bank, including Bedouin and non-Bedouin localities. Participants included livestock keepers, healthcare providers and stakeholders involved in animal, service providers, and public health services, recruited using convenience and referral-based sampling. Structured questionnaires measured livestock husbandry practices including participation in vaccination and testing programmes for brucellosis; receipt of vaccination reminders; awareness of relevant regulations, perceived brucellosis risk to animals and humans; trust in veterinary recommendations; and cross border movement of animals and products. Descriptive statistics summarized responses. Among livestock keepers, logistic regression assessed associations between perceived risk and reported vaccination, with education included in adjusted models.

Results

A total of 70 questionnaires were completed: Among livestock keepers, 84% reported that their livestock were vaccinated against brucellosis, and the same number reported brucellosis testing of their livestock within the prior 12 months. Only 42% reported receiving official vaccination reminders, and 18% reported awareness of Ministry of Agriculture regulations relevant to brucellosis. Reported cross border exchange was uncommon (2% livestock acquisition from Bedouin communities inside Israel; 6% cross border sale). Trust in veterinary advice was moderate to very high among 62%, whereas 54% reported little to no confidence in local leadership for animal health decisions. All service providers reported awareness of

brucellosis and recent outbreaks, but only 20% reported regular zoonotic disease training. Higher perceived animal risk was associated with increased odds of livestock vaccination (OR = 5.81; 95% CI: 1.40 to 24.20; p = 0.016), while perceived human risk was not statistically significant (p = 0.071). Trust in veterinary advice correlated positively with perceived animal risk (rho = 0.586; p 0.001).

Conclusions

Reported vaccination and diagnostic testing were high yet formal supports were limited, including incomplete reminder coverage, low regulatory awareness, and infrequent zoonotic training among providers. Vaccination uptake aligned more strongly with perceived animal risk than perceived human risk. Strengthening routine prevention infrastructure and leveraging trusted veterinary communication within a One Health framework may improve brucellosis control in the southern West Bank.

561 – Integrated One Health Mosquito Control through Targeted Stakeholder Engagement: The Experience of South Tyrol (Italy)

Danilo DOGLIO (1), Filippo CASSINA (2), Christiane HOLZNER (1), Silvia SPERTINI (1), Alberta STENICO (2), Alexander TAVELLA (3), Christian PIFFER (1), Elisabetta PAGANI (1), Dagmar REGELE (1), **Giulia MOROSETTI** (1)

1: Azienda Sanitaria dell' Alto Adige, Italy; 2: Provincia Autonoma di Bolzano, Alto Adige, Italy; 3: Istituto Zooprofilattico delle Venezie, Sezione Bolzano, Italy

Background The expansion of invasive mosquitoes in Europe, particularly *Aedes albopictus*, increases the risk of arboviral diseases such as dengue and chikungunya. With regard to the Alpine region, climate change and mobility of people and goods are gradually expanding suitable habitats, including valleys previously considered at very low risk. As a preventive measure, the Autonomous Province of South Tyrol developed a legally grounded mosquito control programme grounded in a One Health framework, integrating environmental monitoring, public medical and veterinary surveillance, as well as targeted stakeholder engagement. A defining feature of this approach is the systematic identification of specific population subgroups as strategic actors in prevention, using the official regional languages.

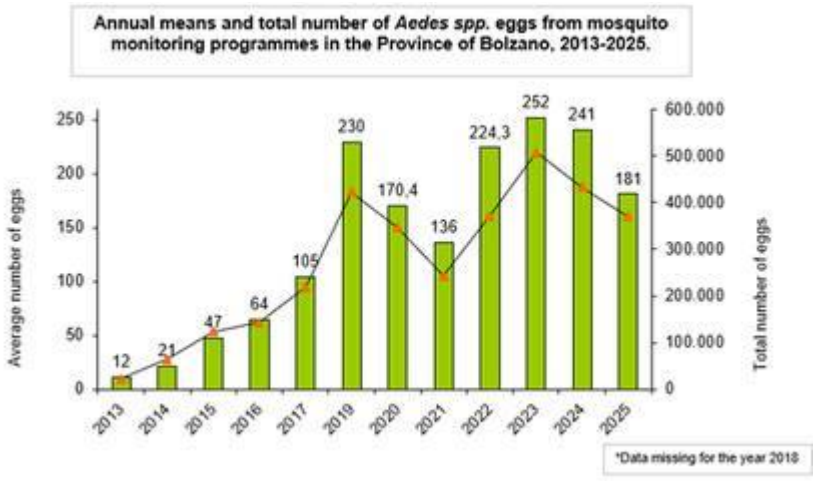
Objectives The programme aims to promote a province-wide mosquito monitoring system; implement environmentally sustainable vector control measures by prioritising larval source reduction and cautious use of larvicides; strengthen integrated One Health governance, health education, as well as engagement of relevant stakeholder groups.

Methods From April to October, entomological monitoring is conducted across most affected areas and high-risk introduction areas using ovitraps and BG-Sentinel traps. Larval control relies primarily on biological larvicides, e.g. *Bacillus thuringiensis israelensis* (Bti), avoiding routine adulticide applications in line with environmental protection principles. The governance structure connects environmental authorities, medical and veterinary public health services, laboratories, and municipalities, thus ensuring coordinated planning and rapid response. Prevention strategies are segmented according to exposure risk and operational responsibility. Identified targets include property managers for shared residential buildings to promote the elimination of standing water in private gardens and terraces; plant nurseries and floriculture businesses for conscious watering; mechanics and tyre retailers, since stored tyres represent potential larval development sites. To enhance early clinical detection of human cases, emergency and urgency physicians are actively involved. The general population is addressed through multilingual communication campaigns.

Results At present, a stable and geographically distributed monitoring network covers the province. *Aedes albopictus* presence is well established in climatically suitable areas, expanding to higher altitudes in the last decade. Other invasive species including *Aedes japonicus* and *Aedes koreicus,* have also been detected. No autochthonous human or animal cases of mosquito-borne diseases have been recorded during the intervention period. Intersectoral coordination improved clarity of institutional roles and operational efficiency. The programme achieved strong stakeholder engagement and compliance, as well as active support from the general population.

Conclusions This experience demonstrates that effective mosquito control in non-endemic regions, such as South Tyrol, requires both continuous integrated One Health governance and precise identification of prevention targets. Empowering professional and community subgroups increases sustainability, accountability, and preventive impact. In the context of climate-driven ecological shifts, active vector

monitoring combined with tailored stakeholder engagement represents a scalable and transferable strategy for regional mosquito control.



Aerial view of Bolzano city, showing one of the critical areas for tiger mosquito density

566 – LAND-AMR: Predicting wildlife-mediated antimicrobial resistance through landscape connectivity

Rita TORRES (1), Ana FIGUEIREDO (1), João CARVALHO (1), Helena FERREIRA (2), Josman PALMEIRA (2)
1: University of Aveiro, Portugal; 2: University of Porto, Portugal

BACKGROUND: Antimicrobial resistance (AMR) is a global public health crisis and a "silent pandemic." Resistant bacteria and genes circulate beyond clinal and agricultural settings, but the role of wildlife in AMR persistence and transmission remains poorly understood. Wild ungulates, highly mobile and present across agricultural, urban, and natural habitats, are largely absent from AMR surveillance, despite their potential to link humans, livestock, and the environment. LAND-AMR advances previous AMR research by integrating landscape connectivity and host movement ecology to address a critical One Health blind spot and by developing a predictive spatial framework for AMR risk assessment.

METHODS: The project focuses on three Portuguese landscapes spanning gradients of agriculture, fragmentation, and human pressure. Wild boar, red deer, and roe deer will be monitored using systematic camera traps to estimate density, activity patterns, and potential contact networks. Non-invasive faecal samples were screened for indicator bacteria (*E. coli*, *Salmonella* spp., *Enterococcus* spp.) and AMR profiles. Previously collected samples (2018 - 2020) were analysed, with a total of 181 faecal samples. The protocols associated with data processing and laboratory analysis are detailed in Torres et al. (2022). Environmental variables reflecting human pressure were assessed as predictors of AMR occurrence using a generalized linear mixed-effects model, with location as a random factor. Ongoing spatial and network-based modelling integrates wildlife movement, environmental predictors, and microbiological data to identify AMR corridors, hotspots and ecological firebreaks.

RESULTS/EXPECTED OUTCOMES: Among 181 samples, 83 (45.8%) were antimicrobial resistant *Enterobacterales* isolates. Resistance was most frequently observed to ampicillin (71.5%) and tetracycline (63.6%), with substantial diversity of ARG detected. Models predicted a higher risk of finding resistance to a greater number of antibiotic classes in wild ungulates inhabiting areas closer to urban areas. Likewise, our model predicted a higher risk of detecting more antibiotic resistance genes in wild ungulates near urban areas. Functional connectivity analyses and predictive spatial modelling are ongoing and are expected to help identify high-risk transmission interfaces.

CONCLUSIONS: LAND-AMR refocuses wildlife-related AMR as a dynamic, landscape-mediated ecological process. By linking host ecology, environmental and human pressures, and microbiological data, the project develops a spatially explicit One Health framework for tailored surveillance and risk management.

573 – Molecular evidence of yaws treponemes in zoos and wildlife reserves, Ghana.

Tabitha Naa KONEY (1,2), Shirley Victoria SIMPSON (1), Olufemi Oladayo FALEKE (2), Benjamin Obukowho EMIKPE (2), Meyir ZIEKAH (3), Gloria Ivy MENSAH (1), Kennedy Kwasi ADDO (1)

1: Noguchi Memorial Institute for Medical Research, University of Ghana, Legon.; 2: School of Veterinary Medicine, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana; 3: Forestry Commission, Wildlife Division, Ghana .

Background: Yaws, a neglected tropical disease caused by *Treponema pallidum* subspecies *pertenue*, remains endemic in Ghana despite years of eradication efforts. Studies suggest that non-human primates (NHPs) may harbour treponemes, potentially acting as reservoirs that complicate elimination strategies. Yet reports on the prevalence and transmission dynamics between humans and NHPs in Ghana remain scarce. We investigated the presence of treponemes in humans and NHPs at human-wildlife interfaces in Ghana and evaluated knowledge, attitudes, and practices (KAP) related to yaws among at-risk populations.

Methods: A cross-sectional study was conducted between July and August 2025 at Accra Zoo, Kumasi Zoo, and Mole National Park. Structured KAP questionnaires were administered to 19 participants (zoo staff, park rangers, and community members). NHP species sampled included *Cercocebus atys* (white-naped mangabeys), *Erythrocebus patas* (patas monkeys), *Chlorocebus sabaeus* (green monkeys), *Papio anubis* (olive baboons), *Cercopithecus petaurista* (lesser spot-nosed monkeys), and *Cercopithecus mona* (mona monkeys). Knowledge was scored as low (0–1 correct responses), moderate (2–3), or high (4–5). Serological screening was performed with HIGHTOP Syphilis Ab rapid diagnostic tests using finger-prick blood from humans (n=19) and serum from NHPs (n=21). DNA was extracted from human stool samples (n=18) and NHP rectal swabs (n=21), followed by amplification of tp*0548* and *polA* genes specific to *T. pallidum.* Amplicons were visualized after gel electrophoresis.

Results: KAP assessment revealed gaps in occupational health preparedness. Only 10.5% of participants had received formal training on zoonotic diseases. While 89.5% consistently wore boots, PPE use was inconsistent: 21.1% never wore gloves, 73.7% never used masks, and 42.1% never wore coveralls. Only 47.4% had been vaccinated (primarily rabies and COVID-19). However, all participants expressed interest in receiving yaws education. Serological testing yielded no positive cases in either humans or NHPs. In contrast, molecular analysis detected *T. pallidum* DNA in 22.2% (4/18) of human samples and 71.4% (15/21) of NHP samples. Specifically, *tp0548* was amplified in 16.7% (3/18) of human samples and 47.6% (10/21) of NHP samples, while *polA* was detected in 5.6% (1/18) of humans and 23.8% (5/21) of NHPs.

Conclusions: NHPs in Ghana harbour *T. pallidum* DNA, with higher detection rates than in humans despite negative serology. Identical gene targets detected in both species at human-wildlife interfaces, combined with documented gaps in occupational health knowledge and biosecurity practices, underscores the need for integrated One Health surveillance. Yaws eradication programs may be insufficient without wildlife monitoring. Incorporating wildlife surveillance and molecular analysis into control programs and strengthening occupational health training for zoo and wildlife workers are essential for early detection of zoonotic reservoirs, improved biosecurity practices, and the integration of One Health approaches into yaws control efforts.

579 – Phenotypic and genomic characterization of antimicrobial resistance in Escherichia coli isolated from food transport containers used in public catering

Levente Hunor HUSZ (1,2), Ákos JERZSELE (1,2), Miklós SÜTH (2,3), Ádám KEREK (1,2)

1: Department of Pharmacology and Toxicology, University of Veterinary Medicine Budapest; 2: National Laboratory of Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health and Food Chain Safety, University of Veterinary Medicine Budapest; 3: Institute of Food Chain Science, University of Veterinary Medicine

Background

Antimicrobial resistance (AMR) is a major global challenge, and within the One Health framework, food-contact environments may contribute to the persistence and dissemination of resistant bacteria along the food chain. Food transport containers used in public catering represent a potentially overlooked environmental niche of food safety relevance. This study aimed to assess the phenotypic and genomic

AMR characteristics of *Escherichia coli* isolates recovered from pressure-relief valve compartments of food transport containers used in institutional catering.

Methods

A total of 93 *E. coli* isolates were examined. Phenotypic antimicrobial susceptibility testing was performed by minimum inhibitory concentration (MIC) determination according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Isolates showing an inhibitor-positive phenotype suggestive of extended-spectrum β-lactamase (ESBL) production were selected for next-generation sequencing to identify antimicrobial resistance genes and regulatory elements potentially influencing their expression.

Results

Phenotypic screening identified 30/93 isolates with an inhibitor-positive phenotype suggestive of ESBL production. Whole-genome sequencing showed that all 30 sequenced strains carried the chromosomal β-lactamase genes *ampC* and *ampH*, whereas classical ESBL genes such as *bla*CTX-M, *bla*SHV, and *bla*TEM were not detected. The observed inhibitor-positive phenotype was therefore most likely associated with *ampC*-linked mechanisms in combination with multidrug efflux systems, including *acrAB* and *mdtEF*, together with regulatory elements such as *emrR*, *baeSR*, *gadX*, and *crp*. Additional resistance-associated determinants related to aminoglycosides, fluoroquinolones, colistin, and tetracyclines were also identified; however, corresponding phenotypic resistance was observed only in a limited number of isolates. These findings indicate that the genomic presence of resistance-associated determinants does not necessarily translate into overt phenotypic resistance without appropriate regulatory background or expression conditions.

Conclusions

Food transport containers used in public catering may harbor *E. coli* strains with multidrug resistance potential, even when classical ESBL genes are absent. The discordance observed between phenotype and genotype highlights the need for integrated phenotypic and genomic surveillance in food-chain environments. From a One Health perspective, environmental AMR monitoring of catering-associated equipment may improve food safety risk assessment and support more targeted hygiene control strategies.

Acknowledgments: Supported by Normative Research Funding Committee (NRC), University of Veterinary Medicine Budapest. Project no. RRF-2.3.1-21-2022-00001 has been implemented with the support provided by the Recovery and Resilience Facility (RRF), financed under the National Recovery Fund budget estimate, RRF-2.3.1-21 funding scheme.

---

584 – Implementing We Care®: One Health in Practice in the Barn

Heather FOWLER

National Pork Board, United States of America

There are numerous examples of the implementation of the One Health approach in different settings, including research and academia. However, industry-specific examples of implementation of One Health practices in animal agriculture are rarely highlighted (Fowler et al 2026 in press). The National Pork Board (NPB) and the farmers they represent have been working in a One Health way every day for decades through the implementation of the six We Care® Ethical Principles (See Figure 1). Given pig farmers' focus on producing safe, healthy, nutritious pork, their training programs, research efforts, and educational resources all map back to the One Health framework via these principles (See Figure 2). Additionally, pig farmers are committed to continuous improvement of their practices to become better stewards of the pigs they raise, the people they support, and the planet upon which they rely for natural resources. Despite these efforts to continuously improve One Health implementation, existing biases often prohibit industry involvement in discussions and limit their ability to be part of a shared One Health solution.

Participants will lgain an understanding of (1) the basic of pork production in the U.S., (2) the We Care® Ethical Principles, and (3) at least two examples of how the US Swine industry applies the One Health approach in daily practice.

589 – “Emerging threat” Crimean Congo Hemorrhagic Fever Virus in Pakistan.

Muhammad ALI
Abdul Wali Khan University Mardan, Pakistan

Introduction: Crimean Congo Hemorrhagic Fever (CCHF), a zoonotic tick-borne disease, spreads through Hyalomma tick bites in animals and direct contact with infected animal blood or fluids in human.

Objectives: This study aimed to determine the seroprevalence of IgG antibodies to Crimean-Congo Hemorrhagic Fever (CCHF) in humans and livestock.It also sought to identify associated risk factors in two districts of Khyber Pakhtunkhwa.An extensive analysis of reported CCHF cases across the province was conducted.Key focus areas included disease prevalence, mortality rates, and evaluation of healthcare infrastructure and management strategies.

Methodology and Results: In Mardan and Malakand districts, 125 households/farms were visited. They collected 1,205 serum samples (livestock=1,029, human=176). Of these, 848 (livestock=762, human=86) were processed for seroprevalence detection via indirect ELISA. District-wise seroprevalence was 13% (n=58) in Mardan and 29.1% (n=117) in Malakand.

From 2019 to 2021, cases reported in tertiary care hospitals were diligently recorded. A total of 207 confirmed cases were documented, out of which 143 patients unfortunately passed away, while 64 patients successfully recovered over various time periods. Comprehensive analysis was conducted on both confirmed and suspected cases.

Among the deceased patients, a majority of them were individuals employed as butchers, farmers, and animal care workers. However, a few cases were observed among drivers, housewives, and healthcare workers.

Conclusion: The data indicate a significant yet sporadic prevalence of Crimean-Congo hemorrhagic fever (CCHF) in both livestock and human populations.Immediate measures are essential to protect public health and ensure economic stability.

597 – Understanding Trust in Veterinary Care and Institutional services among Arab Bedouin Livestock Owners: Application of the Relational One Health Framework

Haneen SHIBLI (1), Julianne MEISNER (1), Anat ROSENTHAL (2)

1: University of Washington, United States of America; 2: Ben Gurion University of the Negev, Israel

Background: The Relational One Health approach emphasizes the interconnectedness of human, animal, and environmental health and provides a lens for understanding zoonotic diseases that are shaped by political, historical, and social conditions. Brucellosis, a zoonotic disease transmitted primarily from livestock, poses specific challenges in communities where livestock hold central economic, cultural, and social importance. In southern Israel, the Arab Bedouin minority (hereafter Bedouins) experiences a disproportionate burden of brucellosis due to structural marginalization, limited access to services, and changing patterns of human–animal interaction driven by land dispossession and compelled urbanization. Building on the Relational One Health framework, the aim of this study was to examine how institutional distrust and displacement to urban locales influence facilitates (or impedes) the transmission of brucellosis.

Methods: A qualitative study was conducted between May 2025 and January 2026. Data collection strategies included Data collection strategies included 29 Key Informant Interviews (KIIs), 30 Oral History interviews, and 12 Transect Walks. Furthermore, 12 Focus groups discussions (FGDs) were conducted (total participants = 81), stratified by gender and age with group sizes ranging from 5 to 10 participants. Participants were recruited from 11 Bedouin towns and villages in southern Israel. Semi-structured guides explored human-animal interactions following urbanization, and levels of trust in veterinary services and authorities. All interviews were conducted in Arabic by trained Arab Bedouin data collectors, audio-recorded, transcribed verbatim and translated into English. Data was analyzed using thematic analysis with validity ensured through audit procedures, reflexivity, and peer debriefing.

Results: Trust emerged as a central theme shaping how Bedouin livestock owners engage with the veterinary and health systems. Participants described a spectrum of experiences ranging from deep mistrust in governmental and veterinary authorities to selective trust in community-based or private veterinary professionals. Poor availability of services, and lack of follow-up were described as the cause of lack of confidence in providers, reflecting frustration with delayed care and high costs. Quality of care and oversight of services, long waiting times and inattentive treatment highlighted perceptions of weak accountability within the veterinary and health systems. Going beyond service delivery, structural inequity was raised as an explanation for intentionally exclusionary regulatory practices. Together, these narratives illustrate how distrust in authorities, perceived neglect, and feelings of unequal treatment shape community engagement with testing, vaccination, and veterinary care.

Conclusions: Situating this work within the Relational One Health framework highlights how environmental, political, and historical conditions shape human–livestock contact networks and create the context in which trust is formed, strained, or lost. The findings point to the need for One Health education and community-based strategies that acknowledge institutional distrust and work collaboratively with local knowledge and community priorities.

599 – Integrating Local Knowledge into a One Health Approach: Livestock Care Among the Arab Bedouin Minority

Haneen SHIBLI (1), Julianne MEISNER (1), **Anat ROSENTHAL** (2)

1: University of Washington, United States of America; 2: Ben Gurion University of the Negev, Israel

Background: Brucellosis, a zoonotic disease transmitted from infected livestock to humans through direct contact or consumption of unpasteurized animal products, poses particular challenges in communities where livestock hold central cultural, social and economic, importance. The Arab Bedouin minority in

southern Israel experience a disproportionate burden of brucellosis due to structural marginalization, limited access to healthcare service, and rapid urbanization. These social processes also shape how people learn about and manage animal health. Building on the Relational One Health framework, the aim of this study was to investigate how Bedouins navigate and interpret knowledge about animal health and brucellosis and to identify how veterinary and public health information interacts with community-based, experiential, and Indigenous knowledge sources.

Methods: A qualitative study was conducted between May 2025 and January 2026. Data collection included 29 Key Informant Interviews (KIIs), 30 Oral History interviews, and 12 Transect Walks. Furthermore, 12 Focus groups discussions (FGDs) were conducted (total participants = 81), stratified by gender and age with group sizes ranging from 5 to 10 participants. Participants were recruited from 11 Bedouin towns and villages in southern Israel. Semi-structured guides explored human-animal interactions following urbanization, and levels of trust in veterinary services and authorities. All interviews were conducted in Arabic by trained Arab Bedouin data collectors, audio-recorded, transcribed verbatim and translated into English. Data was analyzed using thematic analysis with validity ensured through audit procedures, reflexivity, and peer debriefing.

Results: Participants expressed a mix of accurate knowledge and partial or inconsistent knowledge related to animal health and disease prevention. Participants expressed confidence in practices they believed to be protective, such as boiling milk to ensure safety while others pointed to gaps in awareness, particularly in more remote areas where access to services is limited. Concerns about environmental health also varied, with some participants recognizing risks related to common practices of animal care while others were less aware of these issues. Differences in knowledge were shaped by diverse knowledge sources, including veterinarians who provide explanations and treatment, family members who pass down practical experience, community norms that influence everyday decisions and traditional knowledge that continues to guide livestock care among the Bedouin community.

Conclusions: This study highlights how knowledge about animal health among Bedouin communities' households is shaped by a mix of accurate understanding, partial information, and deeply rooted experiential practices. The findings highlight the importance of One Health approach that recognizes and value community-based knowledge while strengthening pathways to reliable information. Supporting locally grounded knowledge alongside accessible veterinary and health services may help reduce brucellosis transmission and promote healthier human–animal–environment relationships in Bedouin communities.

611 – From Donor Dependence to Domestic Ownership: Expert Perspectives on One Health Antimicrobial Stewardship in Asia-Pacific Low- and Middle-Income Countries

Yasodhara D. GUNASEKARA (1,2), Mauricio J. C. COPPO (1,2,3), Ri O. SCARBOROUGH (1,2), Anna E. SRI (1,2), James R. GILKERSON (1,2), Glenn F. BROWNING (1,2), Kirsten E. BAILEY (1,2), Laura Y. HARDEFELDT (1,2)

1: Asia-Pacific Centre for Animal Health, Melbourne Veterinary School, University of Melbourne, Parkville, VIC, Australia; 2: National Centre for Antimicrobial Stewardship, Melbourne Medical School, University of Melbourne, Parkville, VIC, Australia; 3: Instituto One Health, Facultad de Ciencias de la Vida, Universidad Andres Bello, Concepcion, Biobio, Chile

Background: Antimicrobial resistance (AMR) is a growing threat to human, animal, and environmental health. Compared to high-income countries, low- and middle-income countries (LMICs) are predicted to be burdened with the highest impact of AMR. Antimicrobial stewardship (AMS) are strategies and interventions designed to optimise the responsible use of antimicrobials to improve health outcomes, protect their effectiveness for future use, and minimize the development of AMR. Evidence of sustainable implementation of One Health AMS is limited, particularly in LMICs. Methods: This study was designed to explore the current situation and the barriers to, and enablers of, sustainable implementation of One Health AMS in LMICs in the Asia-Pacific region. Four in-person focus group discussions were conducted with human health, animal health, and environmental health experts from Bhutan, Nepal, Pakistan, Papua New Guinea, and Timor-Leste. All selected experts were engaged in the Fleming Fund Programme, and their work aimed to combat AMR in their respective countries. Their experiences and perspectives on current One Health interventions in their countries were explored. Discussions were recorded, transcribed, and a thematic analysis was conducted according to qualitative data analysis principles. Results: Four common themes were identified: silos and differing priorities, recognition of the burden of AMR, stakeholder attitudes, and resource availability. The identified themes interact with and influence

each other, forming a web of relationships that affect sustainable One Health AMS interventions (Figure 1). Current One Health AMS programmes in the studied countries are largely dependent on external donors, and a lack of financial support from the government was identified as a major barrier to the sustainability of these interventions. Siloed operations and differing priorities between the human, animal, and environmental health sectors are also a barrier to One Health AMS. Nearly all participants believed that the One Health approach was important to address AMR, and this shared belief was identified as an enabler. Conclusion: To establish a sustainable One Health AMS in the studied setting, high-impact, low-cost interventions are essential to explore and implement. The introduction of a transition funding plan to all international donors and embedding One Health AMS programmes in the national budget were also identified as important actions. Strengthening of political leadership and policy framework is needed to ensure equitable allocation of resources across all domains of One Health. Additionally, future studies need to focus on exploring the metrics for evaluating co-benefits across sectors for interventions.

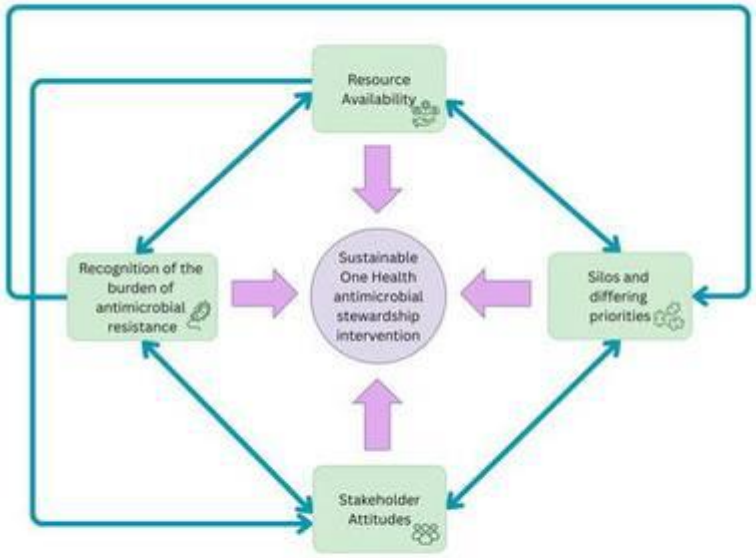


Figure 1: Factors affecting sustainable One Health antimicrobial stewardship interventions in selected low- and middle-income countries in the Asia-Pacific region.

617 – Land-use gradients shape microbial connectivity at the human–animal interface in Cambodia

Pauline VAN LEEUWEN (1), Julia GUILLEBAUD (2), Thavry HOEM (3), Sreyleak HOEM (3), Sithun NUON (3), Anais BOMPARD (4), Erik KARLSSON (3), Veasna DUONG (3), Johan MICHAUX (1,2), Julien CAPPELLE (2)

1: Université de Liège, France; 2: CIRAD, France; 3: Institut Pasteur du Cambodge; 4: INRAE, France

Land-use change reshapes host communities, contact patterns, and microbial exchange at the human–animal interface, with potential consequences for zoonotic emergence. However, integrated evidence across wildlife, domestic animals, and humans remains limited in tropical Southeast Asia. Within the BCOMING project, we generated cross-sectional One Health snapshots across Cambodia to investigate how microbiome diversity, coronavirus circulation, and inter-host microbial connectivity vary across contrasted land-use contexts. We analysed 700 samples collected from humans, bats, rodents, and poultry in three Cambodian provinces spanning urban, rural, and fragmented forest landscapes. Host-associated bacterial communities were characterized using third-generation full-length 16S rRNA metabarcoding, enabling high-resolution taxonomic assignment. In parallel, animal hosts were screened

for coronaviruses, detecting sarbecoviruses in bats, rodent-associated coronaviruses in rodents, and avian coronaviruses in poultry. Questionnaire data from human participents were used to derive an animal-contact gradient reflecting occupation, domestic animal ownership, and daily exposure practices. Microbiome composition was primarily structured by host taxon, but also varied across land-use categories. Coronavirus infection status did not correlated with microbiome imbalance outside of bats, where inter-individual dispersion in community stucture where found, following the Anna Karerina Principle. Fragmented forest systems were expected to support higher bacterial diversity, consistent with greater environmental heterogeneity, whereas rural sites appeared to concentrate conditions more favorable to zoonotic risk through intensified overlap among humans, livestock, peri-domestic animals, and wildlife. Urban settings generally showed more simplified contact configurations and more distinct host compartmentalization. Human microbiome profiles also varied along the animal-contact gradient, suggesting that daily exposure patterns may contribute to structuring bacterial community composition even in the absence of direct viral screening. To further examine potential exchange pathways, we reconstructed inferred transmission networks among hosts based on microbiome community similarity and microbial taxon sharing. These networks suggested stronger inter-host connectivity in rural landscapes, with rodents occupying central interface positions. Together, these results support a One Health framework in which zoonotic risk is shaped not only by biodiversity patterns, but by the interaction between ecological disturbance, host overlap, and microbial exchange. This study provides an integrative baseline for identifying landscapes where spillover conditions may be amplified in rapidly changing tropical systems.

623 – Healthier Cats, Healthier Communities: A One Health Approach to Cat Management in Singapore

Anhui LIN
National Parks Board, Singapore

Background

Urban cat populations present complex One Health challenges, providing wellbeing benefits through human-animal bonds whilst posing zoonotic risks including rabies, toxoplasmosis and ringworm. Overpopulation and irresponsible feeding practices threaten ecological health through environmental contamination, vector proliferation and biodiversity impact.

Singapore's Cat Management Framework (CMF), launched in September 2024, demonstrates an integrated One Health approach to enhancing animal health and welfare whilst safeguarding public and environmental health.

Methods

The CMF integrates mandatory pet cat microchipping and licensing with national disease surveillance systems, enabling rapid contact tracing and outbreak response whilst enhanced traceability increases owner accountability for animal health and welfare. Sterilisation incentives through reduced lifetime licensing fees help address population control. Recognising that socioeconomic determinants affect human, animal and environmental health outcomes, the Pet Cat Sterilisation Support programme targets lower-income households, whilst free microchipping drives alleviate financial barriers to essential veterinary services.

The Trap-Neuter-Rehome/Release-Manage (TNRM) programme reduces free-roaming populations, decreasing risks of cat-related injuries, vector-associated diseases and environmental faecal contamination. Strong partnership between the government, veterinarians, NGOs and the community underpins the TNRM programme.

Cross-sectoral collaboration between human, veterinary and environmental health authorities, social services and NGOs creates a comprehensive One Health approach that addresses the interconnected challenges of pet ownership, public health protection, animal health and welfare. This integrated framework ensures that responsible pet ownership becomes accessible across all socioeconomic levels whilst maintaining robust disease prevention and population management capabilities.

Comprehensive education and outreach communication initiatives target responsible pet ownership and community cat caregiving through diverse channels including traditional and social media, community

and school events. A mandatory free multilingual online pet ownership course and stakeholder-developed community cat caregiving guidelines build health literacy around zoonotic disease prevention, responsible animal care, and environmental impact reduction.

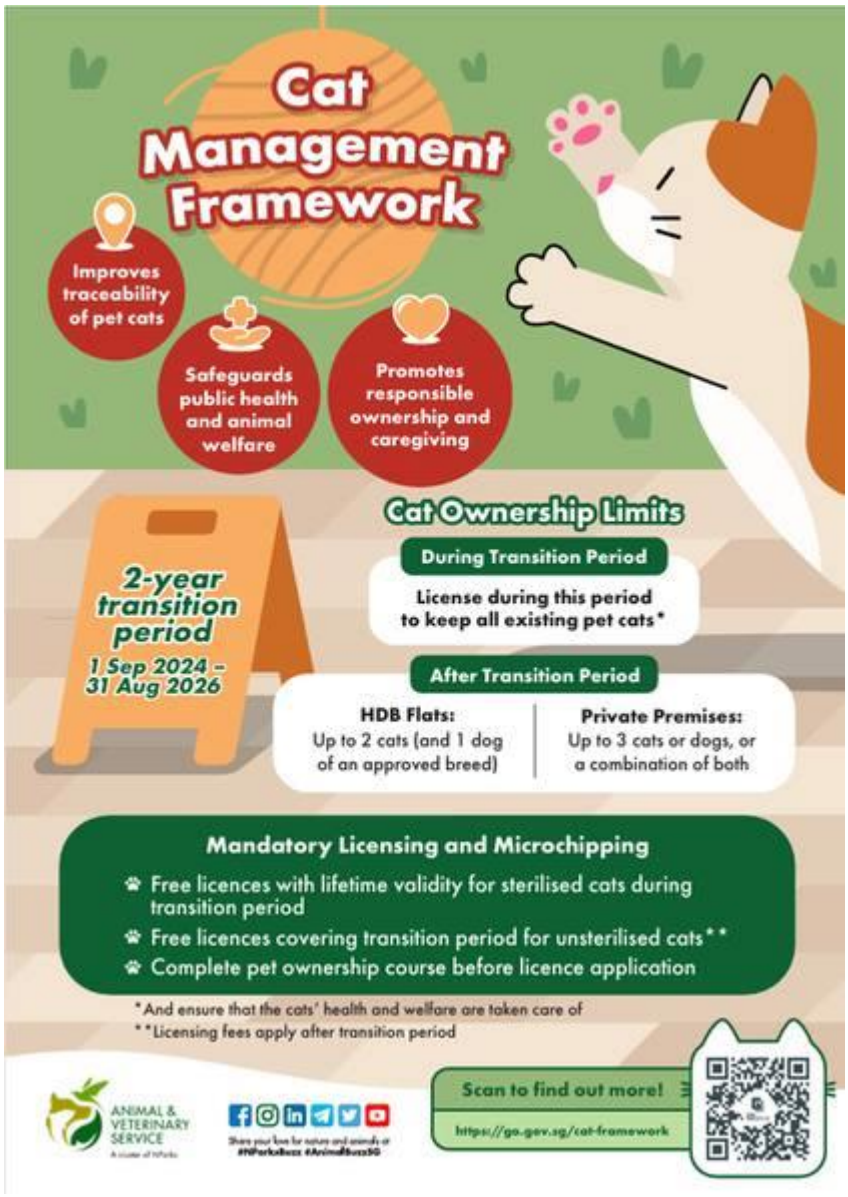
Extensive two-year public consultations incorporating surveys and focus groups with diverse stakeholders ensured robust policy governance. Implementation was informed by Knowledge, Attitudes and Practices studies examining cat ownership and zoonotic disease awareness.

Results

Post-launch outcomes demonstrate significant impact: over 50,000 pet cats licensed with 95% sterilisation rates, over 3,700 cats from lower-income households supported, and over 10,300 cats reached via free microchipping drives. The free-roaming cat population decreased from historical estimates of 60,000 to 13,000 cats. Free-roaming cat population sterilisation rates vary geographically, ranging from 80% in high-rise estates to 20-40% in industrial and low-rise residential areas, highlighting the need for targeted interventions.

Conclusions

Singapore’s CMF exemplifies effective One Health integration in urban animal management. Success stems from multi-sectoral partnerships spanning government health and environmental agencies, veterinary industry, NGOs and communities. The framework's evidence-based approach, combining regulatory measures with support programmes and education, provides a replicable model for urban cat management globally. Sustained success requires continued transdisciplinary collaboration, targeted behavioural interventions and adaptive management strategies.


Cat Management Framework
Improves traceability of pet cats
Safeguards public health and animal welfare
Promotes responsible ownership and caregiving
2-year transition period
1 Sep 2024 – 31 Aug 2026
Cat Ownership Limits
During Transition Period
License during this period to keep all existing pet cats*
After Transition Period
HDB Flats:
Up to 2 cats (and 1 dog of an approved breed)
Private Premises:
Up to 3 cats or dogs, or a combination of both
Mandatory Licensing and Microchipping
Free licences with lifetime validity for sterilised cats during transition period
Free licences covering transition period for unsterilised cats**
Complete pet ownership course before licence application
*And ensure that the cats' health and welfare are taken care of
**Licensing fees apply after transition period
ANIMAL & VETERINARY SERVICE
Scan to find out more!
https://go.gov.sg/cat-framework

631 – Manure-Driven Spread of Antibiotic Resistance Across the Soil–Plant Continuum

Fang WANG, Mariko FUJISAWA, Maria HEILING, Gerd DERCON
International Atomic Energy Agency, Austria

Background

Antimicrobial resistance (AMR) is a major One Health challenge linking environmental, animal, and human health. Agricultural reuse of livestock manure as fertilizer represents an important pathway for the dissemination of antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) into soils and crops, potentially threatening food safety and public health. However, the mechanisms governing antibiotic persistence, ARG transmission, and plant-mediated exposure across the manure–soil–plant continuum remain poorly understood. This study investigated the fate of antibiotics and the dynamics of ARGs across agricultural systems.

Methods

A combination of pot, field, metagenomic, and hydroponic experiments was conducted. Pot trials examined ARG accumulation in carrot rhizosphere, phyllosphere, and tubers following pig manure amendment. Field-scale isotope tracing using 13C-labeled sulfamethoxazole assessed antibiotic fate and ARG responses in lettuce systems with and without swine manure. Paddy field monitoring evaluated ARG dynamics in soil, rice roots, and grains across crop growth stages after compost application. Metagenomic analyses combined with 13C-DNA stable isotope probing identified antibiotic-degrading bacteria (ADB), while hydroponic experiments tested the effect of manure sterilization on endophytic ARGs, MGEs, and pathogens.

Results

Manure application significantly enriched ARGs in carrot rhizosphere and phyllosphere microbiomes and increased ARG bioaccumulation in carrot tubers by up to 124-fold. Estimated daily human ARG intake from manured carrots reached ~3 × 107 gene copies, whereas peeling reduced exposure by 28–91%. In field experiments, 13C-sulfamethoxazole dissipated rapidly in non-planted soils (>98% within 180 days) but accumulated in rhizosphere zones and translocated to lettuce leaves. Co-application with manure increased soil ARG abundance up to 5.35-fold and root enrichment 2.38-fold, with MGEs identified as the primary drivers ($\beta = 0.88$). Compost application elevated ARG abundance in soil and rice roots but did not significantly affect rice grains. Stable isotope probing revealed that antibiotic-degrading bacteria harbored diverse ARGs co-localized with MGEs and degradation genes. Manure sterilization reduced endophytic ARG and MGE subtypes by 50–86% and decreased pathogen abundance.

Conclusions

Manure fertilization promotes AMR dissemination through antibiotic persistence, MGE-mediated transfer, and plant uptake. Although antibiotic residues dissipate rapidly, ARGs persist in plant-associated microbiomes and may contribute to human exposure via food consumption. Integrated mitigation strategies, including manure sterilization and post-harvest processing, are essential to reduce AMR risks at the human–animal–environment interface.

---

632 – The Need for Integrated One Health Approaches in Humanitarian Crises: Going Beyond Livestock Vaccination to Safeguard Livelihoods, Food Security, and Food System Resilience in Sub-Saharan Africa

Shauna RICHARDS (1), Biruk Alemu GEMEDA (2), Wudu Temesgen JEMBERU (2), Guy S ILBOUDO (3), Edward Abworo OKOTH (1), Buke Yussuf WAKO (1), Michel DIONE (4), Theo KNIGHT-JONES (2)

1: International Livestock Research Institute, Kenya; 2: International Livestock Research Institute, Ethiopia; 3: International Livestock Research Institute, Burkina Faso; 4: International Livestock Research Institute, Mali

Background

Humanitarian crises, driven by drought, flooding, and conflict in Sub-Saharan Africa disrupt livestock-based livelihoods essential to small-scale livestock keepers. Livestock vaccination is often one of the primary interventions used to protect food and income sources for smallholder households.. This study examined the role and limitations of emergency livestock vaccination during crises and explored perceptions of livestock keepers on approaches that could enhance resilience, food security, and sustainable livestock systems.

Methods

A retrospective cohort design using mixed methods was applied across five sites: Kenya (n=2), Ethiopia (n=2), and Burkina Faso (n=1), using participatory epidemiology to assess vaccine interventions during crises. Data collection included key informant interviews, focus group discussions, and livestock keeper surveys. Thematic analysis of qualitative data and summary statistics of quantitative data were completed.

Results

In Burkina Faso, conflict compounded by climate shocks prompted a peste des petits ruminants (PPR) vaccine campaign. In Ethiopia and Kenya, drought and flooding triggered mixed ruminant vaccinations. Quantitative data showed weak evidence of reduced morbidity and mortality in vaccinated livestock, with increased household income; however, causality was limited by confounding. Thematic analysis revealed perceived benefits to livelihoods and disease control, but highlighted barriers: limited coverage, exclusion of women and marginalized groups, cold chain failures, funding delays, and weak follow-up. Success was linked to community and government engagement, mobile delivery, and shorter data driven campaigns. Integrated programs combining feed/water/market support, food aid, and WASH support alongside vaccines were most valued by beneficiaries. While emergency livestock vaccination can mitigate disease and protect livelihoods, its impact is maximized when implemented proactively within national frameworks, and strengthens rather than undermines delivery of routine animal health services and vaccination. Emergency funding should support broader stakeholder needs, while maintaining resources for preventive vaccination campaigns that operate beyond crisis timelines.

Conclusions

Emergency livestock vaccination alone offers variable short-term protection but insufficiently contributes to livelihood resilience in complex humanitarian settings. One Health approaches; linking veterinary, human health, and environmental interventions, are critical to achieve sustainable recovery and food-system stability. Embedding vaccination within national One Health and animal health frameworks, alongside crisis-response systems can maximize impact, improve gender inclusion, and reduce long-term vulnerability. Future humanitarian funding for livestock-based livelihoods should prioritize integrated, anticipatory programs that address the shared health determinants of people, animals, and ecosystems.

636 – Population-Level Human-Animal Contact and Wet Market Use in Thailand and northern Ghana: Implications for Zoonotic Spillover

Katy STOKES (1), Eliasu MUMUNI (2), Juthatip WIWATTANAPANTUWONG (3), Michael HEAD (4), Robin GOODWIN (1)
1: University Of Warwick, United Kingdom; 2: University for Development Studies, Ghana; 3: Chulalongkorn University, Thailand; 4: University of Southampton, United Kingdom

Background
Wet markets have been central to zoonotic spillover debates, yet empirical evidence on population-level use and human-animal contact remains limited, especially in low- and middle-income countries. This study investigates wet market engagement and animal practices in Thailand and northern Ghana, with attention to the species and interfaces relevant to zoonotic risk.

Methods
Cross-sectional, in-person surveys were conducted (June-August 2025) among adults in Thailand (n=2000) and northern Ghana (n=2343). Survey domains captured wet market attendance (where live and/or dead animals were sold), frequency of animal contact, species purchased or reared, market characteristics, and infection-related perceptions. Analyses included descriptive statistics and country-specific logistic regression models to identify determinants of wet market attendance.

Results
Patterns of human-animal contact varied across settings. Wet market attendance was higher in Thailand (85.4%; n=1690) than Ghana (29.3%; n=686), yet Ghanaian respondents reported more frequent animal contact at markets, with 29.4% touching animals three or more times per visit compared with 8.8% in Thailand. In both Ghana and Thailand many participants reported visiting markets several times per week (Ghana 54.0%; Thailand 46.9%). Visits were longer in Ghana, 1-3 hours (48.0%), in Thailand most visits lasted less than one hour (71.0%).

In Thailand, only 2.9% of marketgoers purchased live animals (primarily frogs [2.2%] and chickens [0.7%]) illustrating a narrow taxonomic interface dominated by amphibians and poultry. In Ghana, live animal purchasing was widespread among marketgoers (97.4%) and non-marketgoers (86.1%), predominantly involving domesticated birds (chicken 50.1%, guinea fowl 36.9%, duck 3.1%) and grazing mammals (cow 30.3%, goat 28.6%, sheep 21.5%), species associated with a broad range of zoonotic pathogens. Market structures also diverged: Ghanaian markets were mainly outdoor (93.8%), whereas Thai markets were predominantly indoor (83.0%), shaping different ecological exposure contexts.

Determinants of wet market attendance further differentiated risk pathways. Thai market attendance was more likely among females (odds ratio 1.48 [95% CI 1.15-1.90]) and respondents with higher infection worry (1.64 [1.38-1.96]) and lower perceived control (0.78 [0.64-0.96]), whereas Ghanaian attendance aligned with lower infection worry (0.84 [0.76-0.94]), larger household size (1.03 [1.01-1.06]), and extensive home animal rearing (1.42 [1.16-1.75]). Preventive practices reflected these findings: masks and handwashing were more common in Thailand (94.0% vs 42.1 and 82.0% vs 26.4%), while species-specific inspection of animals before purchase was more prevalent in Ghana (51.3% vs 16.1%).

Conclusions
Wet markets represent heterogeneous human-animal interfaces shaped by local ecologies, species assemblages, and behaviour. While attendance was higher in Thailand, Ghanaian marketgoers reported more frequent contact and engagement with live animals, particularly domesticated birds and grazing mammals. These findings suggest that zoonotic exposure is shaped less by wildlife trade than by routine livestock contact across markets and households, highlighting the need for context specific One Health surveillance and risk mitigation strategies.

640 – Four Years of Genomic Surveillance of SARS-CoV-2 in Mecklenburg-Western Pomerania, Germany (November 2021–January 2025): Variant Dynamics and Robust Identification of Viral Recombinants

Anne POHLMANN (1), Ana TZVETKOVA (2), Kathrin LEHMANN (3), Martin BEER (1), Lars KADERALI (2), Nils-Olaf HÜBNER (4), Karsten BECKER (3), Christian KOHLER (3)

1: Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Greifswald - Insel Riems, Germany; 2: Institute of Bioinformatics, University Medicine Greifswald · University of Greifswald, Greifswald, Germany; 3: Friedrich Loeffler-Institute of Medical Microbiology, University Medicine Greifswald, Greifswald, Germany; 4: Central Unit for Infection Prevention and Control, University Medicine Greifswald, Greifswald, Germany

Background

Whole-genome sequencing (WGS) of SARS-CoV-2 is a cornerstone of epidemic surveillance, enabling early detection of emerging variants and supporting public health decision-making. In Germany's federal system, the states are responsible for diagnostics, sampling, metadata collection, and implementation of control measures. The CoMV-Gen project was established in Mecklenburg-Western Pomerania to strengthen regional genomic surveillance through coordinated collaboration between diagnostic laboratories, university hospitals, and public health authorities.

Methods

Clinical samples were selected based on epidemiological relevance and quality criteria and subjected to rapid nanopore-based WGS using harmonized and continuously updated protocols. Sequencing strategies were repeatedly adapted to account for emerging variants and primer mismatches.

Genomic analyses included lineage assignment according to international nomenclature systems, mutation profiling, and time-resolved phylogenetic reconstruction. Recombinant genomes were identified using a multi-step validation approach combining breakpoint analysis with automated and manual inspection of raw sequencing data to distinguish true recombination events from coinfections or laboratory artefacts.

Results

Over a period of more than 50 months, 6,853 SARS-CoV-2 genomes were generated from all counties of Mecklenburg–Western Pomerania, providing a comprehensive overview of regional variant dynamics. Our previous genomic epidemiological analysis covering 2020–2022 demonstrated repeated viral introductions and rapid lineage turnover despite low population density (Kohler et al., 2023, https://dx.doi.org/10.1080/22221751.2023.2245916). As pandemic activity persisted beyond 2022, surveillance was extended through 2025 to capture ongoing evolutionary dynamics.

Successive epidemic waves were characterized by selective sweeps and rapid variant replacement. Delta (21J) temporarily dominated before being displaced by Omicron clades (21K/BA.1, 21L/BA.2, 22B/BA.5), illustrating pronounced intra-variant turnover and strong evolutionary advantages of emerging lineages. Phylogenetic reconstruction revealed both localized clusters and broader regional transmission patterns.

Beyond routinely classified recombinant forms, we identified several previously undescribed SARS-CoV-2 recombinants. Using a stringent multi-layer validation workflow, including systematic breakpoint analysis and detailed manual interrogation of underlying raw sequencing reads, we robustly confirmed true recombination events and unequivocally excluded artefacts arising from coinfections, sequencing errors, or laboratory contamination. This in-depth raw data analysis, extending beyond automated lineage assignment tools, ensured high-confidence characterization of novel recombinant genomes and highlights the added value of meticulous genomic surveillance.

Conclusion

The sustained expansion of molecular surveillance from the early pandemic phase through 2025 underscores the importance of long-term, adaptive sequencing infrastructures beyond acute crisis response. The close integration of routine diagnostics, specialized sequencing facilities, and public health authorities enabled continuous high-resolution monitoring of variant dynamics at the regional level.

Importantly, the combination of harmonized laboratory workflows with in-depth raw data interrogation not only enabled timely detection of variant replacement, but also allowed for high-confidence identification of rare and novel recombinant lineages beyond automated classification approaches. This coordinated and quality-controlled surveillance framework provides a robust model for resilient genomic preparedness against future emerging pathogens.

646 – Developing a One Health Platform: What a Knowledge Broker Can Contribute

Barbara KOVACS, Monika MATT, Elena DE MARTIN
Austrian Agency for Health and Food Safety (AGES), Austria

Background Within the scope of the co-funded European project RAISE (Reinforcing Austrian Integrated Surveillance and Epidemiology), one work package is developing a One Health (OH) surveillance platform for the Austrian agency for Health and Food Safety (AGES) to integrate human, animal, food, and environmental data for risk assessment, outbreak visualization, and early warning/decision support. While the multidisciplinary setting is a strength, dispersed teams, divergent routines, and vocabulary gaps hinder data sharing and coordinated action. We therefore introduced a "knowledge broker" function—bridging domain experts and IT—to align language, expectations, and requirements and to de-risk platform design.

Methods Using a mixed bottom-up/top-down approach, we convened regular interdisciplinary meetings (epidemiology—human & veterinary, medicine, mathematics, sociology/anthropology, economics, biology, and IT). Short pulse surveys and an open collaboration-notes space captured terminology conflicts and elicited requirements. We iteratively curated a shared, living glossary and ran individual ranking exercises (via online forms) followed by plenary discussions to surface discipline-specific "blind spots" in pathogen prioritization. The knowledge broker facilitated sense-making, terminology harmonization, and translation of user needs into technical specifications.

Results A living glossary with initial 17 terms have been established—an unprecedented cross-unit artifact at AGES—documenting where consensus exists and where it does not. For example, "real-time data" spanned responses from ~1 second to ~1 month; "one week" was most frequent, underscoring why ambiguous terms must be operationally defined. Moreover, "platform" itself meant different things to different groups: a data-integration backend, a collaboration space, a public-facing simple tool, or an expert analytical environment. Ranking exercises showed discipline-dependent priorities for zoonotic pathogens, revealing predictable—and remediable—blind spots. These findings guided initial governance for definitions, user-group–specific views, and decision-support requirements.

Conclusions Building an OH platform is as much a socio-technical challenge as a technical one. Early, structured knowledge brokering measurably improves shared language, reduces requirement risk, and surfaces cross-disciplinary blind spots—foundational steps toward interoperable surveillance, clearer alerts, and actionable decision support. We recommend embedding a knowledge broker role (with mandate and methods) in OH IT projects, maintaining a living glossary as a formal deliverable, and treating terminology governance as core infrastructure, not documentation.

---

652 – Bridging Commitments and Capabilities: Support Mechanisms for the Implementation of the Biological Weapons Convention

Sylvain FANIELLE, Remi BACOUILLARD, **James PETTIT**
United Nations Office for Disarmament Affairs, Switzerland

In 2025, the Biological Weapons Convention (BWC), the first disarmament treaty banning an entire category of weapons of mass destruction, celebrated its 50th anniversary. With rapidly advancing technologies and evolving dynamics within the international security framework, the BWC is more relevant than ever and constitutes the sole legally binding instrument addressing the threat of biological weapons.

In such a context, the United Nations Office for Disarmament Affairs (UNODA) actively supports the universalization and effective implementation of the BWC through targeted capacity-building and practical assistance to States. Its efforts focus on strengthening national capacities to prevent, detect, and respond to biological threats, including by helping countries to develop comprehensive legislative frameworks and enhance inter-agency coordination. Relying on tailor-made and innovative approaches to assistance delivery, UNODA's support also fosters expert networks and peer-to-peer exchanges that promote knowledge sharing and technical cooperation among States, while collaborating with regional and international organizations.

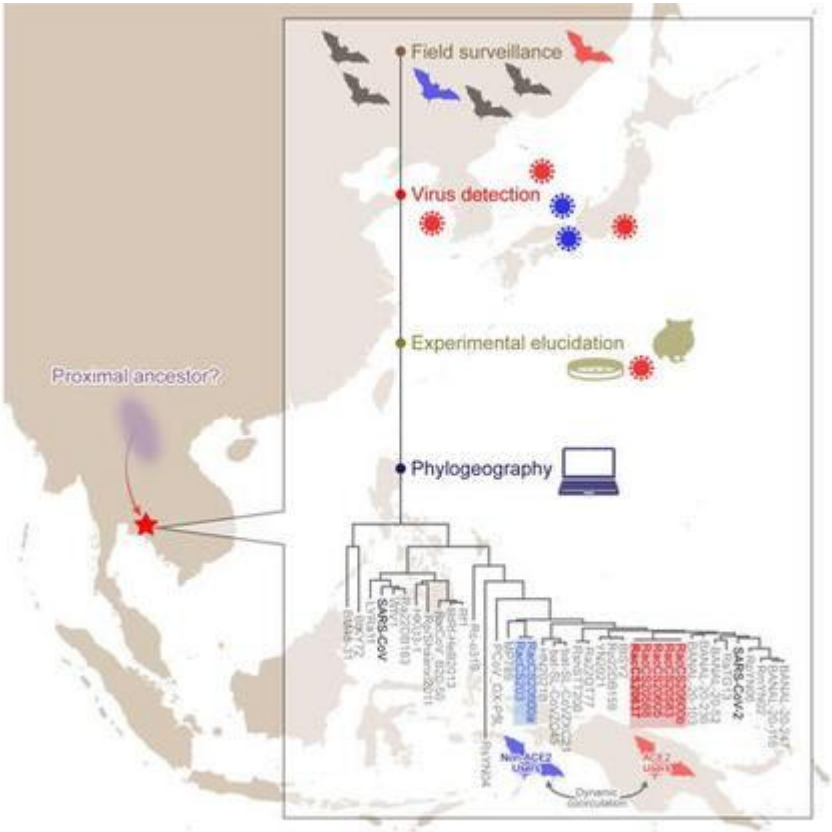
Based on its experience, UNODA will provide an overview of challenges pertaining to BWC implementation as well as the related good practices and lessons learned that contribute to both the full realization of the BWC's objectives and the strengthening of global health and security resilience.

658 – Virological characteristics of SARS-CoV-2-related coronaviruses dynamically circulating in Southeast Asia

Wilaiporn SAIKRUANG (1), Spyros LYTRAS (1), Supaporn WACHARAPLUESADEE (2), Opass PUTCHAROEN (2), Arnon PLIANCHAISUK (1), **Kei SATO** (1)

1: The University of Tokyo, Japan; 2: Thai Red Cross Emerging Infectious Diseases Clinical Center, King Chulalongkorn Memorial Hospital, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand

Following the emergence of SARS-CoV-2 in humans, the scientific community has ramped up its efforts to better understand the biology, ecology and spillover risk of SARS-CoV-2-related viruses (SC2r-CoVs), primarily circulating in horseshoe bats. Here, we present a holistic approach to going from field sampling to experimental, phylogenetic, and ecological characterization of novel SC2r-CoVs. We sampled acuminate horseshoe bats from an artificial cave in Thailand and identified two SC2r-CoV lineages co-circulating in the same population. Our sampling identifies the first co-infection of an ACE2- and a non-ACE2-using SC2r-CoV, raising important implications about the interactions between related coronaviruses that utilize different entry receptors. Despite the new ACE2-using virus's ability to bind to human ACE2, it exhibits reduced fusogenicity and replication *in vitro*, and lower pathogenicity and transmissibility in hamsters compared to SARS-CoV-2, highlighting the latter's key biological differences to its bat-infecting relatives. Finally, we implemented a state-of-the-art phylogeographic approach to trace the movement of the bat SC2r-CoVs presented here across their evolutionary history. We show that some of their genomic segments recently moved from Laos to Thailand, reinforcing the notion that SC2r-CoVs continuously travel across their host ranges in Southeast Asia. The multi-faceted approach we employ here provides comprehensive insights into the biology and ecology of the viruses closest to SARS-CoV-2 and paves the way for effectively assessing the spillover potential of animal viruses.



Understanding the evolutionary trait and virological characteristics of SARS-CoV-2-related coronaviruses

661 – Beyond Construction: Sustaining High-Containment Laboratories in LMICs through One Health Governance

Hokkean LIM (1), Wuchlim KOURK (1), Sema KONG (1), André SPIEGEL (1), Heidi AUERWALD (2), Erik A KARLSSON (1)

1: Institut Pasteur du Cambodge, Cambodia; 2: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (IZSAM), Teramo, Italy

Background: Biosafety and biosecurity are foundational pillars of the One Health framework, particularly in regions where interactions among humans, animals, and ecosystems increase the risk of zoonotic disease emergence and spillover. Biosafety Level 3 (BSL-3) laboratories provide critical containment infrastructure for the detection, surveillance, and research of airborne and high-consequence pathogens. Over the past two decades, international investments have expanded high-containment laboratory capacity in low- and middle-income countries (LMICs). However, long-term operational sustainability remains a major challenge once initial construction and donor support conclude. This study examines the sustained operation of the BSL-3 laboratory at the *Institut Pasteur du Cambodge* (IPC) as a potential governance model for sustaining high-containment laboratory capacity in LMIC settings.

Methods: A governance performance analysis framework was applied to assess the sustainability of the IPC BSL-3 laboratory across four operational domains: regulatory alignment, engineering reliability, workforce capacity, and institutional resource mobilization. Institutional documentation, including internal audit reports, maintenance records, equipment performance verification reports, and staff training activities, was reviewed to evaluate operational continuity, compliance with biosafety standards, and containment integrity.

Results: The IPC BSL-3 laboratory has maintained continuous operation for nearly two decades through internally mobilized institutional resources and integrated technical management systems. Preventive maintenance protocols support critical containment infrastructure, including HVAC pressure-cascade systems, HEPA filtration units, biosafety cabinets, effluent treatment systems, and environmental monitoring platforms. Regular internal audits, emergency preparedness exercises, and multidisciplinary training programs strengthen operational resilience and staff competence. Dedicated engineering and metrology teams support equipment calibration, performance validation, and lifecycle management. Infrastructure redundancy, including diesel generators and uninterruptible power supply systems, mitigates power instability commonly encountered in LMIC contexts. In December 2025, IPC achieved ISO 35001:2019 certification for biorisk management, reflecting the institutionalization of international biosafety standards and performance-based governance.

Conclusions: The Cambodian experience demonstrates that sustainable high-containment laboratory systems require more than infrastructure investment alone. Long-term functionality depends on institutional ownership, integrated technical expertise, preventive maintenance systems, and robust governance structures. Embedding high-containment laboratories within broader One Health governance frameworks can strengthen national and regional preparedness for emerging zoonotic threats. This model provides practical lessons for LMICs seeking to develop resilient laboratory systems that support global health security.

663 – Integrated framework to improve the effectiveness of interventions against rabies and dracunculiasis in sedentary and nomadic communities of the province of Moyen-Chari in Chad

Madjadinan ALLADOUMNGAR (1,2,3), Ndèye Marème SOUGOU (2,3), Kathrin HEITZ-TOKPA (4), Gilbert FOKOU (4), Bassirou BANFOH (4), Jakob ZINSSTAG (5,6), Monique LECHENNE (5,6)

1: Centre de Support en Santé Internationale, N'Djamena, Tchad; 2: Ecole doctorale des sciences de la vie, de la santé et de l'environnement, Dakar, Sénégal; 3: Département de santé publique, Université Cheik Anta Diop de Dakar, Dakar, Senegal; 4: Centre Suisse de Recherches Scientifiques, Abidjan, Côte d'Ivoire; 5: Department of Epidemiology and Public Health, Swiss Tropical and Public Health Institute, Basel, Switzerland; 6: University of Basel, Basel, Switzerland

Background: This study explored the interactions between human and animal health governance to improve the control of this zoonosis in sedentary and nomadic communities in two districts of Moyen-Chari in Chad at the examples of rabies and dracunculiasis, both endemic in this area.

Method: A cross-sectional mixed-methods study was conducted in December 2025, involving 37 human and 3 animal health facilities. Quantitative data was collected from 106 human and 8 animal health professionals on socio-professional characteristics, job satisfaction, knowledge, attitudes, and practices related to rabies and dracunculiasis, as well as resource availability and inter-sectoral collaboration. Clinical data from 80 cases (bite exposures, rabies and dracunculiasis cases) were collected from health facilities. Semi-structured interviews were conducted with 23 community members and 12 health governance stakeholders. Quantitative data was analyzed using R, while interview transcripts were analyzed through thematic content analysis in NVivo 12.

Results: Human health professionals are generally younger and more gender-balanced, whereas animal health professionals tend to be older, predominantly male, and have approximately twice as much professional experience. The male–female ratio was 49.1% in human health and 87.5% in animal health. These ratios are reflected in the refusal of nomadic women to interact with veterinary men for the observation of a dog or to treat a sick ruminant.

Regarding work satisfaction there is a notable difference between health sectors, 95% of human health workers are associated with positive satisfaction, while 75% of their animal health colleagues remain less satisfied. The capacity assessment revealed that the availability of equipment is very limited in animal health structures compared to human health facilities (exp. cold chain lacking in 5% in human health compared to 75% in animal health facilities), highlighting the under-funding of the animal sector also deplored by heads of veterinary posts. Collaboration analysis showed stronger internal collaboration within health centre, while intersectoral collaboration between human and animal health sectors was weaker. Health centres act as frontline structures against zoonoses, but veterinarians are the main drivers encouraging intersectoral collaboration.

Health records showed an average of reported 3.2 bite cases per facility per month (95% CI: 2.4–4.2). Compared with incidence estimates from previous studies, this suggests significant underreporting. Veterinary registries recorded only 29 dogs placed under observation despite 49 reported bite cases, illustrating weak follow-up. Two human and 17 animal guinea worm cases have been documented jointly by human health and the Guinea worm program, including, the animal sector being under-involved.

Conclusion: This study identifies major resource and governance gaps that hinder effective One Health communication and integrated zoonotic disease control in rural Chad. Particularly the veterinary sector, showing a high motivation for intersectoral collaboration should be strengthened to be able to fully assume its role.

670 – Divergent Spatiotemporal Dynamics of Co-Circulating Arboviruses in Brazil, 2014-2024: A Comparative Epidemiological Analysis of Dengue, Chikungunya, and Zika Under Shared Climate and Vector Pressures

Julienne REYNOLDS, Kim STEVENS

Royal Veterinary College, London, United Kingdom

BACKGROUND

Brazil bears one of the highest global arboviral burdens, with dengue, chikungunya, and Zika virus co-circulating under shared *Aedes aegypti* ecology and overlapping climatic drivers. Despite a common transmission system, these arboviruses differ in epidemic history, clinical profile, and surveillance maturity—creating a unique opportunity to disentangle shared environmental drivers from pathogen-specific factors. Understanding their comparative spatiotemporal dynamics is essential for climate-sensitive, integrated arboviral surveillance and control.

METHODS

A retrospective ecological analysis of dengue, chikungunya, and Zika virus was performed across Brazil's 27 federative units from 2014 to 2024 using case data from Sistema de Informacao de Agravos de Notificacao (SINAN) and population denominators from Insituto Brasileiro de Geografia e Estatistica

(IGBE). Annual and monthly incidence rates (per 100,000) and standardized morbidity ratios (SMRs) were calculated by virus and state. Spatial autocorrelation was assessed using Global and Local Moran's I.

RESULTS

Dengue dominated arboviral burden (767.3 per 100,000 per year, 2017–2024), exceeding chikungunya more than four-fold (104.4) and Zika thirteen-fold (13.6). Coinciding with El Niño conditions, Dengue incidence reached a historic peak of 3,038.6 per 100,000 in 2024. All three arboviruses shared February-to-May seasonal peaks aligned with Brazil's rainy season; Zika peaked earliest, followed by dengue, then chikungunya—consistent with differing extrinsic incubation periods in *Aedes aegypti*. Large dengue outbreaks consistently followed El Niño years (2015–2016, 2018–2019, 2023–2024). Southern states remained consistently low across all three viruses, reinforcing a north-south climate gradient in transmission risk. There was statistically significant high-high spatial clustering of dengue in Goiás (SMR 2.6), Distrito Federal (2.2), and Minas Gerais (2.1) with twice as many cases observed as expected. Global autocorrelation was not statistically significant for chikungunya or Zika. Chikungunya SMRs peaked in Ceará (3.4) and Tocantins (3.0) before progressive geographic expansion toward the Central-West and Southeast (2022–2024), with Mato Grosso do Sul reaching SMR 11.4 by 2024, increasingly mirroring dengue's high-burden geography. Despite low absolute incidence, Zika demonstrated the highest state-level SMR in the dataset (Tocantins, 5.7), underscoring the value of population-standardized metrics.

CONCLUSIONS

Despite sharing an ecological niche and a single primary vector, dengue, chikungunya, and Zika display distinct spatiotemporal signatures possibly shaped by the interplay of climate, vector dynamics, host immunity, and surveillance capacity. Shared seasonality support climatological conditions—potentially mediated through *Aedes aegypti* population dynamics—as key drivers of transmission across all three viruses. Chikungunya's expanding geographic footprint signals a transition toward dengue-like burden patterns. Ongoing incorporation of 2025 data will further elucidate patterns which may be disrupted by the 2023 dengue state of emergency. Integrated, climate-aware, multi-pathogen surveillance is urgently needed to anticipate co-epidemic risk, particularly as climate change continues to expand suitable vector habitats across Brazil and globally.

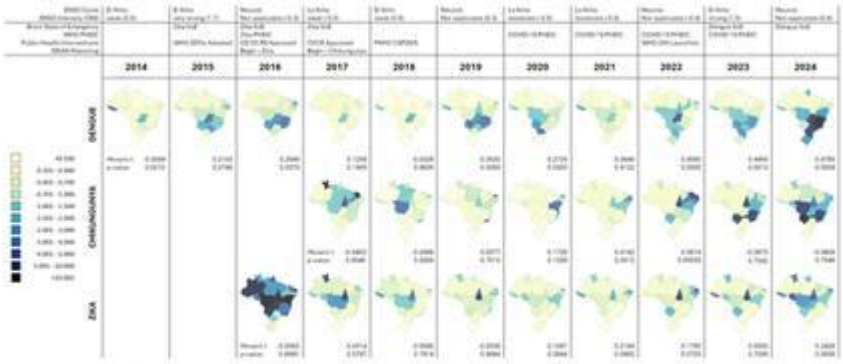


Figure 9: Annual standard morbidity ratios of dengue, chikungunya, and Zika virus, Brazil (2014-2024). *Grid of choropleth maps showing annual standard morbidity ratios for each virus by state from 2014-2024. Each row represents one virus; each column represents a calendar year. Immediately below each map is its corresponding Global Moran's I (top value) and associated p-value (bottom value). A single shared legend is used across all maps. The figure includes a header indicating a given year's ENSO phase and intensity, national states of emergency, WHO PHEIC declarations, public health intervention milestones, and changes to SINAN reporting. Standard morbidity ratios were calculated using case data from Sistema de Informação de Agravos de Notificação (SINAN) and populations estimates from Brazilian censuses.*

Figure 10: Monthly standard morbidity ratios of dengue, chikungunya, and Zika virus, Brazil (2014-2024). *Grid of choropleth maps showing monthly standard morbidity ratios for each virus by state from 2014-2024. Each row represents one virus; each column represents a calendar month. Immediately below each map is its corresponding Global Moran's I (top value) and associated p-value (bottom value). A single shared legend is used across all maps. The figure includes a header with seasonal, climatic, and meteorological average for each month, including temperature, precipitation, humidity, atmospheric pressure, and wind speed. Standard morbidity ratios were calculated using case data from Sistema de Informação de Agravos de Notificação (SINAN) and populations estimates from Brazilian censuses.*

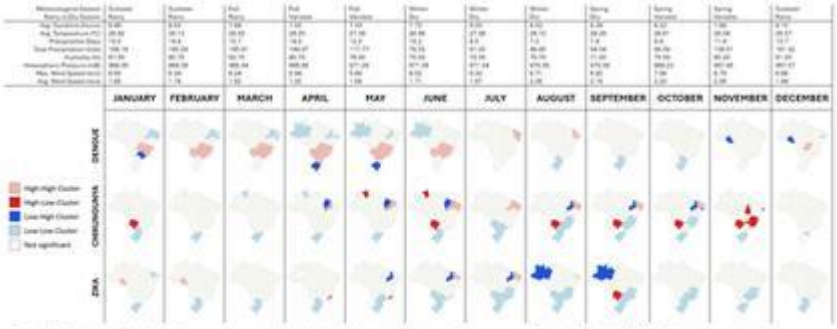


Figure 13: Anselin Local Moran's I cluster maps for monthly standard morbidity ratios of dengue, chikungunya, and Zika virus, Brazil (2014-2024). *A grid of local Moran's I cluster maps depicting spatial associated for monthly standard morbidity ratios by state for each virus. Each row represents one virus; each column represents a calendar month. A single shared legend is used across all maps. The legend classifies clusters into High-High, Low-Low, High-Low, and Low-High spatial associations. The figure includes a header with seasonal, climatic, and meteorological average for each month, including temperature, precipitation, humidity, atmospheric pressure, and wind speed. Standard morbidity ratios were calculated using case data from Sistema de Informação de Agravos de Notificação (SINAN) and populations estimates from Brazilian censuses.*

677 – A National Mentoring and Skills Development Training Program in One Health

Wilson RUMBEIHA, Laura VANWINKLE, LaCole BLACKSHIRE
University of California Davis, United States of America

Background and Purpose: Action Track 6 of the One Health Joint Plan of Action calls for integrating the environment into One Health. while Action 6.4 calls for development of transdisciplinary One Health (OH) training programs. Currently, OH is facing a major challenge: the lack of engagement of toxicologists and/or people with toxicology knowledge in OH transdisciplinary research and practice. This is partly due to inadequate training of toxicologists in skills essential for successful transdisciplinary OH research and/or a lack of awareness of opportunities in this field, as OH is not offered as a major at most undergraduate institutions. The University of California, Davis is leading a consortium of institutions including the Society of Environmental Toxicology and Chemistry (SETAC), Meharry Medical College, and Iowa State University to develop a national mentoring and skills development training grant in One Health (MSDT One Health). The program targets early career scientists and undergraduate students in STEM fields.

Methods: MSDT-One Health has three specific aims (SA). SA1: Develop and deliver a year-long mentoring program for STEM undergraduate students. SA2: Develop and deliver a year-long professional development training and mentoring program for early career scientists (Post-docs, Fellows, Project Scientists, Assistant Professors) to increase their awareness of the opportunities in OH research and to increase their knowledge and ability to obtain funding necessary to conduct OH research, including community-engaged toxicology research. SA3: Develop case studies and e-modules at the intersection of OH and toxicology and make them freely available globally. The program, which is mostly virtual, is delivered through a combination of assigned modules and case studies, in-person and virtual workshops, webinars, attendance at a national OH conference, and 1:1 mentoring with near peer and senior mentors. Training duration is 1 yr.

Results: In Yr1 (2025- 2026) we trained 20 undergraduate mentees, and 9 early-career scientists, from across the United States. Yr 2 recruitment (2026-2027) is currently ongoing and will conclude in April 2026. Training includes a 1-wk workshop on transdisciplinary and community based research, grant writing workshops, assigned case studies and modules, and webinar attendance.

Conclusions: Expected outcomes include a) a total of 100 undergraduate students mentored in OH with a toxicology emphasis; b) 5-10 early career scientists securing intramural seed funding and 2-3 early career scientists securing extramural funding to conduct OH research with community engagement components; c) development of highly interactive case studies in one environmental health toxicology (5) and learning modules on OH (3) to be widely available for training undergraduates and early career researchers. Ultimately, this research education program in OH and toxicology will strengthen the biomedical research enterprise by increasing the number of scientists with the necessary knowledge, skills and networks to engage in transdisciplinary OH research. Supported by NIGMS R25GM160671

682 – Seasonal and Spatial Dynamics of Enterococcus and Antimicrobial Resistance in a One Health Dairy Ecosystem in Western Canada

Shawn HOOGSTRA (1), Cassandra KLAAS (1), Jillaine KUELKER (1), David MAHONEY (1,2), Mark LUBBERTS (3), Catherine CARRILLO (4), Alyssa GOLDEN (5), Irene MARTIN (5), Tim MCALLISTER (6), Rahat ZAHEER (6), **Rhiannon WALLACE** (1)

1: Agassiz Research and Development Center, Agriculture and Agri-Food Canada, Agassiz, BC, Canada; 2: Department of Community Health and Epidemiology, Faculty of Medicine, Dalhousie University, Halifax, NS, Canada; 3: Summerland Research and Development Center, Agriculture and Agri-Food Canada, Summerland, BC, Canada; 4: Ottawa Laboratory (Carling), Canadian Food Inspection Agency, Ottawa, Ontario, Canada; 5: National Microbiology Laboratory Branch, Public Health Agency of Canada, Winnipeg, MB, Canada; 6: Lethbridge Research and Development Center, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada

Antimicrobial resistance (AMR) in *Enterococcus* poses an emerging One Health concern due to its capacity for environmental persistence and cross-sector transmission. This two-year longitudinal study investigated the spatial and seasonal distribution of *Enterococcus* across interconnected animal, environmental, and human wastewater compartments in a peri-urban region of western Canada. We aimed to i.) characterize *Enterococcus* species across varying stages of dairy cow maturity, farm environments and nearby municipal wastewater systems and ii.) determine the AMR profiles and genomic relationships of *E. faecalis* and *E. faecium*. Among the 1,133 *Enterococcus* isolates collected, over 24 species were identified, with *E. hirae* (*n* = 319) being the most prevalent followed by *E. faecium* (*n* = 256) and *E. faecalis* (*n* = 223). Species distributions varied significantly by season across most sample types. Antimicrobial susceptibility testing of *E. faecalis* (n = 58) and *E. faecium* (n = 61) isolates revealed four, multi-drug resistance *E. faecalis* isolates, with resistance to tetracycline (18%) and quinupristin-dalfopristin (18%) most common. Genomic analysis of *E. faecalis* (n = 158) and *E. faecium* (n = 171) isolates revealed 36 resistance determinants, with *aac(6')-Ii*, *lsa(A)*, *msr(C)*, *tet(M)* and *tet(L)* being the predominant resistance genes. Phylogenomic analysis revealed high diversity within both species, comprising 88 sequence types (STs) for *E. faecalis* and 100 for *E. faecium*, including 46 novel STs. Most of the closely related isolates (≤10 SNPs) originated from the same sample type and site (>74%), reflecting localized transmission dynamics. Evidence of cross-domain exchange and seasonal persistence was confined to organic dairy farms, while no genomic relatedness was observed between livestock-associated isolates and those from wastewater. These findings show that dairy-associated *Enterococcus* populations are diverse yet spatially contained, with limited connectivity to the human wastewater domain. Targeted One Health surveillance can help identify localized points to guide AMR mitigation in regions of intensive dairy production.

688 – Evaluating Arctic Community-Based Surveillance for Brucellosis Risk in Caribou and Muskoxen: Process Mapping, Sample Completeness, and Diagnostic Timeliness

Mohammod Misbah UDDIN (1), Susan KUTZ (1), Fabien MAVROT (1), Kugluktuk Angoniatit ASSOCIATION (2), Olokhaktomiut Hunters and Trappers COMMITTEE (3), Ekaluktutiak Hunters and Trappers ORGANIZATION (4), Lisa-Marie LECLERC (5), Naima JUTHA (6), Dayna GOLDSMITH (1,7), Jamie ROTHENBURGER (1,7), Niroshan THANTHRIGE-DON (8), Om SURUJBALLI (8), **Karin ORSEL** (1)

1: Faculty of Veterinary Medicine, University of Calgary, Calgary, AB T2N 4Z6, Canada.; 2: Kugluktuk Angoniatit Association, 13 Klengenberg St., Kugluktuk, NU X0B 0E0, Canada.; 3: Olokhaktomiut Hunters & Trappers Committee, P.O. Box 161, Ulukhaktok, NT X0E 0S0, Canada.; 4: Ekaluktutiak Hunters & Trappers Organization, 4 Mitik St., Cambridge Bay, NU X0B 0C0, Canada.; 5: Department of Environment, Government of Nunavut, P.O. Box 377, Kugluktuk, NU X0B 0E0, Canada.; 6: Department of Environment and Climate Change, Government of Northwest Territories, PO Box 1320, Yellowknife, NT, X1A 2L9, Canada; 7: Canadian Wildlife Health Cooperative, Alberta Region, Calgary, AB, Canada; 8: Canadian Food Inspection Agency, Ottawa Laboratory (Fallowfield), 3851 Fallowfield Road, Ottawa, ON, K2J 4S1, Canada

Background:

Inuit and First Nations in the Canadian Arctic rely on harvested caribou and muskoxen for food security. A priority zoonotic concern is brucellosis (*Brucella suis* biovar 4). Community-based wildlife health surveillance (CBWHS) has operated for >13 years in three communities (Kugluktuk and Cambridge Bay, Nunavut; Ulukhaktok, Northwest Territories). Harvesters submit a standardized “sample kit” and are encouraged to report any abnormal tissues discovered while processing carcasses. The objective was to use a formal framework to evaluate the CBWHS for process mapping, kit/data completeness, diagnostic timeliness, and accuracy of harvesters’ detection of *Brucella*-associated abnormalities.

Methods:

Guided by the SERVAL surveillance evaluation framework, we 1) mapped the CBWHS process by literature review and key-informant discussions; and 2) analyzed kit-submissions (Jan 2022-Sep 2025) of the Dolphin and Union (DU) caribou (n=118 kits) and muskoxen (n=180 kits) to measure sample-kit completeness, datasheet completeness, and *Brucella* diagnostic timeliness. To assess the accuracy of harvesters' suspicion of true *Brucella* infection with culture available for 38/746 submissions, we ran a Monte Carlo simulation (10,000 iterations) with sensitivity informed by the cultured subset and high specificity reflecting mostly healthy/seronegative submissions. Positive and negative predictive values (PPV, NPV) were estimated across assumed prevalences of 5-20%.

Results:

The CBWHS process had two operational streams: active kit-based and passive diagnostic monitoring. Diagnostic cases had three entry points: reported at kit submission, detected during screening, or submitted outside the kit. Rightsholders and Stakeholders involved harvesters, co-management bodies, territorial and federal agencies, and the university research team. Kit completeness (six required samples) varied by species and harvest communities and was high for muskoxen (86.1% with 6/6) and moderate for DU caribou (47.5% with 6/6; 28.8% with 5/6). Across communities, muskox kits were consistently complete, whereas DU caribou kits were more often partially complete in Cambridge Bay and Ulukhaktok than in Kugluktuk. Data sheet completeness was generally high, apart from DU caribou body condition (46.6%). Among brucellosis-confirmed cases, non-suspect cases by harvesters took 60 days longer to reach initial screening than suspect cases. In the culture subset (n=38), apparent sensitivity of harvesters' suspicion of brucellosis was 63.3% (95% CI 45.5-78.1), consistent with the beta posterior mean sensitivity of 62.5% (45.4-78.2). PPV of harvesters' suspicion increased with assumed prevalence from 26.0% (15.4-41.4) at 5% prevalence to 61.6% (46.3-77.0) at 20% prevalence, while NPV decreased from 97.9% (96.9-98.8) to 90.6% (86.8-94.4).

Conclusions:

CBWHS functions as a dual-purpose system involving many partners and complex communication structures. Capacity building should prioritize harvester training to improve kit completeness and lesion recognition for speeding screening and risk communication to reduce zoonotic exposure. Harvesters' suspect classification was likely truly infected, while non-suspects were usually truly negative. Overall, community-based detection supports One Health by monitoring wildlife health to safeguard public health.

---

695 – Assessing the applicability of the Tripartite SIS Operational Tool to structure integrated surveillance for neglected parasitic zoonoses in data-limited settings

Katrina DI BACCO (1,2,3), Fidèle KABERA (1,2), Raphael DE SOUZA AGUIAR (4,5), Mary WIKTOROWICZ (4,5), Hélène CARABIN (1,2,3)

1: Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, Canada; 2: Groupe de recherche en épidémiologie des zoonoses et santé publique (GREZOSP), Saint-Hyacinthe, Canada; 3: Centre de recherche en santé publique (CReSP), Montreal, Canada; 4: School of Global Health, York University, Toronto, Canada; 5: Dahdaleh Institute for Global Health Research, Toronto, Canada

Background

Neglected parasitic zoonoses rarely have formal surveillance systems due to low policy prioritization, fragmented data infrastructures and limited intersectoral information sharing. The Tripartite Zoonoses Guide Surveillance and Information Sharing Operational Tool (SIS-OT) was designed to establish or strengthen coordinated, multisectoral surveillance and information sharing for zoonotic diseases. However, its applicability in contexts where surveillance data and infrastructure are sparse is not well described. We aimed to assess whether the SIS-OT could be adapted to develop a roadmap for integrated surveillance of neglected parasitic zoonoses in Canada.

Methods

The SIS-OT pre-planning and portions of the assessment components were applied to four endemic zoonotic parasites in Canada of which the definitive hosts are companion animals and wildlife :

Toxoplasma gondii, *Toxocara* spp., *Baylisascaris procyonis*, and *Echinococcus* spp. Initial steps included pathogen prioritization through interdisciplinary expert consultation, a desktop review of existing surveillance programs and data sources, and stakeholder mapping across human health, veterinary, wildlife, and public health sectors. A structured multi-sector workshop and a stakeholder survey were conducted to document surveillance infrastructure, laboratory capacity, data-sharing practices, and opportunities for cross-sector linkages. These activities were used to identify structural gaps and barriers to advancing integrated surveillance.

Results

Application of the SIS-OT revealed fragmented surveillance structures, limited accessibility of existing data, and minimal cross-sector coordination and information exchange on these zoonoses. Fourteen experts contributed to the prioritization and system mapping process. Thirty collaborators responded to the stakeholder survey and an additional 30 participated in a national workshop. None of the targeted infections are federally reportable in humans in Canada, and in animals *Echinococcus* spp. and *T. gondii* are annually notifiable. Reporting systems for neglected parasitic zoonoses thus remain largely fragmented. Human diagnostic data are frequently maintained in isolated laboratory or institutional databases and are rarely consolidated nationally. Companion animal diagnostic data are predominantly held by private laboratories, limiting accessibility for governments and researchers. Wildlife data are more widely available through the Canadian Wildlife Health Cooperative but rely primarily on animals found dead, biasing surveillance signals. A gap identified was the absence of population-level human prevalence data. Subsequent nationally representative serosurveys identified measurable exposure, with preliminary seroprevalence estimates ranging from 1% to 10% across the four zoonoses. Stakeholders identified inconsistencies in public risk communication. In response, a public-facing website and educational videos were developed to support knowledge translation and prevention messaging.

Conclusion

In data-limited contexts, the SIS-OT can serve as a structured decision-support framework to identify surveillance gaps and guide targeted evidence generation on neglected zoonoses. However, it cannot be used to link surveillance systems when sectoral surveillance infrastructure is fragmented or absent. This study demonstrates how operational One Health tools can be adapted to support data-informed prioritization before integrated surveillance systems are established.

---

705 – Comprehensive Evaluation of Knowledge and Attitudes Toward Ebola and Marburg Viruses Among Students and Professionals in Sédhiou, Senegal.

Yacine CISSE (1,2), Aminata TOURE (1,2), Tracie YOUBONG (2), Ezechiel Prosper NOALI (3), Amadou SECK (2), Daniel YONGA (2), Simone SOSO (4), Somine DOLO (4), Amadou Yeri CAMARA (5), Thierry Lamare FOUAPON ASSEDI NJATOU (4), **Deborah THOMSON** (4), Noel Magloire MANGA (1)

1: UFR Sciences de la Santé, Université Assane Seck de Ziguinchor, Sénégal; 2: One Health Lessons®, Dakar, Sénégal; 3: One Health Lessons®, Ouagadougou, Burkina Faso; 4: One Health Lessons®, Washington DC, USA; 5: Regional Health Department of Sedhiou, Sénégal

Background: Enhancing One Health knowledge and surveillance for zoonotic diseases poses significant challenges in Senegal. Ebola and Marburg virus diseases, prioritized zoonoses, remain public health threats, with the latest outbreak reported in February 2025 in neighboring Guinea. This study assessed students' and professionals' knowledge and practical attitudes regarding Ebola and Marburg in southern Senegal.

Methods: In our study on an innovative One Health approach to zoonotic surveillance in the Sedhiou region of Senegal, conducted from January 2025 to March 2026, we conducted a cross-sectional, quantitative, descriptive study between April 11 and April 18, 2025. An 8-hour training session, organized by One Health Lessons® (OHL), took place at Assane Seck University in Ziguinchor. This training utilized a variety of materials, including slide presentations and game cards. Knowledge assessments were conducted both before and after the training. Additionally, we developed a survey questionnaire to evaluate participants' knowledge and practical attitudes concerning the Ebola and Marburg viruses, as well as to collect socio-demographic information.

Results: A total of 109 participants were surveyed: 63.9% were students, while 26.1% were professionals. The average age of the participants was 29 years, and the sex ratio (M/F) was 2:0. Before the training, the overall level of knowledge about Ebola and Marburg was 78%. Only 32% of participants demonstrated a good understanding of the reservoirs for Ebola and Marburg. The most commonly recognized symptoms were sudden high fever (24%) and unexplained bleeding (24%), followed by vomiting and severe diarrhea (21%). The two main transmission routes identified were contact with infected blood or body fluids (34%) and the consumption of infected bushmeat (35%). Before the training, the most widely recognized preventive measure was avoiding contact with sick individuals.

After the training, the overall knowledge level increased to 89%. Forty-six percent of participants demonstrated a good understanding of the reservoirs for Ebola and Marburg viruses. The main symptoms remained widely recognized; however, certain symptoms, such as itchy skin rash and muscle pain accompanied by extreme fatigue, saw improved recognition rates, rising from 15% to 16% and from 18% to 21%, respectively. Awareness of contact with infected fruit bats as a transmission route increased slightly from 28% to 30%, indicating improved recognition of this risk. The regular disinfection of surfaces and hands also saw a small increase, rising from 24% to 27%, as did proper meat cooking, which increased from 21% to 26%.

Conclusion: This study confirms that a concise, interactive training program significantly enhances comprehension of risks associated with priority zoonotic diseases. For sustained public health practice, these training modules should be systematically integrated into the academic and professional curricula for students and stakeholders in Senegal's health sector.

---

708 – Implementing One Health in Practice: Lessons from 18 transdisciplinary projects addressing health risks in wildlife trade

Hongying LI (1,2), Beate HENRICHFREISE (3), Johannes KEIL (3), Michael NAGEL (3), Craig STEPHEN (4,2), Jamie REASER (2,5), **Chadia WANNOUS** (6)

1: Columbia Climate School, Columbia University, United States of America; 2: Steering Committee of the International Alliance against Health Risks in Wildlife Trade, Bonn, Germany; 3: Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH, Secretariat of the International Alliance against Health Risks in Wildlife Trade, Bonn, Germany; 4: The McEachran Institute, British Columbia, Canada; 5: Smithsonian-Mason School of Conservation, Virginia, United States; 6: World Organisation for Animal Health (WOAH)

Background

Wildlife trade is recognized as a driver of biodiversity loss and zoonotic disease emergence, yet translating global commitments into effective prevention measures remains challenging. One Health emphasizes integrated approaches across human, animal, and environmental health, but practical examples of implementation—particularly at the wildlife trade interface—remain limited. To address this gap, the International Alliance against Health Risks in Wildlife Trade supported a portfolio of transdisciplinary projects aimed at reducing zoonotic spillover risks while strengthening collaboration among health, conservation, and governance actors. This study synthesizes lessons from the implementation of these projects to identify enabling factors, barriers, and practical pathways for operationalizing One Health approaches to prevent zoonotic disease risks.

Methods

A qualitative synthesis was conducted across 18 projects implemented in 23 countries in Africa, Asia, and the Americas, along with one global initiative. These projects applied interdisciplinary approaches combining social and behavioral research, legal and governance analysis, and pathogen surveillance to address health risks associated with wildlife trade. Data was sourced from project documentation, implementation reports, and cross-project reflections produced by implementing teams and partners. The analysis examined implementation strategies, partnership models, and contextual factor influencing project implementation and outcomes. Particular attention was given to cross-sector collaboration, governance mechanisms, and the integration of local knowledge systems, cultural practices, and gender considerations in the design of risk-reduction strategies.

Results

Across diverse contexts, the projects demonstrated that effective zoonotic risk reduction requires context-specific implementation strategies rather than standardized approaches. Interventions prioritized upstream prevention and emphasized locally grounded solutions aligned with cultural practices and existing governance structures. These projects catalyzed cross-sector collaboration among public health, veterinary, environmental, and conservation stakeholders, functioning as practical case studies of One Health implementation. They strengthened local capacity for risk awareness, surveillance, and response, while identifying policy and regulatory entry points to improve governance of wildlife trade. Partnerships among governments, research institutions, civil society organizations, and local communities enabled coordinated action. However, the synthesis also highlighted persistent barriers to OH implementation, including fragmented institutional mandates, limited sustained financing, and operational challenges in translating pilot interventions into long-term programs.

Conclusions

The findings suggest that effective implementation of One Health approaches requires more than scientific evidence; it depends on enabling governance environments, cross-sector partnerships, and sustained investment in locally grounded prevention strategies. Community-led engagement and trust-building were critical for aligning health, conservation, and livelihood priorities. These experiences demonstrate how targeted investments and collaborative platforms can operationalize One Health principles in complex real-world settings. By linking implementation lessons from wildlife trade interventions with broader global commitments, this synthesis provides practical insights for strengthening One Health strategies and financing mechanisms aimed at preventing future pandemics while advancing biodiversity conservation and health security.

---

713 – Long-Term Ambient Air Pollution and the Incidence of Primary Open-Angle Glaucoma: A Retrospective Cohort Study

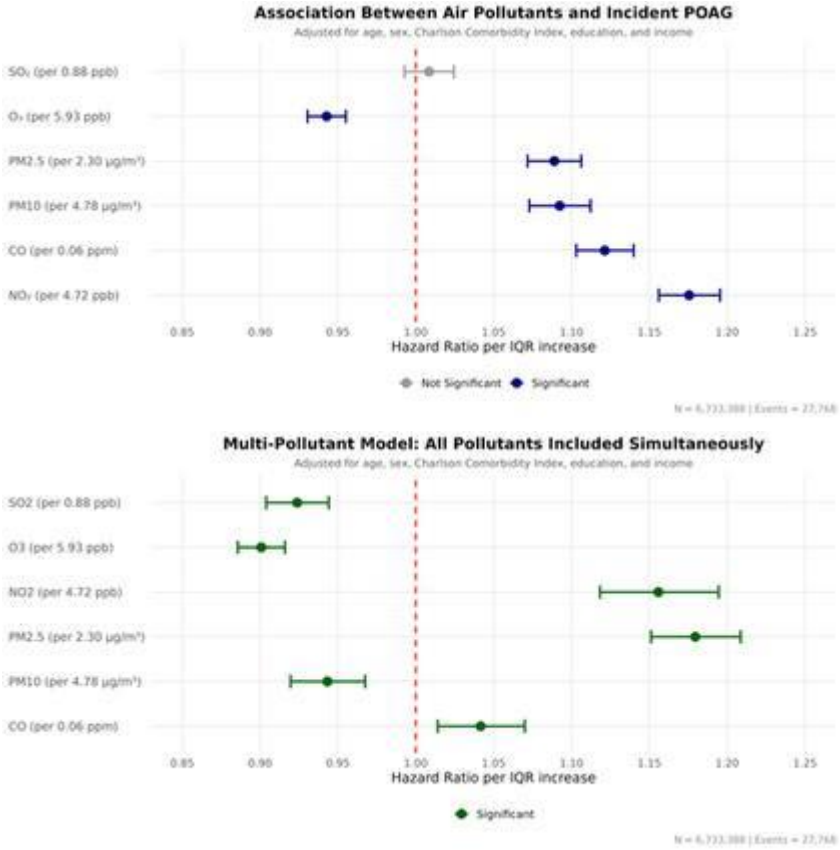
Aparna REDDY, Zachary WAKEFIELD, Xiangxue XIAO, Sophia WANG
Stanford, United States of America

Background: Glaucoma is a leading cause of irreversible blindness, affecting 80 million individuals worldwide. Primary open-angle glaucoma (POAG) is known as the “silent thief of sight” as it is asymptomatic until advanced stages, highlighting the importance of prevention and early detection. Major known risk factors include demographics, genetics, and lifestyle. Fine particulate matter (PM2.5) from air pollution is known to cause oxidative stress and inflammation from reactive oxygen species, which may contribute to the development of POAG. Thus, the purpose of this study was to evaluate the association between long-term exposure to air pollution and the risk of developing POAG.

Methods: We conducted a retrospective cohort study using US-based insurance claims data from the Merative™ Marketscan® Commercial Database and air quality estimates from the Center for Air, Climate, and Energy Solutions (CACES) Land Use Regression Model to identify the association between long-term ambient air pollution (PM2.5, PM10, CO, NO2, O3, SO2) and POAG. Our study population included 6,733,388 individuals with no prior glaucoma diagnoses and county-level air pollution exposure from 2007 to 2010. Analysis was conducted using Cox proportional hazards regression models, adjusting for age, sex, Charlson Comorbidity Index, median income, and college education. Individual pollutant models, in which each pollutant was analyzed separately, and a cumulative model, in which all pollutants were included in a single model simultaneously, were conducted. A correlation matrix and VIF’s confirmed the lack of collinearity among the pollutants in the cumulative model.

Results: In the individual models (Figure 1), four of the six air pollutants were significantly associated with increased risk of POAG. NO2 showed the strongest association, with a hazard ratio (HR) of approximately 1.19 per 4.72 ppb increase. CO was associated with an HR of 1.15 per 0.06 ppm increase, followed by PM2.5 (HR ≈ 1.11 per 2.30 μg/m³ increase) and PM10 (HR ≈ 1.10 per 4.78 μg/m³ increase). O3 was associated with a decreased risk of POAG, and SO2 was not statistically significant. In the multipollutant model (Figure 2), adjusting for co-pollutants, NO2 and PM2.5 had the highest hazard ratios of approximately 1.17 (per 4.72 ppb increase) and 1.18 (per 2.30 μg/m³ increase), respectively. CO was also positively associated with POAG risk (HR ≈ 1.05 per 0.06 ppm increase).

Conclusion: This large U.S.-based retrospective cohort study of over 6.7 million individuals demonstrates that long-term exposure to ambient air pollution, especially NO2, PM2.5, and CO, is associated with an increased risk of incident POAG. These findings support existing evidence that chronic exposure to air pollutants may contribute to the risk of POAG through inflammation and oxidative stress.



724 – Antimicrobial-Resistant Bacteria and Resistance Gene Profiles in the Yambaru Forest, a World Natural Heritage Site in Okinawa, Japan

Kei NABESHIMA (1), Ayaka OKADA (2), Manabu ONUMA (1)

1: National Institute for Environmental Studies, Japan, Japan; 2: Gifu university

Background: Antimicrobial resistance (AMR) is a major global public health threat and is often described as a silent pandemic. Inappropriate antimicrobial use in human medicine and livestock production has accelerated the emergence and spread of resistant bacteria through the acquisition and dissemination of antimicrobial resistance genes (ARGs). Our previous study suggested that migratory birds may introduce ARGs into Japan, and fecal samples from Okinawa showed a more diverse ARG profile than those from other regions. Since 2022, antimicrobial-resistant *Pseudomonas aeruginosa* has also been sporadically isolated from wildlife in the Yambaru forest of Okinawa. These findings raised concern that AMR and ARGs may already be infiltrating the local environment. This study assessed AMR risk in the Yambaru forest by integrating pathological and bacteriological investigations of wildlife carcasses with metagenomic surveillance of ARGs in wildlife feces and environmental water.

Methods: Four lung samples from Ryukyu long-furred rats (*Diplothrix legata*) suspected of bacterial pneumonia were collected between 2023 and 2025. For fecal surveillance, rectal feces from 15 road-killed rats were examined. For environmental surveillance, 14 water samples were collected from seven major river systems in 2024 during summer and winter. Bacteria isolated from lung samples were analyzed by whole-genome sequencing using Nanopore Flongle. DNA from fecal and water samples was extracted with the EZ2 PowerFecal kit, libraries were prepared using the QIAseq xHYB AMR Panel, and sequencing was performed on the NovaSeq X. ARG profiles were analyzed using GeneGlobe and evaluated against 17 important antimicrobial classes in human and veterinary medicine.

Results: Bacteriological examination identified two P. aeruginosa isolates and a novel *Rodentibacter* species. One *P. aeruginosa* strain was resistant to ciprofloxacin, enrofloxacin, orbifloxacin, and gentamicin, and belonged to sequence type ST274, the same genotype as a strain isolated in 2023. In environmental water, ARGs associated with 15 of the 17 target antimicrobials were detected at 10 or more sampling points, excluding meropenem and aztreonam. Rifampicin- and isoniazid-resistance genes were detected at all sites. The plasmid-associated colistin resistance gene mcr-1.1 was detected in a winter sample from Sosu Beach, and the tigecycline resistance gene tetX was widely distributed across Okinawa. In rat feces, ARGs for the same 15 antimicrobial categories were detected in at least three pools. The ESBL-associated beta-lactamase gene CTX-M-56 was detected in all rat sampling areas, and several ARGs overlapped with those found in environmental water.

Conclusions: These results provide the first evidence that both AMR bacteria and diverse ARGs are present in wildlife and the environment of the Yambaru forest, suggesting ecological linkage and circulation of ARGs within this forest ecosystem.

730 – Assessment of knowledge, attitudes, and practices regarding zoonotic diseases and the socio-economic impact of zoonotic outbreaks to strengthen disease surveillance system in Cambodia

Tu Tu Zaw WIN (1), Bunna CHEA (2), Theng KOUCH (2), Naiheak BAN (2), Sonita MANG (2), Sokha CHEA (3), Samon SRENG (4), Flavie GOUTARD (5)

1: ASTRE, CIRAD, Bangkok, Thailand; 2: Royal University of Agriculture (RUA), Phnom Penh, Cambodia; 3: Wild Conservation Society (WCS), Phnom Penh, Cambodia; 4: Preah Norodom Sihamoni General Education and Technical High School, Cambodia; 5: ASTRE, CIRAD, Hanoi, Viet Nam

Background: Cambodia represents a critical hotspot for emerging diseases, where complex interactions among wildlife, livestock, and human populations facilitate pathogen spillover and zoonotic threats. This study aimed to evaluate awareness of zoonotic diseases, the socio-economic impact of zoonotic disease outbreaks, and to identify factors influencing preventive behaviours and community surveillance.

Methods: A cross-sectional household survey was conducted in 11 villages in Stung Treng Province, involving 421 households. Descriptive analyses were undertaken to characterize community knowledge, attitudes, and practices (KAP) related to zoonotic diseases, and the perceived impacts of zoonotic disease outbreaks on households.

Results: The majority of respondents were male farmers (n = 318, 75.53%), with over half having attained primary-level education (n = 213, 50.59%). More than half of the respondents earned ≥USD1,000 (n = 229, 54.39%). Primary income sources were based on crop farming (n = 384, 91.21%) and livestock husbandry (n = 104, 24.70%), with poultry being the most commonly raised species (n = 253 out of 338, 75.52%). Awareness of zoonotic diseases was generally robust, particularly regarding animal-to-human transmission (n = 366, 87.14%), and was particularly high for zoonoses (rabies n = 177 (42.04%), avian influenza n = 255 (60.57%)). Majority of respondents (90.74%) recognized the importance of zoonotic diseases (90.74%), acknowledged animal-to-human transmission (88.12%). Preventive measures, including human vaccination (n = 376, 89.31%), livestock vaccination (n = 360, 85.51%), hand hygiene after contacting sick animals (n = 393, 94.54%), and safe food handling including not eating the meat of sick animals or animal found dead (n = 387, 91.92%), were widely recognized. However, gaps in understanding remained regarding human-to-animal transmission (n = 184, 43.71%), wildlife-associated risks such as rodents and bats (less than 50%). Despite widespread awareness, a significant gap between knowledge and practice was observed. Animal vaccination coverage remained low (n = 83, 19.71%), and high-risk food behaviours such as the consumption of raw meat (n = 199, 47.27%) were prevalent. From 2020 to 2025, respondents rarely identified zoonotic outbreaks other than COVID-19. Affected households reported income loss as the most significant challenge, followed by reduced access to food, health care, and education. Community involvement in surveillance or health-related roles (n = 47 out of 419, 11.22%) was limited, predominantly involving human health workers (n = 32 out of 47). Respondents identified training, awareness campaigns, and informational materials as essential strategies for improving community engagement.

Conclusion: Findings indicate that communities in Stung Treng demonstrated high awareness of common zoonotic diseases and preventive measures. However, knowledge gaps persisted regarding wildlife-

related transmission and preventive practices did not always align with reported knowledge. Further analyses, regression modeling, will be conducted to identify socio-economic and behavioural factors influencing community engagement in surveillance and adoption of preventive measures.

738 – Preparing for the Future of Research and Education in One Health—A Scenario Planning Exercise toward 2050 from Una Europa University Alliance

Bruno GONZALEZ-ZORN (1,4), **Alessandra SCAGLIARINI** (2,4), **Lisa BODEN** (3,4), Una Europa ONE HEALTH SSC (4)

1: Complutense University of Madrid, Spain; 2: Univesrity of Bologna, Italy; 3: University of Edimburgh, UK; 4: Una Europa

BackgroundDespite growing recognition of the need for interdisciplinary and cross-sectoral approaches, the future trajectory of One Health research, education, and governance in Europe remains uncertain due to evolving social, technological, economic, environmental, and geopolitical drivers. This work presents a strategic foresight exercise conducted as part of a Una Europa initiative within the Una Europa One Health Focus Area, aiming to explore plausible futures for One Health research and education in Europe by 2050 and identify priorities to strengthen interdisciplinary collaboration and policy impact.MethodsA participatory foresight process using scenario planning methodology was conducted within the Una Europa alliance of European universities. Interdisciplinary stakeholders participated in workshops designed to explore long-term uncertainties affecting One Health. The process began with a SWOT analysis (Strengths, Weaknesses, Opportunities, Threats) to assess the current landscape of One Health research, education, and collaboration across partner institutions. Participants then identified and ranked drivers of change across social, technological, economic, environmental, and political domains according to their impact and uncertainty. The most critical uncertainties were grouped into thematic axes of change, forming the basis for the development of future scenarios for the European One Health landscape in 2050.ResultsThree key axes of uncertainty were identified: foreign policy orientation (globalist vs. isolationist), research landscape (researcher-led vs. technology-driven), and public trust in governance and scientific institutions (high vs. low). Combining these dimensions generated three plausible future scenarios. These range from a globalist, researcher-driven future with high public trust, characterized by strong interdisciplinary collaboration and open science, to a technocratic and isolationist future with low public trust, where algorithm-driven research systems, disciplinary silos, and misinformation dominate. A third scenario reflects a continuation of current trajectories, where One Health remains prominent in academia but faces an implementation gap between research, policy, and practice.ConclusionsThis One Health foresight action highlights that the future success of One Health will depend not only on scientific innovation, but also on governance, public trust, interdisciplinary collaboration, and effective science–policy interfaces. Strengthening FAIR data sharing, expanding interdisciplinary education, and improving stakeholder engagement will be essential to ensure that One Health research translates into actionable solutions for global health challenges.

740 – Operationalizing One Health in West Africa: Strengthening Regional Governance, Workforce Development and Integrated Zoonotic Surveillance in the ECOWAS region

Lionel Soléte SOGBOSSI (1), Virgil Kuassi LOKOSSOU (1), Guy Gerard KOUAME (2), Aishat USMAN (1), Tieble TRAORE (3), Félix AGBLA (1), Melchior Athanase AÏSSI (1)

1: West African Health Organisation, Côte d'Ivoire; 2: Private Sector, Côte d'Ivoire; 3: World Health Organisation Regional Office for Africa,Senegal

Background

West Africa faces recurrent zoonotic and emerging public health threats requiring coordinated multisectoral surveillance and timely information sharing. The West African Health Organization has led regional efforts to operationalize One Health in Member States through governance frameworks, workforce development, and the Tripartite Zoonoses Guide operational tools to strengthen epidemic intelligence.

Methods

Between 2022 and 2025, WAHO supported key Tripartite Guide Operational Tools, including the Surveillance and Information Sharing Operational Tool (SIS-OT), the Joint Risk Assessment Operational Tool (JRA OT), and the Workforce Development Operational Tool (WFD OT). This support involved regional Training-of-Trainers workshops and national workshops in each participating country, engaging human, animal, and environmental health sectors.

Countries used the SIS-OT workbook to evaluate their surveillance capacities across five domains, leading to the creation of five-year national roadmaps for integrated zoonotic surveillance.

Additional initiatives included the ECOWAS One Health Leadership Course for Anglophone and Francophone professionals, community-level One Health awareness training, and the expansion of digital surveillance systems like Surveillance, Outbreak Response Management and Analysis System (SORMAS).

Results

SIS-OT assessments were conducted in six ECOWAS Member States (Guinea, Mali, Senegal, Sierra Leone, Nigeria, and Côte d'Ivoire) revealed 60–85% of capacities at the lowest levels, with systemic gaps in legal frameworks, interoperability, laboratory networks, and accountability.

Sierra Leone recorded 84% of activities at the foundational capacity level, while Nigeria reported 56.3% at level 1, and only two activities were fully completed. Each country developed a five-year costed roadmap. Regionally, WAHO finalized the ECOWAS One Health Strategy (2025–2029), and a governance manual to institutionalize multisectoral coordination. Trained 104 One Health leaders and 222 intermediate-level professionals across Anglophone and Francophone countries, established a regional Risk Communication and Community Engagement technical working group, and expanded SORMAS surveillance.

Conclusions

WAHO's integrated approach has accelerated One Health operationalization in ECOWAS. Evidence-based national roadmaps, regional governance frameworks, and workforce development initiatives have strengthened epidemic intelligence. Sustaining interoperable data governance and embedding SIS-OT within regional health security mechanisms will be critical to consolidate gains.

---

743 – Discourse analysis of OHHLEP publications, interviews, and meeting synthesis provides new insights about One Health definition and implementation levels.

William ADDEY (1), Cyril MASSELOT (1), Serge MORAND (2)

1: Université Marie et Louis Pasteur, France; 2: Université de Montpellier France

Background: Following the publication of a One Health (OH) definition by OHHLEP Term 1 members (OT1) as the balance and optimization of human, animal, and environmental health, we sought to understand the most commonly referred lexicon and how concepts were used by the scientists and the quadripartite. To better understand what the authors and the quadripartite intended to say, we gathered all available material published by OT1.

Methods: A Discourse analysis was conducted of interviews with OT1 members, meeting syntheses, the annual report on the WHO website, and the OT1 members' scientific publication. After verifying acceptability, usability, and homogeneity, each corpus was analyzed using Iramuteq software (Pélissier, 2017; Ratinaud, 2020) in accordance with proven statistical practices (Reinert, 1983). This made it possible to obtain a mapping of the textual forms and to identify specific isotopies. These statistical calculations allowed the grouping of lexicon profiles (Table 1) , the visualization of dendrograms (Graph 1) , and the representation of discourse profiles using Correspondence Factor Analysis (Graph 2).

Results: The study reveals distinct differences among the three corpora, each employing a unique language and emphasis. The examination of scientific publications indicates a tendency towards practical, problem-oriented discussions that operationalize theoretical concepts into actionable tools. The interviews highlight a tension between institutional frameworks and real-world human experiences, with a stark dichotomy between biological themes and top-down health policy implementation. The synthesis, authored by the quadripartite's secretary, is marked by highly structured discourse that favors formal guidance. For example, while in interviews scientists frame collaboration in terms of "discipline" and "transdisciplinary" engagement, publications describe it as "coordination" among the quadripartite

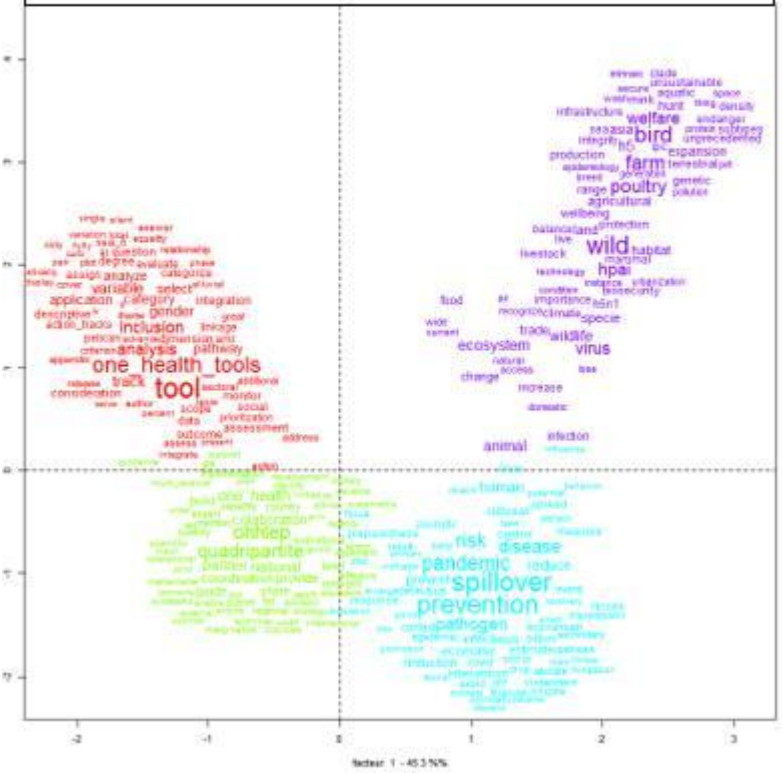
and national authorities. The synthesis referred to collaboration as “thematic updates” or “drafting'” illustrating a progression from lived interdisciplinary challenges to procedural consensus-building.

Conclusions: The study illustrates how individual scientists, scientific collectives, and institutions implement the OH framework at varied levels. The lexical distinctions reflect a spectrum of discursive functions, from the holistic aspects of OH in the interviews to the instrumental focus in publications, to the very procedural discourse of institutional synthesis. The absence of high chi-square values for terms such as plant, youth, death, fish, or ocean underscores OH's historical ties to zoonoses and to top-down public health approaches. Indeed, neither wildlife nor the environment is yet perceived as a solution for human health; rather, they primarily represent risks requiring management, with nature-based solutions being still overlooked in favor of human-centric interventions. Furthermore, the ongoing separation between environment and human concerns, as well as biological and psychosocial elements, indicates that some disciplines have yet to be effectively integrated and that there may be a lack of the necessary language to address overlapping risks.

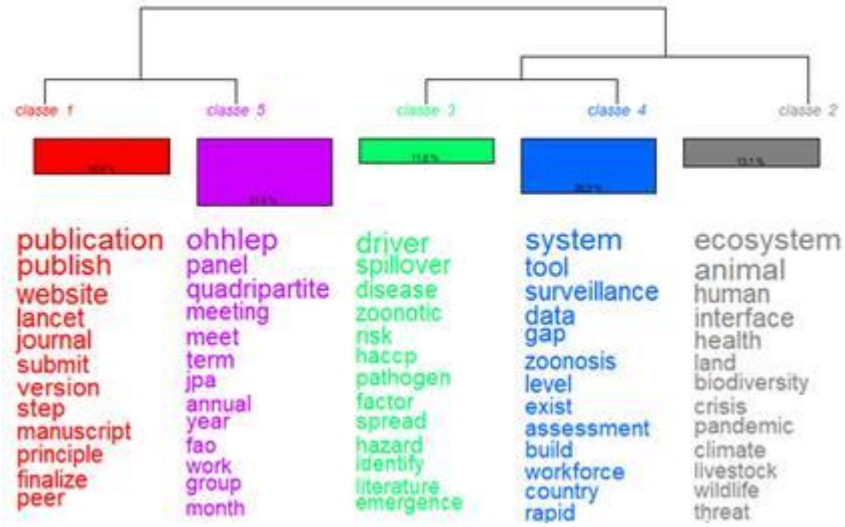
Table 1 of discourse profiles of the interview corpus

Classe 1 (11.8%)	χ2	Classe 2 (22.4%)	χ2	Classe 3 (30.5%)	χ2	Classe 4 (35.3%)	χ2
woman	74.7	definition	63.9	work	86.3	animal	98.2
reality	68.3	level	55.4	discipline	78.8	human	64.6
knowledge	61.0	ohhlep	39.0	science	63.2	healthy	56.7
cycle	59.5	partner	36.9	scientist	37.5	planet	46.9
indigenous	55.6	one_health	35.4	transdisciplinary	32.3	ecosystem	45.0
life	48.1	national	33.4	social	30.7	food	43.1
listen	44.6	high	32.2	project	20.4	specie	43.1
relate	43.0	country	29.5	medicine	18.3	environment	40.8
feel	38.3	principle	28.9	interdisciplinary	18.3	wildlife	34.8

Graph 2 : Correspondence Factor Analysis of the publication corpus



Graph 1 : Dendrogram of the synthesis corpus



745 – Strengthening early detection of wildlife disease through ranger-based digital surveillance: preliminary findings from the Wildlife Health Watch program in Kenya

Shaleen ANGWENYI (1,2), Nelly BARGOIYET (1,3), Stephen CHEGE (4,5), Francis GAKUYA (6), Samuel KAHARIRI (7), Isaac LEKOLOOL (8), Macon OVERCAST (1), **James HASSELL** (1,3,9)

1: Global Health Program, Smithsonian's National Zoo & Conservation Biology Institute, Smithsonian Institution, Washington, DC, USA; 2: Mpala Research Centre, Nanyuki, Kenya; 3: International Livestock Research Institute, Nairobi, Kenya; 4: San Diego Zoo Wildlife Alliance, San Diego, CA, USA; 5: VetinWild, Nanyuki, Kenya; 6: Wildlife Research and Training Institute, Naivasha, Kenya; 7: State Department for Livestock Development, Nairobi, Kenya; 8: Kenya Wildlife Service, Nairobi, Kenya; 9: Yale School of Public Health, New Haven, CT, USA

Background

Early detection of wildlife disease events is critical for preventing zoonotic spillover and strengthening global health security. However, systematic wildlife health surveillance remains limited across many biodiverse landscapes, particularly in regions where wildlife, livestock, and human populations interact closely. Rangers patrol these ecosystems daily and represent an underutilized frontline workforce for disease detection. Wildlife Health Watch (WHW) is a ranger-led surveillance initiative in Kenya that integrates workforce training, mobile reporting tools, and cross-sector data sharing to strengthen early warning of wildlife health events at the wildlife–livestock–human interface.

Methods

Between 2023 and 2025, WHW was implemented across 20 wildlife conservancies and protected landscapes in Kenya. Rangers received targeted training in wildlife health observation, syndromic recognition, safe reporting procedures, and One Health principles. A digital mobile platform (EarthRanger) enabled standardized reporting of wildlife morbidity, mortality, injuries, and abnormal behaviour during routine patrols. Submitted observations are transmitted in near real time to a centralized database and shared with wildlife veterinarians, wildlife authorities, and partner institutions to support verification and response.

An evaluation of the surveillance system is currently underway using the SERVAL (Surveillance Evaluation) framework, assessing attributes including reporting frequency, geographic coverage, timeliness, and perceived utility for early detection of and decision-making for wildlife health events.

Results

Preliminary implementation data demonstrate the feasibility of integrating ranger networks into wildlife disease surveillance systems. To date, more than 1,000 rangers have been trained across participating conservancies, creating a distributed surveillance network spanning approximately 10,000km2 of rangeland ecosystems. Rangers have submitted over 200 structured wildlife health observations through EarthRanger, including reports of mortality events, injuries, and syndromic disease indicators across multiple wildlife taxa.

Early findings suggest improved communication between field teams and veterinary responders and enhanced situational awareness of wildlife health events, and timely notification of potential risks at wildlife–livestock–human interfaces. Ranger participation has also enhanced local One Health capacity and awareness, building a network of trained frontline observers. The approach is scalable and could inform wildlife health surveillance models across other landscapes. Ongoing analyses are evaluating reporting patterns, spatial distribution of alerts, and system performance indicators through the SERVAL evaluation process.

Conclusions

Ranger-based surveillance represents a scalable and cost-effective approach to strengthening wildlife disease detection in biodiverse ecosystems where formal veterinary surveillance capacity is limited. By combining frontline workforce development with digital reporting and cross-sector data sharing, WHW demonstrates how decentralized surveillance networks can contribute to integrated One Health monitoring systems.

Final results from the ongoing SERVAL evaluation will further assess the system's performance and inform opportunities to scale ranger-based wildlife health surveillance as part of national and regional early warning frameworks.

749 – Knowledge, attitudes, and practices toward zoonotic disease transmission among wildlife farmers in Vietnam

Ha Thi Thanh NGUYEN (1,2), F. Lindahl JOHANNA (1,2,3), Steven LAM (4), Hung NGUYEN-VIET (4), Sinh DANG-XUAN (2), Fred UNGER (2), Jiaxin LING (1), Ake LUNDKVIST (1), Hu Suk LEE (5), Bernard BETT (4)

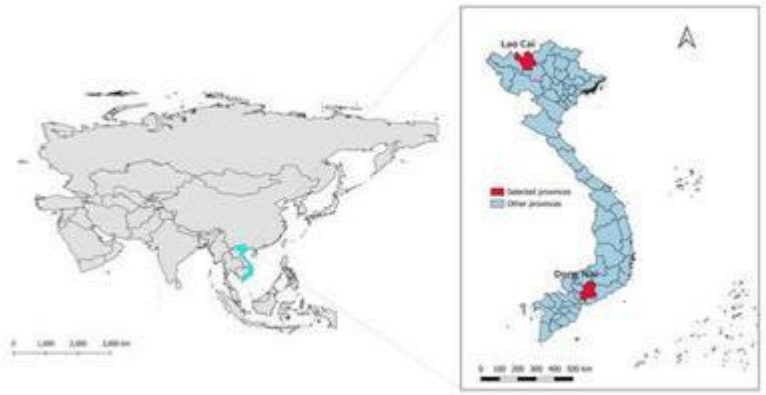
1: Zoonosis Science Center, Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden; 2: International Livestock Research Institute, Vietnam; 3: Swedish Veterinary Agency, Uppsala, Sweden; 4: International Livestock Research Institute, Nairobi, Kenya; 5: College of Veterinary Medicine, Chungnam National University, Daejeon, Republic of Korea

Background: Wildlife farming and trade in Southeast Asia contribute to the growing threat of zoonotic diseases. Despite the diversity of species farmed and the varying levels of risk they may pose, biosecurity practices among wildlife farmers remain underexplored. This study aimed to assess the knowledge, attitudes, and practices (KAP) of wildlife farmers in Vietnam to inform targeted interventions for zoonotic risk reduction.

Methods: A mixed-methods study was conducted among 210 wildlife farmers who raised bats, bamboo rats, civets, and wild boars in Lao Cai and Dong Nai provinces, Vietnam, between October 2023 and March 2024. Quantitative data were collected via structured questionnaires, and qualitative insights were obtained through 30 key informant interviews and two focus group discussions. Linear mixed-effects regression and thematic analysis were applied to explore KAP scores and associated factors.

Results: Wildlife farmers demonstrated relatively high knowledge (mean score: 10.1/13, 77.7%), positive attitudes (mean score: 41.3/50, 82.6%), and moderate preventive practices (mean score: 14.1/30, 47.0%). Farmers with college or above education had higher knowledge scores (Estimated marginal mean (EMM) = 11.8; 95% confidence interval (CI): 10.2 – 12.8) compared to those with no formal education (EMM = 7.8; 95% CI: 4.0 – 11.1). Farmers solely engaged in wildlife farming had lower attitude scores (EMM = 41.7; 95% CI: 37.8 – 45.0) than farmers who also worked as government employees (EMM = 46.1; 95% CI: 43.3 – 48.2). Farming bats (EMM = 8.5; 95% CI: 5.8 – 11.4) had lower practice scores compared to farming civets (EMM = 15.8; 95% CI: 13.0 – 18.6), and farmers consumed wild meat had lower practice score (EMM = 12.3; 95% CI: 9.5 – 15.2) than those did not (EMM = 14.5; 95% CI: 11.9 – 17.0). Qualitative findings revealed that many farmers normalised risky practices, prioritised convenience and personal experience over disease knowledge, and avoided reporting illnesses due to mistrust in veterinary authorities and fear of negative consequences.

Conclusion: This study highlights low risk perception and gaps between knowledge and practices among wildlife farmers, underscoring the urgent need for One Health interventions that promote low-cost preventive measures, build trust with authorities, and deliver targeted health education for reducing zoonotic risks.



756 – Are Canine Rabies Vaccination Campaigns Sustainable? A Scoping Review of Global Implementation and the One Health Approach.

Charlotte RENDINA (1), Kim R. VAN DAALEN (2,3), Rakesh CHAND (1,4), Yinka S. OYELEKE (5), James L.N. WOOD (1)

1: Department of Veterinary Medicine, University of Cambridge, Cambridge, UK; 2: British Heart Foundation Cardiovascular Epidemiology Unit, Department of Public Health and Primary Care, University of Cambridge, Cambridge, UK; 3: Heart and Lung Research Institute, University of Cambridge, Cambridge, UK; 4: School of Veterinary Medicine, University College Dublin, Dublin, Ireland; 5: Independent researcher

BackgroundEliminating dog-mediated human rabies by 2030 depends on sustained canine vaccination supported by effective surveillance and multisectoral coordination. Although vaccination campaigns are widely implemented, how they are organised, financed, and embedded within national systems is often poorly documented. We mapped the global literature on canine rabies vaccination campaigns and examined patterns related to sustainability and One Health integration.

MethodsWe conducted a scoping review following Joanna Briggs Institute and PRISMA-ScR guidance. Four databases (CABI Global Health, PubMed, Scopus, and Web of Science) were searched from inception to September 2025 without language restrictions. Grey literature from five international organisations, particularly websites, was also screened. Studies describing the implementation of canine rabies vaccination campaigns were eligible. Data were extracted at the campaign level on campaign duration, leadership, funding, stakeholder involvement, sustainability measures, and indicators consistent with One Health approaches. Descriptive analyses summarised campaign characteristics. Associations between selected campaign features were examined using Fisher's exact tests and modified Poisson regression.

ResultsSeventy-nine records describing 71 distinct vaccination campaigns across 39 countries between 1950 and 2025 were included. Most campaigns were short-term (66%). Reporting focused primarily on operational delivery metrics, including numbers of dogs vaccinated (86%) and vaccination coverage (82%), whereas downstream outcomes such as reductions in human or animal rabies cases were less frequently reported. Among campaigns reporting vaccination coverage, 31% reached the recommended 70% coverage threshold across the entire campaign period and geographic scope. A further 36% achieved the 70% threshold at least once during implementation, for example, within a specific year of a multi-year campaign or in particular geographic areas, even if overall coverage did not consistently meet this level.

Most campaigns were led by local government authorities, often with technical or financial support from external partners (63%). Sustainability measures were reported in 63% of campaigns, but these were most often framed as planned continuation rather than evidence of institutional integration. Over half of campaigns (62%) reported at least one feature consistent with a One Health approach. Campaigns with such features were more likely to report sustainability indicators than those without them (80% vs 44%; relative risk 1.8, 95% CI 1.1–2.8; p=0.004).

ConclusionsPublished evidence on canine rabies vaccination campaigns emphasises short-term operational delivery rather than long-term integration within health systems. Explicit reporting on governance, financing, and institutional embedding remains limited. Strengthening the integration of vaccination and surveillance within national systems, supported by sustained domestic investment and multisectoral coordination, will be important for achieving the global goal of eliminating dog-mediated human rabies by 2030.

768 – Towards synergy: better integration of the Environmental domain in One Health

Aleid BOUMAN, **Marieke DE COCK**, Nikki THIE
National Institute for Public Health and the Environment, Netherlands, The

Background: One Health surveillance seeks to monitor, control, and prevent infectious disease outbreaks at the intersection of human, animal, and environmental health. Although environmental surveillance—defined as the monitoring of infectious agents in environmental matrices such as water, soil, and air—is crucial for understanding zoonotic transmission pathways, the environmental domain remains underrepresented in practical One Health applications. Inconsistent terminology and different interpretations further complicate the integration of the environment within One Health. This study aims to clarify the definitions and scope of 'environmental surveillance' and 'environmental health' as used in the One Health scientific community; to map current types and practices of environmental surveillance; and to synthesize the benefits, opportunities, and challenges of integrating the environmental domain within One Health approaches.

Methods: A scoping review is currently being conducted to examine the literature on environmental inclusion in One Health, with particular attention to discrepancies in terminology and practice. Moreover, qualitative data will be collected through interviews and questionnaires with professionals working in the One Health field.

Expected results: This research will deliver a comprehensive overview of the role and use of the environment within One Health infectious disease research, highlight challenges, and present opportunities for improved integration of the environmental domain in One Health and One Health surveillance activities.

Conclusions: At the time of abstract submission, this is still work in progress, so no conclusions can be drawn yet.

772 – One Health in Social-Ecological Systems: Analysing the interdependence of natural resource use, livelihoods and human and animal health in Mongolia

Artemiy DIMOV (1,2,3), Ariane RHOMBERG (1,2,4), Chimedtseren BAYASGALAN (5), Burmaa DASHBAL (6), Amy BIRKINSHAW (7), Beat REIDY (7), Beatrice FILIPPINI (1,2), Rejifu NUREDING (1,2), Stephanie ZAVALA (1,2), Hussein MUKTHAR (1,2), Günther FINK (1,2), Jakob ZINSSTAG (1,2)
1: Swiss Tropical and Public Health Institute, Switzerland; 2: University of Basel; 3: University of Zürich; 4: University of Gothenburg; 5: Mongolian University of Life Sciences; 6: Mongolian Rangeland Research Centre; 7: Bern University of Applied Sciences

Background: Sustainability is founded on the interdependence of three principal pillars: society, economy, and environment. Their interactions shape the resilience of complex systems. In Mongolia, which encompasses the world's most extensive temperate grassland, these interrelations are particularly critical. Increasing livestock populations and pressures on communal rangelands have raised widespread concerns about overexploitation and the emergence of a "tragedy of the commons." Within the One

Health Social-Ecological Systems (OHSES) framework, this study explores how natural resource management, livestock health, and pastoral livelihoods interact. It seeks to show how both individual and group decisions affect ecological sustainability, economic viability, and the health of people and animals. Methods: An ex-ante simulation was conducted for Tuv Province, Mongolia, covering 2010–2023. A coupled system model was developed to integrate environmental variables, livestock population dynamics, brucellosis epidemiology, resource availability, and herder income generation. Several counterfactual scenarios were evaluated: (i) continuation of current high livestock density with brucellosis control, (ii) transition toward a reduced yet ecologically sustainable livestock with brucellosis control, and (iii-iv) both population approaches without vaccination. To evaluate how actors interact, scenarios were also analysed with a game-theoretic method. This enabled analysis of cooperative and non-cooperative choices for grazing and disease control. Results: Simulations revealed strong, non-linear links among ecology, the economy, and health. Among sustainable livestock herders, incomes dropped by about 30%, highlighting the trade-off between short-term profit and long-term balance. In vaccination scenarios, herders were almost indifferent to participating, as both vaccination costs and brucellosis impacts were minimal during near-elimination or pre-epidemic phases. The net carbon balance of the grassland-livestock system was neutral or slightly positive when comparing grassland carbon capture to emissions from enteric fermentation. Conclusions: The analysis shows that sustainability in Mongolian rangelands results from many rational, decentralised decisions. Fewer livestock improve ecological and climate stability, but lower household incomes. This signals the need for policies that account for ecological impacts, such as payments for ecosystem services or targeted subsidies. The OHSES framework helps integrate environmental, economic, and health factors into a single model. This method provides evidence for adaptive governance and policy, relevant to shared resources beyond Mongolia.

780 – The Certificate of Advanced Studies in One Health at the University of Bern: using continuing education as a living lab for intersectoral and transdisciplinary collaboration

Camille DORAS

University of Bern, Veterinary Public Health Institute, Switzerland

Background

Implementing the One Health approach requires professionals to collaborate across sectors, disciplines, and institutional mandates – yet opportunities to develop such competencies during professional training remain limited.

The Certificate of Advanced Studies (CAS) in One Health offered by the University of Bern is a unique continuing education programme in Switzerland. It was specifically designed to bring together professionals from diverse sectors and disciplinary backgrounds who seek to develop competencies for applying the One Health approach in their practice. In addition to providing foundations in One Health concepts, the programme emphasises experiential learning through hands-on activities and collaborative exercises. Participants engaged in group work and practical assignments that are intentionally structured to maximise disciplinary and sectoral diversity within each cohort. These activities function as *living labs*, enabling participants to experience first-hand the challenges and opportunities associated with communication, negotiation, and collaboration across professional silos.

In this session, we will present and discuss in the first part (20min presentation + 10min discussion) how these participatory group activities simulate real-world intersectoral/transdisciplinary collaboration. We will also share feedback from students regarding their learning experience and the perceived value of these activities.

In a second part (45min), session participants will be invited to engage in a facilitated multi-actor role-play designed to simulate cross-sectoral decision-making processes. This exercise will allow participants to experience the dynamics and challenges inherent to collaborative One Health initiatives. The session will conclude with a 15-min reflection on sectoral mandates, priorities, and the complexity of negotiating solutions across disciplines and sectors.

Impact

This session will illustrate how educational programmes can be designed to foster competencies for intersectoral and transdisciplinary collaboration. By presenting the CAS One Health programme as a

pedagogical *living lab,* it highlights practical approaches for strengthening the capacity of future One Health practitioners to work across disciplinary and institutional boundaries, an essential condition for effective One Health operationalisation.

Educational outcome

Participants will gain insight into the dynamics of collaborative One Health initiatives, including power asymmetries, institutional mandates, and divergent stakeholder interests, and reflect on strategies to navigate these complexities in practice. They will also learn from a continuing education program that can inspire similar initiatives for this critical and rarely offered training opportunity for practising professionals.

Talk

Feedback from the CAS One Health: how group activities served as experiencing first-hand the challenges of collaboration for One Health

Speaker

Salome Dürr**,** Prof. Dr. med. vet., Veterinary Public Health Institute, University of Bern

Simon Rüegg, Dr. med. vet., Vetsuisse Faculty, University of Zurich

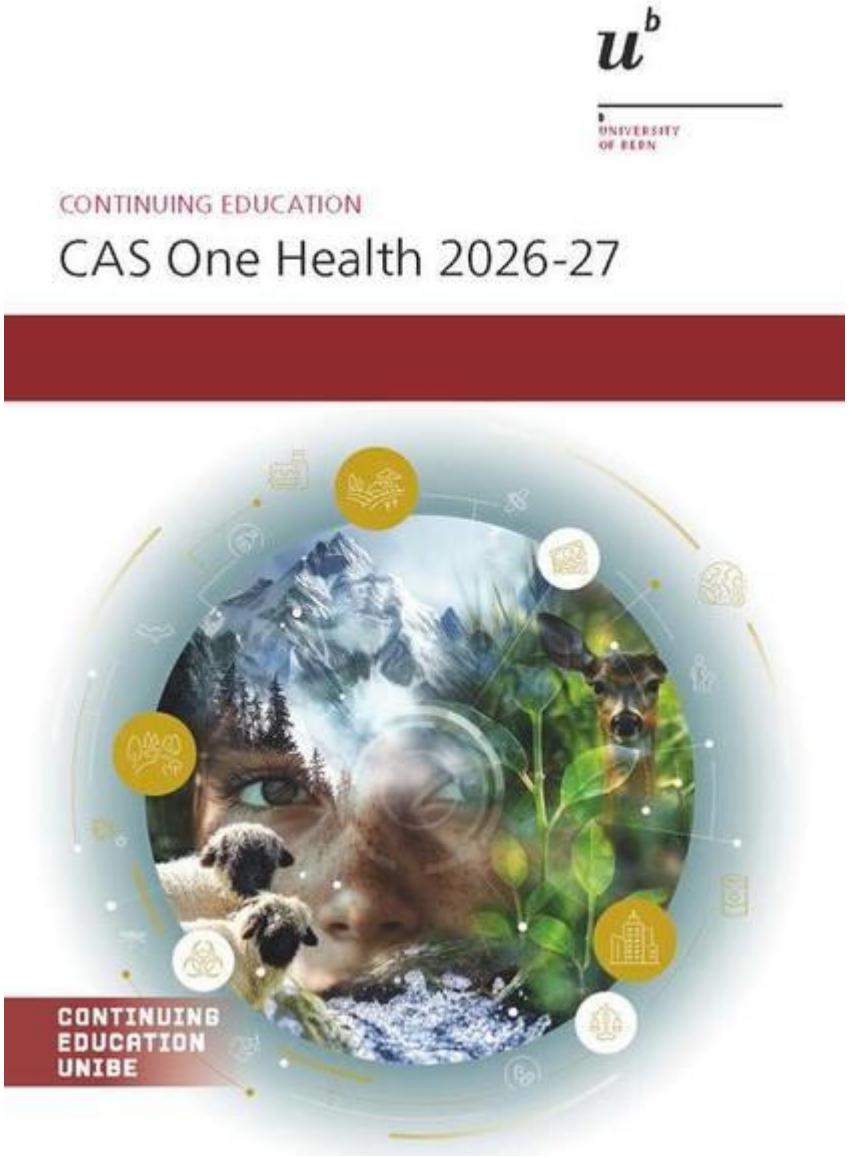
Senior chair

Jakob Zinsstag,Prof. Dr. med. vet., SwissTPH, University of Basel

Junior chair

Camille Doras,Dr. med. vet., Veterinary Public Health Institute, University of Bern

Lars Straub, PD Dr., Institute of Bee Health, University of Bern



791 – Influence of white-tailed deer abundance on tick-borne disease dynamics in periurban parks: preliminary findings

Jessica HAINAULT (1,2,3), Ariane DUMAS (2,4), Jean-Philippe ROCHELEAU (5), Catherine BOUCHARD (2,4), Jean-Pierre TREMBLAY (6), Ariane MASSÉ (2,8), Gabriel TEJ (7), Kirsten CRANDALL (9), Patrick A. LEIGHTON (1,2,3), Cécile AENISHAENSLIN (1,2,3)

1: Department of Pathology and Microbiology, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada; 2: Groupe de Recherche en Épidémiologie des Zoonoses et Santé Publique, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada; 3: Centre de recherche en santé publique de l'Université de Montréal et CIUSSS du Centre-Sud-de-l'Île-de-Montréal, Université de Montréal, Montréal, QC, Canada; 4: pplied Public Health Sciences Directorate, Science and Policy Integration Branch, Public Health Agency of Canada, Saint-Hyacinthe, QC, Canada; 5: Department of Animal Health, Cégep de Saint-Hyacinthe, Saint-Hyacinthe, QC, Canada; 6: Department of Biology, Faculty of Science and Engineering, Université Laval, Québec, QC, Canada; 7: Yamaska National Park, Société des établissements de plein air du Québec, Roxton Pond, QC, Canada; 8: Ministère de l'Environnement, de la Lutte contre les changements climatiques, de la Faune et des Parcs, Québec, QC, Canada; 9: Direction des risques biologiques, Institut national de santé publique du Québec, Montréal, QC, Canada

Background: White-tailed deer (*Odocoileus virginianus*) are the primary reproductive hosts for the black-legged tick (*Ixodes scapularis*), the principal vector of tick-borne diseases (TBD) in North America. As TBD rise globally due to climate change, understanding the ecological interactions between deer, ticks, and

pathogens is crucial for public health. This study evaluates how spatio-temporal variations in deer abundance influence TBD risk in periurban nature parks. The main hypothesis is that increased deer abundance is positively associated with higher risk of TBD, a relationship further modulated by habitat-specific environmental factors.

Methods: A longitudinal study was conducted across 50 plots within five periurban nature parks in southern Quebec, Canada, previously identified as high-exposure sites to TBD for humans and pets, and varying ecological integrity and deer abondance: two in Montréal, two in Montérégie and one in Estrie. Ticks were collected via drag sampling, from June to November 2023.Three key indicators of risk were measured: the density of *Ixodes* spp. ticks, the prevalence of various pathogens in collected ticks, and the presence of other emerging tick species. The relative abundance of deer was measured using camera traps in each study plot. Environmental characterization was conducted across all plots and included assessments of microclimatic conditions, vegetation composition and structure, as well as soil moisture levels. Multivariate statistical models are being developed to assess how deer abundance and environmental conditions influence tick density and infection prevalence at the plot level.

Results: Preliminary analysis highlights significant spatial heterogeneity in entomological risk across the five parks. Two distinct risk profiles were observed. The park with the highest nymphal proportion of infection for *Borrelia burgdorferi* (42.11%) presented a low nymphal density (0.25/100 m²) (Tab. 1). In contrast, the park with the highest nymphal density (2.09/100 m²) had a significantly lower proportion of *B. burgdorferi* infection (15.75%) (Tab.1). Overall, the density of infected nymphs per 100 m² varied substantially between parks, from 0 to 0.33/100 m2 (Tab. 1). Four pathogens co-circulated across the study sites : *Borrelia miyamotoi*, *B. burgdorferi*, *Anaplasma phagocytophilum*, and *Babesia odocoilei,* with the latter two detected at all sites (Tab. 1). The results are preliminary and analysis is still ongoing for the deer component and environmental characterization. However, camera traps recorded a mean of 371 deer detections per park over a 129-day period.

Conclusion: These preliminary findings highlight a marked heterogeneity in entomological risk within periurban parks. The high nymphal densities and significant proportion of infected ticks underscore the complexity of TBD dynamics. Ongoing analysis will correlate these findings with camera trap data and environmental metrics to determine the threshold of deer abundance that significantly influence tick-borne disease risk. This research will facilitate the development of evidence-based wildlife management and public health intervention strategies.

Table 1. Ecological characteristics of the five study parks, Québec, Canada, 2023.

Variable	Montréal-BIB	Montréal-PAP	Montégérie-MIC	Montérégie-MSB	Estrie-YAM
Deer abundance	Low	High	High	High	Low
Tick density	Moderate	Low	Moderate	High	High
Ecological integrity	High	Low	Low	High	High
Detected pathogens	Bb, Ap, Bo	Ap, Bo	Bb, Bm, Ap, Bo	Bb, Bm, Ap, Bo	Bb, Bm, Ap, Bo

Notes:
Deer abundance: Low (≤ 5 deer/km²); Moderate (5-10/km²); High (> 10 deer/km²)
Tick density: Low (≤ 0.20 nymphs/100 m²); Moderate (0.20–0.30 nymphs/100 m²); High (> 0.30 nymphs/100 m²).
Ecological integrity: Low, moderate or high.
Detected pathogens: Bb= *Borrelia burgdorferi*; Bm= *Borrelia miyamotoi*; Ap= *Anaplasma phagocytophilum*; Bo= *Babesia odocoilei*

793 – World Veterinary Environmental Alliance - Global collaboration on climate, sustainability and biodiversity

Jeannet KESSELS
World Veterinary Environmental Alliance

The veterinary profession stands at a pivotal moment in human and ecological history. Climate change, biodiversity loss, and environmental degradation are accelerating beyond safe planetary boundaries, with profound implications for animal health, human wellbeing, and global sustainability.

The World Veterinary Environmental Alliance (WVEA) has been established in response, to focus and amplify the veterinary voice in environmental action, offering a positive, coordinated, science-based, and compassionate approach to protecting our shared future.

WVEA brings together national and multinational veterinary associations, universities, veterinary sustainability groups, and industry, sharing resources across five focus areas - Global Policy, Education, Biodiversity and Sustainability In-Clinic and On-Farm. Sharing practical sustainability and emissions reduction is key.

This presentation introduces WVEA's Strategic Plan for 2026, under the banner 'Act Locally, Collaborate Globally', emphasizing the unique strengths of veterinarians as trusted, science-informed advocates who work across every community, species, and ecosystem.

WVEA invites you, and your veterinary organisation, to join. See www.worldvetalliance.org

800 – A systematic approach to identify Group A Streptococcal (GAS) antigens as targets for novel vaccine design to prevent and manage GAS autoimmune sequelae. (The iSPY-Net Study)

M Taariq SALIE (1), Shiranee SRISKANDAN (2), Liesl ZÜHLKE (3,4), Kelin ENGEL (1), Clinton MOODLEY (5), Kimona RAMPERSADH (1,6), Caitlin MEYER (1,6), **Mark E ENGEL** (1,6)

1: AFROStrep Research Initiative, Cape Heart Institute, Dept of Medicine, University of Cape Town, South Africa; 2: Section of Adult Infectious Diseases, Dept of Infectious Disease, Hammersmith Campus, Imperial College London, London, UK; 3: Children's Heart Disease Research Unit, Dept of Pediatrics, University of Cape Town; 4: Office of the VP, South African Medical Research Council, South Africa; 5: National Health Laboratory Service (Groote Schuur Hospital) & Med Microbiology, University of Cape Town, South Africa; 6: Cochrane SA, South African Medical Research Council, South Africa

Background:

An initial Group A Streptococcus (Strep A) infection, through dysregulated immune responses, may result in autoimmune sequelae such as the chronic non-communicable cardiovascular disease, Rheumatic heart disease (RHD). Although Strep A exposure is common, progression to RHD occurs in only a subset of individuals, suggesting that antigen-specific immune recognition plays a central role in disease pathogenesis. Our research, (The iSPY-Net study) sought to establish a human immune-guided antigen discovery platform, to interrogate immunodominant Strep A antigens with potential relevance to immune-mediated mechanisms underlying GAS Sequelae.

Methods:

National blood bank donated Intravenous immunoglobulin (IVIG) was utilised as a population-level archive of human polyclonal immune memory, reflecting the cumulative natural exposure to Strep A. Polyclonal IgG was immobilised onto activated chromatography resin serving as an affinity matrix for selective antigen–antibody binding. Incubation with protein extracts from highly prevalent GAS in our community enabled enrichment of GAS proteins.

Results

We have successfully produced enhanced IVIG from prominent GAS strains. Eluted proteins are to be subjected to proteomic analysis to identify immunodominant GAS antigens.

Conclusion:

We have utilised a phased approach to identify GAS antigens most frequently recognised by human immunity rather than selected solely by pathogen abundance. This platform provides a framework to prioritise antigen-specific immune targets that may contribute to the transition from acute GAS infection to chronic non-communicable cardiac disease. This work lays the foundation for rational immune-based preventive strategies, including the development of interventions aimed at reducing the global burden of RHD.

805 – Environmental Disaster and Dengue Dynamics: Evaluating the Impact of the Brumadinho Tailings Dam Collapse on Dengue Epidemiology in Minas Gerais, Brazil (2014–2023)

Gabriel R. FERNANDES (1), Aline B. M. VAZ (2), Wanderson K. de OLIVEIRA (3), Paula L. C. FONSECA (4), Eric R. G. R. AGUIAR (5), Nádia L. OLIVEIRA (6), Bruna C. LOPES (7), César R. MOTA FILHO (7), André B. S. SANTOS (8), Múcio L. P. de CASTRO (9), **Carlos E. STARLING** (10)

1: Instituto René Rachou - Belo Horizonte (Brazil); 2: Departamento de Educação Médica. Universidade Professor Edson Antônio Velano (UNIFENAS). Belo Horizonte (Brazil); 3: Hospital das Forças Armadas. Faculdade de Medicina do Centro Universitário (Uniceplac). Brasília (Brazil); 4: Departamento de Genética, Ecologia e Evolução. Universidade Federal de Minas Gerais (UFMG). Belo Horizonte (Brazil); 5: Departamento de Engenharias e Computação. Universidade Estadual de Santa Cruz (UESC). Ilhéus (Brazil); 6: Instituto Butantan. São Paulo (Brasil); 7: Departamento de Engenharia Sanitária e Ambiental. Universidade Federal de Minas Gerais (UFMG). Belo Horizonte (Brazil).; 8: Departamento de Engenharia Hidráulica e Ambiental. Universidade Federal do Ceará (UFC). Fortaleza (Brazil); 9: Pathos Ltda. Belo Horizonte (Brazil); 10: Infection Control Ltda. Belo Horizonte (Brasil)

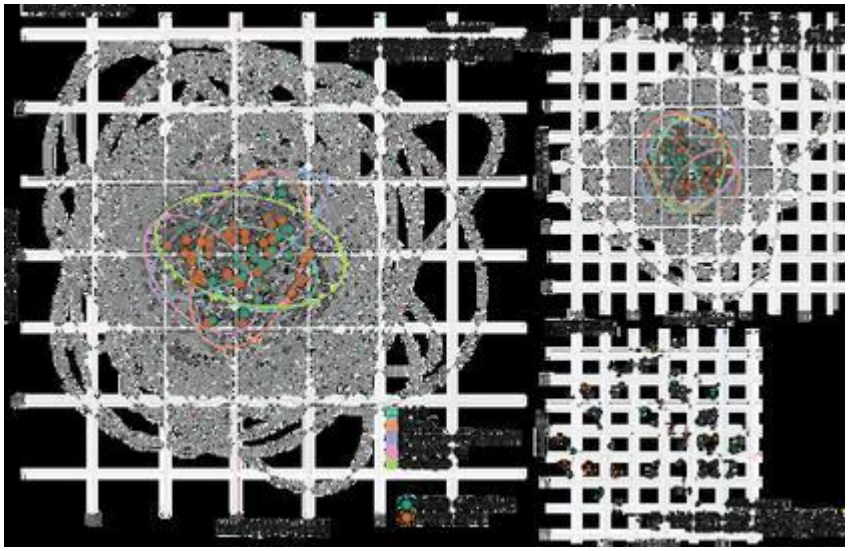
Introduction:Environmental disturbances can reshape ecological conditions that influence vector populations and the transmission dynamics of mosquito-borne diseases. In January 2019, the collapse of a mining tailings dam in Brumadinho (Minas Gerais, Brazil) released millions of cubic meters of mining

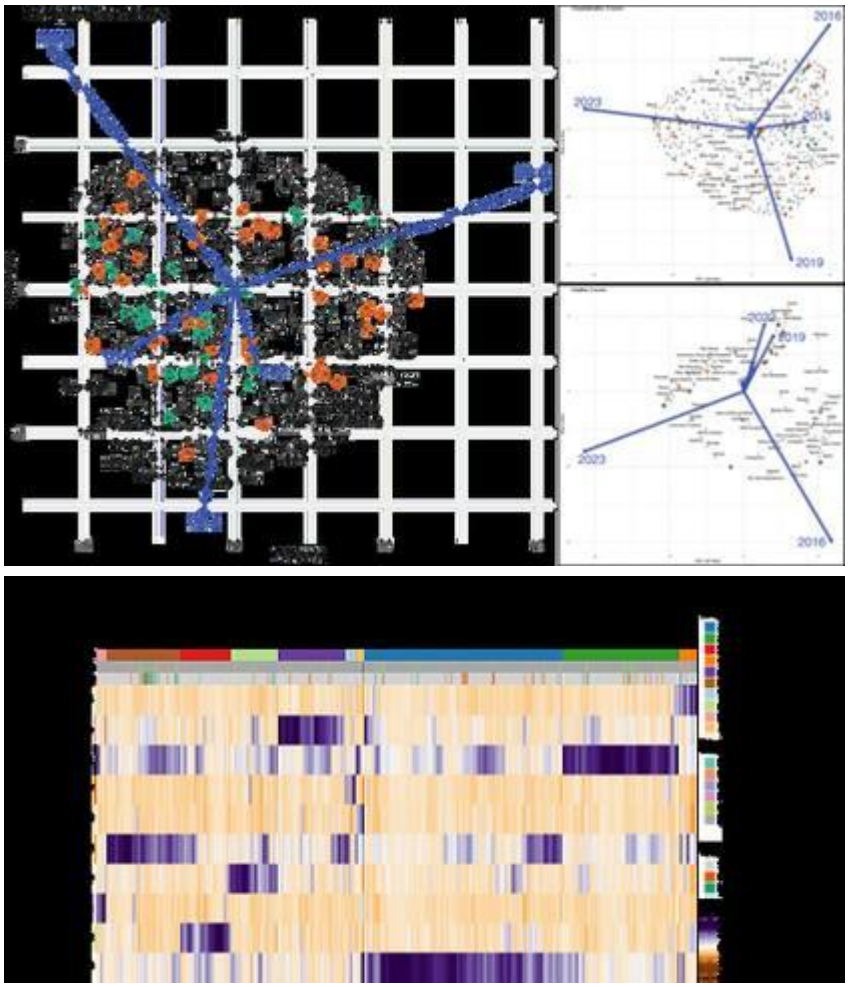
waste into the Paraopeba River basin, producing one of the largest environmental disasters in Brazilian history. Such disruptions may alter aquatic ecosystems, modify mosquito breeding environments, and potentially affect dengue transmission. Within a One Health perspective, understanding how environmental shocks influence disease dynamics is essential. This study evaluates whether the Brumadinho disaster — alongside the COVID-19 pandemic — altered the spatio-temporal patterns of dengue incidence in Minas Gerais between 2014 and 2023.

Methods:A retrospective ecological study was conducted using dengue surveillance data from the Notifiable Diseases Information System (SINAN), hospitalization records from the Hospital Information System (SIH), and mortality data from the Mortality Information System (SIM). Minas Gerais municipal dengue notifications were standardized with Z-scores to pinpoint epidemic peaks over time. Hospitalization and mortality rates were calculated per 100,000 inhabitants. Municipalities located within the Paraopeba River basin were analyzed as environmentally exposed territories potentially impacted by the dam collapse. Similarities in epidemiological patterns among municipalities were evaluated using Euclidean distance. Spatial and temporal structures were explored using Principal Coordinates Analysis (PCoA) and Principal Component Analysis (PCA). Drivers of epidemiological variability were assessed through PERMANOVA.

Results:Municipal clustering patterns in PCoA were primarily structured by geographical and administrative health regions rather than environmental exposure. PERMANOVA indicated that administrative health region explained 45% of the variability in dengue notifications, 31% in hospitalizations, and 43.9% in mortality [Figure 1]. In contrast, municipalities located within the Paraopeba River basin - representing potential environmental exposure to the mining disaster - accounted for less than 1% of the variability. PCA identified epidemic years (2016, 2019, and 2023) as the principal temporal drivers of dengue dynamics, as show in Figures 2 and 3. Despite widespread disruptions to health systems during the COVID-19 pandemic, dengue notifications in 2020 remained close to expected levels.

Conclusions:Despite a large-scale environmental disturbance affecting river ecosystems and surrounding territories, dengue epidemiology in Minas Gerais remained predominantly governed by stable spatial and seasonal transmission patterns. These findings suggest that persistent ecological suitability and regional transmission cycles may outweigh the short-term effects of isolated environmental shocks. However, sustained global environmental changes - including climate shifts, land-use modification, and ecosystem degradation - may exert long-term selective pressures on vector ecology and transmission dynamics, potentially reshaping dengue epidemiology over extended time scales. Understanding this distinction is critical for anticipating vector-borne disease risks within a changing planetary health context.





815 – A One Health Analysis of Socio-Cultural Drivers of Dog Vaccination and Post Exposure Prophylaxis Uptake: Evidence from Rural Communities in Ebonyi State, Nigeria

Terese Gabriel ORUM (1,6), Oiza Gloria MAGAJI (2), Ogbonna NWAMBEKE (3), Awashima ATI (4), Josephine ADEKOLA (5)

1: Galore Public Health Initiatives, Nigeria; 2: Regional Disease Surveillance System Enhancement Project, Abuja, Nigeria; 3: Ebonyi State Ministry of Health, Abakaliki, Ebonyi State, Nigeria; 4: Department of Nursing Science, Faculty of Medical Sciences, University of Jos, Nigeria; 5: Adam Smith Business School, University of Glasgow, Glasgow, G11 6EY, UK; 6: Department of Veterinary Public Health and Preventive Medicine, University of Ibadan, Nigeria

Background: Rabies is a 100% fatal zoonotic disease causing an estimated 59,000 human deaths each year, with most infections arising from dog bites. In Nigeria, rabies remains a major public health concern, contributing an estimated 1,600 deaths annually. Persistent transmission reflects gaps in health-seeking and disease prevention behaviors shaped by cultural beliefs and trust in healthcare providers, both traditional and biomedical. Mary Douglas' cultural theory defines four orientations: hierarchical reflects trust in authority and expert rules; egalitarian reflects collective, community-driven decisions; individualist reflects self-reliance and weak regulation; and fatalist reflects low control and resignation. We examine how these orientations, together with the Social Amplification of Risk Framework, shape dog vaccination practices and post-exposure prophylaxis (PEP) uptake in rural communities in Ebonyi State, Nigeria.

Methods: A mixed-methods design was used to examine sociocultural drivers of dog vaccination and PEP uptake. A structured questionnaire was administered to 646 randomly selected residents in Abakaliki and Ishielu communities in Ebonyi State. Quantitative data was analyzed descriptively and with Firth's logistic regression to identify predictors of vaccination behavior, PEP uptake, risk perception, and misinformation exposure. Qualitative data from four focus group discussions and fourteen key informant interviews were

thematically analyzed and interpreted using Mary Douglas' cultural theory and the Social Amplification of Risk Framework. Ethical approval and informed consent were obtained.

Results From questionnaires, dog vaccination coverage was 65.9%, despite 75.7% expressing negative perceptions of the vaccine. Over 40% reported dog bites, of whom 36.8% sought traditional treatment, while PEP uptake remained low, with 54.0% not receiving PEP. Regression analyses showed no significant socio-demographic or attitudinal predictors of dog vaccination or PEP uptake. However, middle-aged adults were significantly more likely to encounter misinformation about rabies than younger adults (OR: 1.56, 95% CI: 1.00–2.43), and individuals worried about rabies after a dog bite had higher odds of misinformation exposure (OR: 1.50, 95% CI: 1.03–2.16), indicating risk-driven information-seeking patterns. Qualitative findings provided explanatory depth, reflecting Mary Douglas' orientations. Veterinary and health workers voiced hierarchical views, favoring vaccination enforcement and WHO-recommended PEP uptake. Community leaders expressed egalitarian perspectives, presenting rabies control as a shared responsibility. Rural women and traders conveyed fatalistic beliefs, suggesting little control over dog-vaccination decisions. Men with experiences of dog bites tended toward individualistic reasoning, relying on personal judgment and traditional remedies. While all orientations appeared, hierarchical and egalitarian views were most influential in shaping how rabies risk was amplified or attenuated within rural communities.

Conclusion: Rabies prevention in rural communities of Ebonyi State reflects cultural worldviews, risk perception, and access to information. Low dog vaccination and PEP uptake persist alongside rising misinformation. Hierarchical and egalitarian orientations shape community actions. Tailoring One Health strategies with these cultural dynamics will support sustainable rabies-elimination efforts.

Figure 1: Conceptual framework illustrating cultural orientations and rabies risk dynamics in Rural Areas of Ebonyi State, Nigeria

819 – Human depopulation reshapes antimicrobial resistance dynamics in wildlife through population-level transmission

Shiori IKUSHIMA (1), Keita FUKASAWA (1), Akira YOSHIOKA (1), Kahoko TOCHIGI (1), Hisashi KOMATSU (2), Masahiko KABEYA (3), Manabu ONUMA (1), Masanori TAMAOKI (1), Seiji HAYASHI (1)

1: National Institute for Environmental Studies; 2: Fukushima Prefectural Center for Environmental Creation; 3: Fukushima Prefectural Wildlife Symbiosis Center

Background

Antimicrobial resistance (AMR) in wildlife is often interpreted as a spillover consequence of anthropogenic contamination. However, the effects of long-term human depopulation on AMR dynamics remain poorly understood. After the Fukushima Daiichi Nuclear Power Plant accident, large areas have remained uninhabited since 2011. Reduced human activity has led to rapid wildlife population growth and expansion into former human settlements. To elucidate how depopulated landscapes influence AMR dynamics in wildlife, we investigated the distribution and transmission patterns of quinolone-resistant

Escherichia coli (QRE) and third-generation cephalosporin-resistant *E. coli* (3CRE) in wildlife and environmental samples from the long-term evacuation zone (EZ) and surrounding inhabited areas (OUTSIDE) in Fukushima.

Methods

Rectal swabs were collected from 593 wild animals in EZ and OUTSIDE, together with 23 environmental samples. Ecological and anthropogenic drivers of QRE occurrence were evaluated using generalized additive models (GAMs) incorporating wildlife density estimated from camera trap surveys, land-use variables, and livestock indices. Whole-genome sequencing was performed for QRE and 3CRE isolates. Core genome single-nucleotide polymorphism (cgSNP) analysis was conducted to assess genomic relatedness and potential transmission patterns. AMR and virulence gene profiles were analyzed using NMDS and PERMANOVA to evaluate differences among host species and regions. For isolates carrying *bla*CTX-M-15, flanking sequences were compared to characterize the associated mobile genetic element structure.

Results

Despite minimal anthropogenic pressure in the EZ, the prevalence of QRE in wild boars was significantly higher than in surrounding inhabited areas. cgSNP analysis revealed extensive clonal sharing among wild boars in the EZ, suggesting within-population transmission. Consistent with this genomic pattern, GAM analysis demonstrated that QRE carriage increased with local wild boar density, supporting density-associated clonal expansion. In raccoons and masked palm civets, QRE carriage was associated with built-up and agricultural land, and isolates frequently carried ExPEC/UPEC-associated virulence genes. These findings indicate exposure to human-modified environments. Additionally, the clinically important ESBL gene *bla*CTX-M-15 was disseminated across host species via a conserved mobile genetic element, highlighting horizontal gene transfer occurring alongside clonal spread.

Conclusions

In depopulated landscapes, increased wildlife density may facilitate the amplification and persistence of AMR bacterial lineages even under reduced anthropogenic pressure. In contrast, AMR patterns in raccoons and masked palm civets remained associated with human-modified environments. These findings highlight that AMR dynamics in wildlife may be shaped by both ecological processes and anthropogenic contamination. Integrating wildlife population management into One Health AMR risk assessments will therefore be essential in depopulated landscapes undergoing human re-inhabitation. More broadly, these findings provide a conceptual basis for understanding AMR dynamics in depopulated landscapes, which are increasingly observed in rural and abandoned regions worldwide.

---

828 – Closing the Host–Pathogen Gap: A Portable Nanopore Assay for Integrated One Health Surveillance

Anna S. FOMSGAARD (1,6), Irene K. MEKI (2), Charles E. LAMIEN (2), Limmey KHUN (1), Janin NOUHIN (1), Brian N. MERRITT (3), Peter THIELEN (3), Sivyi CHHAY (4), Giorgio GONNELLA (4), Roslyn HICKSON (5,7), Paul F. HORWOOD (5,6), Erik A. KARLSSON (1)

1: Virology Unit, Institut Pasteur du Cambodge, Pasteur Network, Phnom Penh, Cambodia; 2: Animal Production and Health Laboratory, Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture, Department of Nuclear Sciences and Applications, International Atomic Energy Agency, Vienna, Austria; 3: John Hopkins Applied Physics Laboratory, Maryland, United States; 4: Unit for Bioinformatics and AI Applications, Institut Pasteur du Cambodge, Phnom Penh, Cambodia; 5: Australian Institute of Tropical Health and Medicine, James Cook University, Cairns and Townsville, Queensland, Australia; 6: College of Science and Engineering, James Cook University, Cairns, Queensland, Australia; 7: Commonwealth Scientific Industrial Research Organisation (CSIRO), Townsville, Queensland, Australia

Background

Comprehensive early warning systems can mitigate spillover and outbreak impacts, particularly in resource-limited settings with multiple zoonotic interfaces. Rapid pathogen detection typically prioritizes virus identification, while host identification is often conducted separately or not performed at all. Integrating host identification can substantially enhance genomic surveillance. The Pan-viral integrated indexed Primer (PiiP) assay, presented at the 8th World One Health Congress, targets major zoonotic virus genera; *Alphainfluenzavirus*, *Coronavirus*, *Orthoflavivirus*, and *Lyssavirus*, with recent expansion to

Orthopoxvirus, *Alphavirus*, and *Orthoebolavirus*. However, pathogen detection alone provides limited ecological context for source attribution and transmission. To address this gap, COI integrated indexed Primers (CiiP) were developed for parallel animal DNA barcoding, enabling simultaneous detection of zoonotic viruses and host species within a unified workflow deployable at the point-of-sampling.

Methods

Oxford Nanopore indexes integrated into the primers of both the PiiP and CiiP assays, eliminated conventional library preparation steps, reducing the workflow from 22 to 12 hands-on steps. The CiiP assay includes a triplex COI primer pool across invertebrate, vertebrate, and avian taxa to maximize host detection coverage. The PiiP and CiiP assay were harmonized to identical extraction protocols, PCR conditions, and library preparation, generating barcode-specific outputs for viral cDNA/DNA and host DNA reads. The CiiP assay was evaluated using direct animal and environmental samples from 67 unique species representing mammals, birds, reptiles, insects, arachnids, marsupials, and monotremes across Europe, Australia, and Southeast Asia.

The workflow was also deployed in a portable field laboratory at live bird markets in Phnom Penh and bat roosting caves in northwestern Cambodia. Sequencing was performed for two hours using a MinION Mk1D, with real-time virus classification in Basestack (v2.4.7) using MyTax2 and host identification in a custom pipeline with a COI-database.

Results

Species-level identification was achieved for 90.3% of samples, with three uncharacterized and remaining to genus-level. Simultaneous pathogen–host attribution was demonstrated across multiple zoonotic systems, including camelpox virus in camel, mpox virus in agile mangabey, SARS-CoV-2 in Eurasian beaver, and rabies virus in buffalo, cats, and Bengal fox. Influenza A and Gammacoronavirus were detected in avian hosts and environmental samples, including cage swabs and air samples collected at live bird markets in Cambodia. The portable laboratory processed samples from extraction to sequencing in under seven hours detecting pathogens and host DNA under tropical field conditions during both wet and dry seasons.

Conclusions

Reducing health risks at human–animal–environment interfaces require surveillance systems that are rapid, adaptable, and deployable in the field. The PiiP–CiiP assays enable simultaneous pathogen and host species detection directly at high-risk interfaces in a decentralized and analytically automated workflow. This approach provides improved ecological context for zoonotic surveillance and supports more actionable One Health systems.

---

830 – Community and Household investigation of Campylobacter in Kids – CHICK

Jordana BURDON BAILEY (1,2), Alfred MENYERE (2), Nicola WILLIAMS (1), Nigel CUNLIFFE (1), Gina PINCHBECK (1), Jennifer CORNICK (1,2)

1: University of Liverpool, Malawi; 2: Malawi Liverpool Wellcome Research Programme

Background:

Campylobacter is an important and common cause of childhood diarrhoea in resource limited settings. Diarrhoea is associated with increased mortality risk in children under five years old, and negatively impacts physical and neurological development. Asymptomatic carriage is common and is linked to reduced height gain in Tanzanian children. While*Campylobacter* infection is typically foodborne in high resource settings, studies from Africa suggest additional transmission routes may be important drivers of paediatric infection and illness. However, this has not been previously investigated in Malawi. We assessed associations between demographic and household factors and *Campylobacter*-associated diarrhoea in Malawian children.

Method:

We conducted a case-control study of children under five years old living in urban Blantyre, Malawi. Cases were children with diarrhoea that were *Campylobacter* positive (n=48). Controls were age and neighbourhood matched children without diarrhoea (n=82) from different households. Stools were

collected from case and control children. To investigate potential transmission pathways, we administered household questionnaires, and collected samples of water, the environment, and stool samples from up to 2 household members, and animals in the households. We used culture and polymerase chain reaction (PCR) to assess *Campylobacter* presence in samples. Multivariable analysis, controlling for sex, was used to assess associations between demographic, hygienic and environmental factors and *Campylobacter*-associateddiarrhoea.

Results:

Campylobacter was detected in 179 samples of which 70 were *C. jejuni* or *C. coli*; 6 were *C. lari* and 104 were identified only as *C. spp*; One sample had two *Campylobacter* spp. Asymptomatic carriage was common: 42.68% of controls, and 43.10% of all household members. *Campylobacter* was detected in 6.67% and 4.88% of environmental samples; 4.17% and 4.88% of water samples; 40% and 20% of animal stool samples (case and control respectively). Children with *Campylobacter*-associated diarrhoea were more likely to have adult(s) in the household with diarrhoea in the previous seven days (OR 7.02; 95% CI 1.20-40.94, p = 0.02), to have *Campylobacter* positive environmental samples (OR 6.674; 95% CI 1.530-29.11, p = 0.01), and less likely to have a dedicated food preparation area (OR 0.07; 95% CI 0.01-0.74, p = 0.01). Cases were significantly younger than controls (OR 0.93, 95% CI: 0.90-0.97, p 0.001). Asymptomatic carriage was not associated with age of either controls (OR 0.998, 95% CI: 0.97-1.03, p = 0.98) nor household members (OR 0.98, 95% CI: 0.95-1.01, p = 0.18).

Conclusions:

Our results identify clear associations between demographic and environmental factors and *Campylobacter*-associated diarrhoea. These associations suggest potential educational interventions aimed at reducing *Campylobacter*-associated diarrhoea in young children. Focusing interventions on improving household hygiene practices may lead to decreased symptomatic transmission of diarrhoeal pathogens between adults and children. Further, dedicated household food preparation areas may decrease the likelihood of *Campylobacter*-associated diarrhoea in children.

843 – Leveraging Carbon Markets to Mitigate Environmental Antimicrobial Resistance through Nature-Based Solutions

Bridget KOBUSINGYE

Medical Research council/ Uganda Virus research institute, Uganda

Background

Antimicrobial resistance (AMR) represents a critical threat to global health security, with environmental compartments serving as major reservoirs and amplifiers for resistance gene emergence and spread. Continuous inputs of antibiotics and resistant determinants from pharmaceutical effluents, agricultural runoff, and untreated wastewater drive selection pressures in aquatic and terrestrial ecosystems at sub-therapeutic concentrations. Current global AMR governance prioritizes clinical and agricultural sectors, resulting in chronic underinvestment in environmental interventions. Concurrently, carbon markets channel billions annually into ecosystem restoration, offering an innovative, underutilized mechanism to integrate climate finance with One Health objectives and address environmental AMR drivers synergistically.

Methods

We conducted a narrative evidence synthesis integrating environmental AMR research with carbon finance mechanisms to propose a conceptual policy framework. This framework assesses opportunities to strengthen carbon credit certification standards by embedding AMR-specific indicators, including reductions in antibiotic residues and antibiotic resistance genes (ARGs). It incorporates science-based targets for antibiotic concentrations in receiving waters to ensure quantifiable public health benefits. Emphasis is placed on nature-based solutions (NBS) such as constructed wetlands, mangrove restoration, and sustainable land management that concurrently enhance carbon sequestration and provide ecosystem services for AMR attenuation through filtration, adsorption, biodegradation, and plant uptake.

Results

Restored wetlands and mangroves act as effective natural biofilters, substantially reducing antibiotic residues and ARGs while generating verifiable carbon credits. Incorporating AMR metrics into established carbon verification protocols could redirect climate finance toward high-priority pollution hotspots, including pharmaceutical manufacturing zones and intensive agricultural areas identified in global river contamination assessments. This strategy creates market-driven incentives for advanced wastewater treatment and ecosystem restoration, harnessing existing financial instruments without necessitating new funding mechanisms.

Conclusions

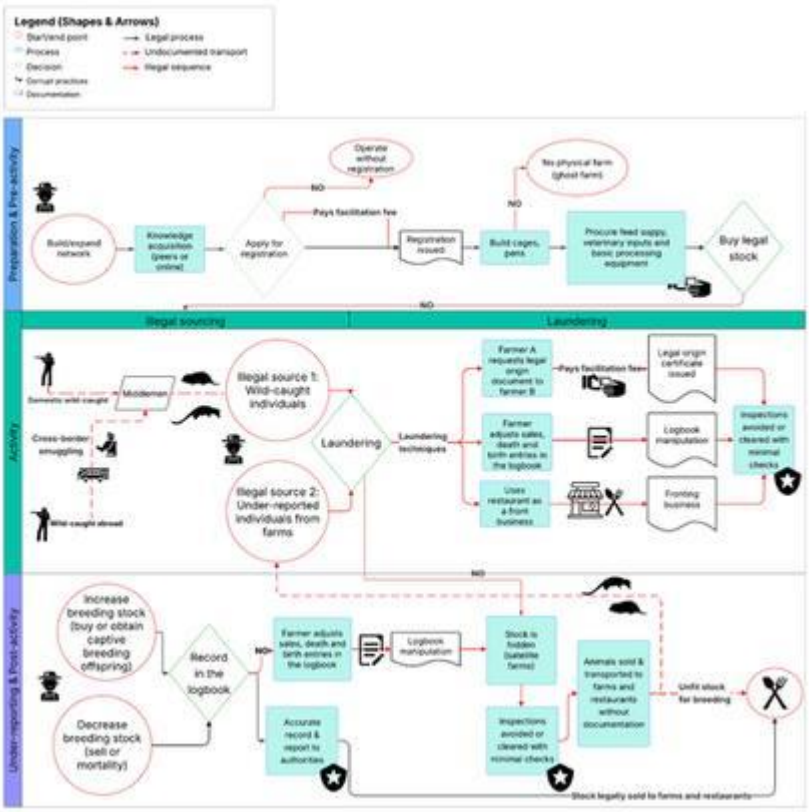
Carbon markets offer a transformative policy instrument to bridge climate finance and One Health governance, generating co-benefits for climate mitigation and environmental AMR reduction. Integrating rigorous, science-based AMR indicators into carbon credit frameworks would establish powerful economic incentives to tackle these interconnected planetary crises. Urgent development and adoption of AMR-inclusive certification standards could significantly expand the global AMR governance toolkit, delivering substantial health, environmental, and climate co-benefits at scale.

850 – From forests to chopsticks: Mapping semi-legal wildlife supply chains in Vietnam

Aitor IBÁÑEZ ALONSO (1), Thien Khoa NGUYEN PHUC (2), Trong Dat CAO TIEN (3), Thi Mai TRINH (4), Daan VAN UHM (5)

1: KU Leuven, Belgium; 2: Fulbright University Vietnam; 3: Vinh University, Vietnam; 4: United Nations Development Programme (UNDP), Vietnam; 5: Utrecht University, the Netherlands

The exploitation of wildlife for meat consumption—both legal and illegal—poses major conservation, animal welfare, and public health risks. While scholarship often centers on CITES-listed species, other species remain comparatively underexamined. Focusing on the semi-legal trade in two widely bred and consumed species in Vietnam—civets and bamboo rats—this study examines the scale of the illegal trade embedded within ostensibly legal businesses, and employs Crime Script Analysis (CSA) to map the illegal activities through two complementary scripts: a farm-based and a restaurant-based CSA. The analysis draws on 107 interviews, including 63 semi-structured interviews with farmers and restaurant operators and 44 interviews with other stakeholders, complemented by direct observations. Findings indicate that more than half of respondents (34/63) openly acknowledged engaging in illegal sourcing, even in front of authorities. Moreover, eight farms operated entirely outside the regulatory system or maintained unregistered satellite locations, while two-thirds (24/38) of registered farms reported having operated without registration for several years. Under-reporting and logbook manipulations were widespread in more than half of the farms (26/43), while ritualized inspections and facilitation payments contributed to lax regulatory oversight. Understanding these procedural dynamics provides a foundation for targeted interventions essential not only for conservation but also for strengthening zoonotic disease surveillance within a One Health framework.


Legend (Shapes & Arrows)
Start/end point
Process
Decision
Corrupt practices
Documentation
Legal process
Undocumented transport
Illegal sequence
Preparation & Pre-activity
Activity
Under-reporting & Post-activity
Illegal sourcing
Laundering
Build/expand network
Knowledge acquisition (peers or online)
Apply for registration
Operate without registration
Pays facilitation fee
Registration issued
Build cages, pens
No physical farm (ghost farm)
Procure feed supply, veterinary inputs and basic processing equipment
Buy legal stock
NO
Middleman
Illegal source 1: Wild-caught individuals
Illegal source 2: Under-reported individuals from farms
Laundering
Laundering techniques
Farmer A requests legal origin document to farmer B
Legal origin certificate issued
Logbook manipulation
Fronting business
Increase breeding stock (buy or obtain captive breeding offspring)
Decrease breeding stock (sell or mortality)
Record in the logbook
Stock is hidden (satellite farms)
Animals sold & transported to farms and restaurants without documentation
Inspections avoided or cleared with minimal checks
Accurate record & report to authorities
Stock legally sold to farms and restaurants

CHINA
MYANMAR
LAOS
VIETNAM
THAILAND
CAMBODIA
MALAYSIA
ThaiNguyen
LangSon
VinhPhuc
BacGiang
BacNinh
QuangNinh
HaNoi
HaiDuong
HungYen
HoaBinh
HaiPhong
ThanhHoa
NgheAn
HaTinh
BinhPhuoc
LamDong
BinhDuong
DongNai
BinhThuan
HoChiMinh
LongAn
BaRia-VungTau
TienGiang
Bamboo rat farm
Civet and bamboo rat farm
Civet farm
Restaurant
0
250
500 km

852 – Integrated Wildlife Surveillance and Capacity Building for Zoonotic Pathogen Detection in Laos

Chittaphone VANHNOLLAT (1), **David SAFRONETZ** (2), Philippe BUCHY (1)

1: Institut Pasteur du Laos, Lao People's Democratic Republic; 2: National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg Canada

Background

Lao People's Democratic Republic (Lao PDR) is situated within Southeast Asia, a global hotspot for the emergence and re-emergence of zoonotic pathogens, including coronaviruses, influenza viruses, bunyaviruses, and paramyxoviruses. Spillover events are typically detected only after human infections occur, highlighting the critical need for proactive wildlife monitoring and early warning systems. Furthermore, strengthening laboratory capacity for detecting high-consequence viral pathogens (HCVPs) remains essential for regional preparedness. This study aimed to integrate active field surveillance of wildlife reservoirs with enhanced laboratory diagnostic capacity to improve early detection of emerging pathogens at the human-animal-environment interface.

Methods

Through a collaboration between Institut Pasteur du Laos, National Microbiology Laboratory (Canada), Faculty of Environmental Sciences of Laos, and National Animal Health Laboratory (Ministry of Agriculture and Forestry, Laos), we conducted active field surveillance targeting wild animals, including bats, rodents, and small mammals, combined with local wet market surveys. Biological samples were collected and screened using diagnostic approaches, including PCR assays and next-generation sequencing. Concurrently, enhanced biosafety and biosecurity training was implemented for laboratory personnel handling specimens potentially containing HCVPs, including formalized training of a biosafety officer to oversee daily laboratory operations.

Results

Preliminary analyses revealed the presence of multiple viral families including *Coronaviridae*, *Paramyxoviridae*, *Hantaviridae*, and *Flaviviridae* circulating in wildlife populations and at market interfaces. These detections highlight the diversity of viruses present in Lao ecosystems. The integrated approach successfully combined field surveillance with molecular characterization while simultaneously strengthening institutional capacity for handling biological specimens that may contain high-consequence pathogens.

Conclusions

This study demonstrates the value of integrating field and molecular surveillance within a One Health framework for early detection of zoonotic pathogens. The multi-faceted approach combining ecological surveillance, advanced diagnostics, and capacity building strengthens regional preparedness and supports the development of early warning systems to ultimately mitigate the risk of zoonotic spillover events with pandemic potential.

---

862 – Voucher-verified DNA barcodes for South African bats: A tool to strengthen zoonotic disease biosurveillance

Marinda DE VRIES (1), Marike GELDENHUYS (1), Teresa KEARNEY (2,3), Rochelle RADEMAN (1), Wanda MARKOTTER (1,4)

1: Centre for Viral Zoonoses, Department of Medical Virology, University of Pretoria, Pretoria, Gauteng, South Africa; 2: Ditsong National Museum of Natural History, Pretoria, South Africa; 3: Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa; 4: Future Africa Platform, University of Pretoria, Pretoria, Gauteng, South Africa

Background: Reliable identification of wildlife reservoir hosts is essential for understanding pathogen diversity, host-virus associations, and the ecological processes that shape zoonotic spillover risk. Wildlife biosurveillance studies frequently rely on genetic reference databases that may contain incomplete or misidentified sequences, creating uncertainty in host identification during pathogen surveillance. This challenge is particularly pronounced in bats, which host a high diversity of zoonotic viruses and include many morphologically similar species that are difficult to distinguish in the field.

Methods: To address this limitation, we developed a voucher-verified DNA barcode reference library for bat species in South Africa, linked to previously collected museum specimens obtained during pathogen surveillance activities. DNA was extracted from archived tissue samples associated with morphologically confirmed voucher specimens. Multiple mitochondrial markers (COI, CytB, and 12S rRNA) were amplified using PCR and sequenced using Sanger sequencing. Sequences were quality-checked, assembled, and compared with publicly available databases to identify discrepancies. The dataset includes specimens (n=130) representing 58% of bat species known from South Africa, with efforts made to include voucher specimens of the same species sampled from multiple geographic regions across the country to account for geographic variation. Each barcode sequence was linked to specimen vouchers, geographic metadata, and curated reference records to ensure traceability, reproducibility, and long-term verification.

Results: The resulting reference library (366 sequences) provides a curated and traceable genetic dataset for reliable species identification of South African bats. By linking molecular barcodes to verified museum vouchers and associated metadata, the dataset improves the accuracy of host identification during wildlife biosurveillance and pathogen discovery. The library includes sequences for species not previously represented for all targeted barcode regions and captures geographic representation across multiple regions of South Africa, enabling assessment of intraspecific geographic variation. In collaboration with taxonomic experts, the dataset also contributed to the description of a previously unrecognised bat species and highlighted several taxa showing genetic divergence that may represent cryptic diversity requiring further taxonomic investigation.

Conclusion: Voucher-verified DNA barcode libraries are valuable tools for zoonotic disease surveillance, improving the reliability of wildlife host identification and strengthening host-virus association studies. Linking genetic data to archived museum voucher specimens and curated metadata highlights the importance of closer collaboration between disease ecologists, taxonomists, and natural history collections. Expanding biodiversity-linked reference resources across countries and wildlife host groups, including other zoonotic pathogen reservoirs such as rodents, would strengthen zoonotic risk assessment and support more integrated One Health approaches to emerging infectious diseases.

866 – Persistent colonization and zoonotic transmission of colistin-resistant Escherichia coli in different chicken farming systems in Vietnam

Thi Ngoc Minh HUYNH (1,2), Phuc Diem HO (1), Yen Xuan HUYNH (1), Mai Huynh HO (4), Hieu Quoc THAI (4), Julian PARKHILL (5), Trung Vinh NGUYEN (1,2,3), Hoa Thi NGO (1,2)

1: Oxford University Clinical Research Unit, Centre for Tropical Medicine, Ho Chi Minh City, Vietnam.; 2: Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom.; 3: Department of Veterinary Medicine, College of Agriculture, Can Tho University, Can Tho, Vietnam.; 4: Sub-Department of Animal Health, My Tho, Tien Giang, Vietnam.; 5: Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom.

Background: Antimicrobial resistance (AMR) is a major challenge to global public health. Colistin, the last-resort antibiotic for treating multi-drug-resistant Gram-negative bacteria for human infections, was ranked the 2nd highest for antimicrobial usage (AMU) on farms. Colistin resistance is driven by agricultural AMU and the spread of the plasmid-mediated *mcr-1* gene, which poses a potential risk of transmission from livestock to humans. In Tien Giang, we identified the co-existence of the two farming systems with different AMUs approaches: conventional farms with farmers' experience-based AMU and cooperative farms with AMU managed by licensed veterinarians. In this study, we aim to determine if the above-mentioned farming systems may differently impact the prevalence and long-term carriage of colistin-resistant *Escherichia coli (E. coli)*.

Methods: Chicken-farm boot swabs and human stool samples from each of the 24 farms were longitudinally collected throughout a full production cycle, with the final sampling occurring at the start of the subsequent flock. Microbiological culture was carried out to determine the prevalence of AMR bacteria and perform antimicrobial susceptibility testing (AST). Whole-genome sequencing (WGS) was performed on 321 *E. coli* isolates, followed by de novo assembly and core-genome alignment. Pairwise core-genome single nucleotide polymorphisms (SNPs) distances were calculated to assess genetic relatedness between isolates.

Results: The proportion of colistin-resistant E. coli was lower compared to that of the total coliforms. While the prevalence of colistin-resistant coliforms in conventional-farm chicken samples was higher than that of the cooperative ones, no clear difference was observed in human samples from those

systems. Colistin-resistant bacteria persisted between flocks indicating either long-term carriage or re-introduction of an ongoing circulated strain in the farm. Usage of different antibiotic classes in chicken farming, particularly macrolides (*OR*= 10.60, 95% CI= 2.59-71.70), was significantly associated with the presence of the mcr-1 gene, while certain antibiotics like sulfonamides (*OR*= 0.14, 95% CI= 0.05-0.37) and quinolones (*OR*= 0.20, 95% CI= 0.07-0.50) appeared to be protective. Farm hygiene practices such as changing shoes (*OR*= 0.43, 95% CI= 0.17-0.94) and disinfecting with lime powder (*OR*= 0.24, 95% CI= 0.13-0.43) were shown to reduce risk of *mcr-1* gene spread. Using WGS, we were able to detect 17 sharing events (long-term carriage, zoonotic sharing and household transmission) with differences in core-gene SNPs distance ≤ 10.

Discussion: The findings provide research-based local data to reinforce the compliance to biosecurity in farming practice at all farm- scales to ensure AMR reduction on farms, which will lead to prevent the transmission of AMR to human population.

Variable		Odds Ratio [1]	Lower 95% CI	Upper 95% CI	*p-value*
Usage of the antibiotic class					
	Sulfonamides	0.14	0.05	0.37	<0.001
	Quinolones	0.20	0.07	0.50	<0.001
	Macrolides	10.60	2.59	71.70	0.003
	Tetracyclines	1.77	0.76	4.33	0.20
	Beta-lactams	2.02	0.85	4.67	0.10
Usage of vitamins		0.10	0.03	0.28	<0.001
Farming practices					
	Disinfect rearing area with lime powder	0.24	0.13	0.43	<0.001
	Changing shoes prior entering the farm	0.27	0.11	0.61	0.003

[1] *OR* = Odds Ratio; CI = Confidence Interval; *p* <0.05 considered statistically significant

Table 1: Risk factors associated with the presence of *mcr-1*-harbouring isolates. Odds ratios (ORs) and 95% confidence intervals (CIs) were estimated using multivariable logistic regression. *OR* < 1 indicates a protective association, whereas *OR* > 1 indicates increased odds of *mcr-1* detection.

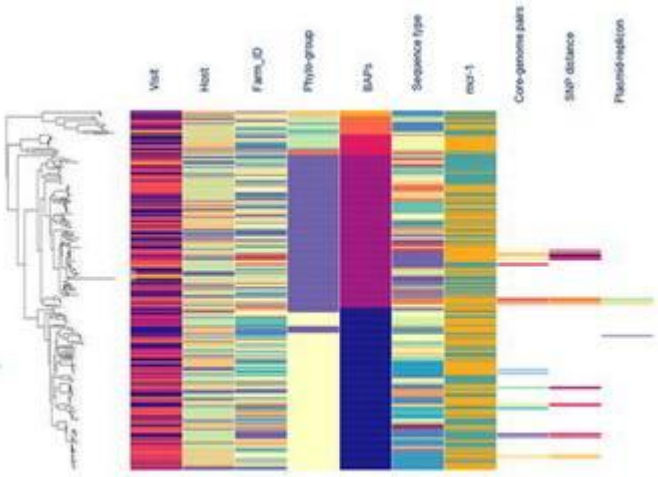


Figure 1: **Phylogenetic tree was reconstructed using core-genome alignment of 321 Escherichia coli genomes.** Maximum-likelihood tree based on core-genome alignment of 321 isolates. Colored bars indicate epidemiological and genomic characteristics, including host, farm ID, phylogroup, sequence type, mcr-1 presence, and pairwise core-genome SNP distance. Clusters with ≤10 SNPs indicate close genetic relatedness and potential transmission events.

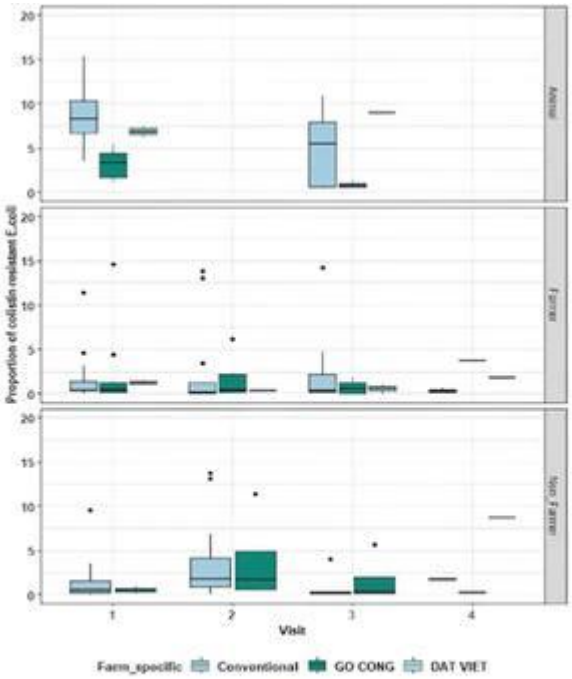


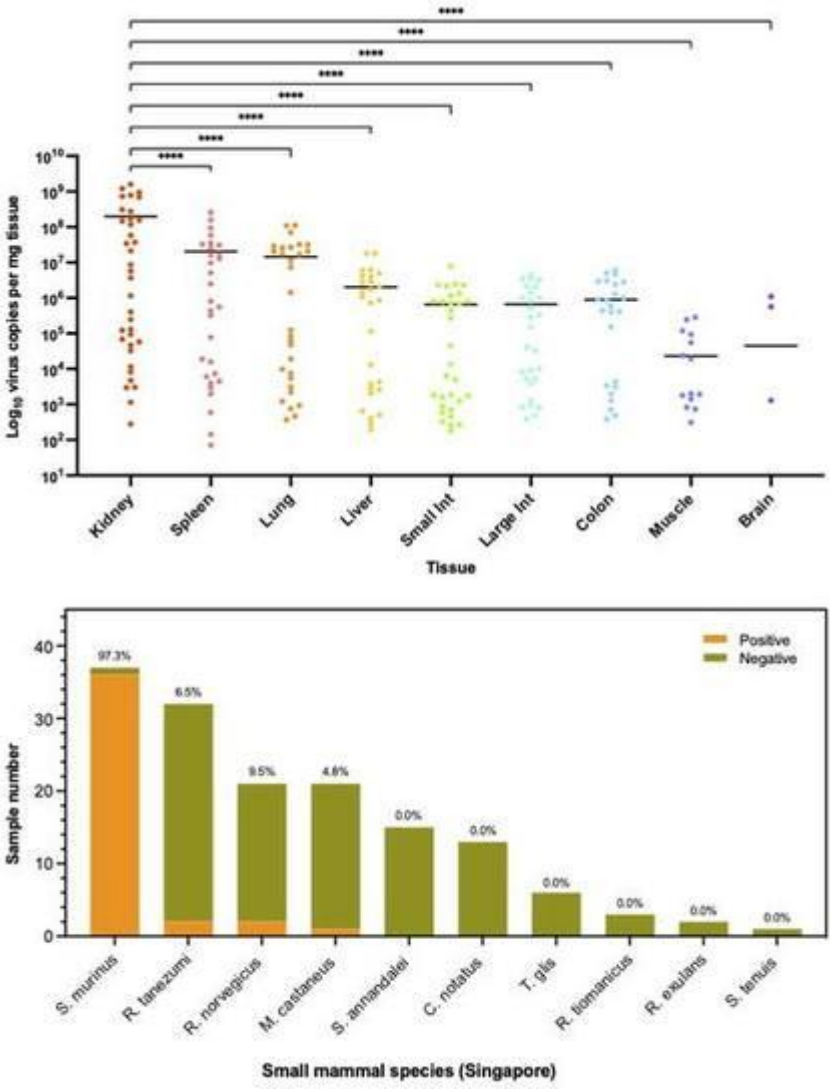
Figure 2: Proportion of colistin-resistant *Escherichia coli* stratified by hosts and farming types. Boxplots show the distribution of the proportion of resistant isolates by farm type: conventional farms and cooperative farms (GO CONG and DAT VIET).

870 – Cencurut virus (CENV): A shrew-borne Orthonairovirus with an expanded host range in urban rodents from Singapore

Dolyce LOW (1), Peter CRONIN (1), Siti-Humairah BINTE-MOHD-RODHI (1), Janin NOUHIN (2), Limmey KHUN (2), Sophoannadedh RATH (2), Vireak HEANG (2), Erik KARLSSON (2), Yvonne SU (1), Gavin SMITH (1)

1: Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore; 2: Virology Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia

Cencurut virus (CENV) is a shrew-borne *Orthonairovirus,* phylogenetically classified as a member of the *Thiafora Orthonairovirus*genogroup first detected in Asian house shrews (*Suncus murinus*) in Singapore in 2023. Orthonairoviruses are typically tick-borne viruses that infect a wide range of avian and mammalian hosts, including humans. However, no arthropod hosts have been described for members of the *Thiafora Orthonairovirus* genogroup. Since the discovery of CENV we initiated further studies to investigate host range and tissue tropism. Here we screened tissues (brain, colon, muscle, kidney, large intestine, liver, lung, small intestine and spleen) from 37 Asian house shrews. Results indicate that CENV establishes systemic infection in *S. murinus*, with high viral loads detected across all examined organs. The highest viral load was observed in the kidney, ranging from 2.8 x 102 to 1.6 x 109 viral copies per mg of tissue (mean = 2.0 x 108), followed by the spleen, lung, liver, colon, large intestines, small intestines, brain, and muscle. We also report the first detection of CENV in rodents, specifically urban species including *Rattus norvegicus*(n=2/21), *R. tanezumi* (n=2/31) and *Mus castaneus* (n=1/21). CENV was not detected in peri-urban species such as *Callosciurus notatus, R. exulans, R. tiomanicus, Sundamys annandalei, Sundasciurus tenuis* or *Tupaia glis*, though this may be due to small sample sizes (n=113). A larger sample set (n=715) from Cambodia – including *Suncus murinus, R. exulans, R. norvegicus, R. rattus, R. argentiventer, Mus* spp., and *Bandicota* spp. – all tested negative for CENV (0%), suggesting CENV may be endemic to Singapore. Future work will focus on generating rodent-derived CENV genomes to investigate potential host-switching mutations and conducting serological studies to assess *Orthonairovirus* exposure in small mammals and humans to clarify the ecological range and potential zoonotic risk of this virus.



873 – Beyond Infrastructure: Multilevel drivers of meat safety risk at traditional food markets in a Low-Middle-Income Indigenous setting

Harsha KUMARI, Uday HAJONG, Adenson KHARBULI, Melari NONGRUM, Rajiv SARKAR
Indian Institute of Public Health, Northeast Regional Hub, India

Background

Globally, 600 million people fall sick annually from foodborne diseases; largely linked to animal-source foods which act as carriers of zoonotic pathogens (*Salmonella*, *Campylobacter*, *E. coli)*. This burden is disproportionately higher in low- and middle-income countries. In India, the north-eastern indigenous tribes, culturally prefer an animal-origin diet sourced from traditional food markets. However, varied operational standards and regulatory oversight at such informal community hubs, present inherent zoonotic disease transmission risks. This mixed-methods study aims to explore the *meat market hygiene from slaughter to sale in traditional food markets* in urban Meghalaya, a hilly tribal state in northeast India.

Methods

A cross-sectional survey was conducted among 235 retail meat vendors across 14 traditional food markets using stratified sampling approach. An adapted questionnaire assessed *food safety knowledge and practices* using 30 and 20 items, respectively. Responses were considered satisfactory using the 75th percentile thresholds (21 points for knowledge and 12 points for practices). Descriptive statistics

summarized sociodemographic characteristics. Associations were tested using univariate logistic regression and reported as odds ratios with 95% confident intervals. In-depth interviews (10) were conducted with purposively selected abattoir workers and retail meat handlers to gain deeper insights into slaughter to sale practices. Qualitative data was analyzed thematically.

Results

Among retail vendors, 60% did not reach the 75th percentile knowledge threshold (mean ± SD: 19.6 ± 2.8). Likewise, 64.3% did not meet the practice threshold (mean ± SD: 10.7 ± 2.3). Education ≥10th standard (OR: 2.5, 95% CI: 1.1–5.7) and possession of food safety license (OR: 3.6, 95% CI: 1.2–10.7) were associated with better *knowledge* only. Almost all (97%) retail meat vendors reported hand washing before and after meat handling reduces contamination risks; however, only 18% were consistently practicing handwash. Majority (94%) cleaned the knives, slaughter and storage areas, but only few (17%) used personal protective gear. Qualitative findings corroborated the quantitative results demonstrating non-uniform exposure to formal food safety and meat processing training. Infrastructure-wise, lack of cold chain logistics for meat storage and transport was observed. The pre-post slaughter health inspection of livestock was not uniformly regulated. Environmentally, waste disposal systems for the meat by-products were largely negligible in this setting. Despite the aforementioned resource constraints, meat handlers acted as responsible stakeholders in meat safety governance by excluding drug treated sick animals from the slaughter chain.

Conclusions

The study highlights meat safety challenges at traditional food markets in low resource settings are shaped by interconnected behavioral, infrastructural and regulatory factors. These factors may influence zoonotic disease transmission. Addressing these gaps requires coordinated interventions, including vendor education, improved market facilities, and routine inspections to promote safer meat handling. Lastly, regular monitoring and surveillance by the Food Safety and Standards Authority of India may sustain the long-term benefits.

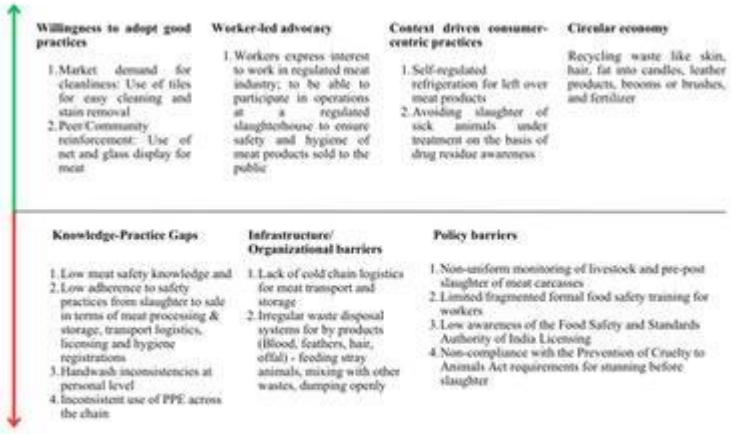


Figure 1. An Integrated Conceptual Model of Meat Safety among Retail Vendors and Abattoir Workers: Identifying Key Gaps and Intervention Points in a Low-Resource Indigenous Setting. The red arrow indicates the negative drivers and the green arrow indicates the positive drivers.

Supporting figures and tables

Table 1. Responses to Questions Assessing Food Safety Knowledge among Meat Handlers in Shillong, Meghalaya, India (n = 235)

Statements & Options	Responses n (%)
Understanding of the term "Food safety"	180 (76.6%)
Understanding the meaning of safe meat handling practices	214 (91.1%)
An ideal place to store raw meat	107 (45.5%)
Correct temperature for storing meat	37 (15.7%)
Safe method to stop the growth of bacteria	102 (43.4%)
Leftovers of processed meat be stored	217 (92.3%)
Importance of inspecting meat	190 (80.9%)
Regular hand washing before and after meat handling reduces the risk of contamination	228 (97%)
Is it advisable to wash hands after handling waste or garbage	233 (99.1%)
Eating and drinking in the workplace can increase the risk of meat contamination	29 (12.3%)
Using gloves while handling meat will reduce the risk of contamination	119 (50.6%)
Safe meat handling to avoid contamination and diseases is part of your job responsibilities	234 (99.6%)
Using different knives and cutting boards for meat and offal is important	199 (84.7%)
Proper cleaning and sanitisation of working surfaces and tools reduce the risk of meat contamination	230 (97.9%)
Knives, hooks, and cutting boards can be a source of food contamination	121 (51.5%)
Keeping working surfaces and utensils clean reduces the risk of illness for consumers	233 (99.1%)
Insects (flies, cockroaches, etc.) and pests (rats, mice, etc.) can be a source of contamination to raw meat	225 (95.7%)
Consumption of contaminated meat can cause diarrhoea	221 (94%)
Awareness of microbes like E. coli, Staphylococcus, etc.	16 (6.8%)
Microbes are present on the hands, skin, nose, and ears of healthy meat handlers	132 (57%)
The word "clean" is the same as the word "sanitised"	152 (64.7%)
Cross-contamination can occur when microorganisms from contaminated meat are transferred by the meat handler's hands or utensils to another surface or meat	220 (93.6%)
Contaminated meat always shows visible changes in colour, odour, or taste	224 (95.3%)
Can people with open skin diseases and injuries should handle raw meat	183 (77.9%)
Climate change can affect the quality of meat	186 (79.1%)
It is important to evaluate the health status of meat handlers before employment	196 (83.4%)
Regular training will improve meat safety and hygiene practices	228 (97%)
Awareness of the requirement to obtain a license under the Food Safety and Standards Act, 2006, or FSSAI	35 (14.9%)

Table 2. Participant characteristics influencing food safety knowledge and practices

Variables	Food safety knowledge level				Food safety practice level			
	Satisfactory	Unsatisfactory	p-value	Odds Ratio (95% CI)	Satisfactory	Unsatisfactory	p-value	Odds Ratio (95% CI)
Age (years)								
18-29	32(34.78)	60(65.22)	-	Reference	14(15.22)	78 (84.78)	-	Reference
30-44	48(42.48)	65(57.52)	0.26	1.38 (0.78-2.44)	13(11.50)	100 (88.50)	0.43	0.72(0.32 - 1.62)
45-65	14(46.67)	16(53.33)	0.24	1.64 (0.71 - 3.78)	1 (3.33)	29 (96.67)	0.11	0.19(0.02 - 1.52)
Sex								
Male	83(40.3%)	123(59.7%)	0.8	1.104 (0.49-2.45)	27(13.11)	179 (86.89)	0.165	4.22(0.55-32.32)
Female	11(37.9%)	18(62.6%)	-	Reference	1(3.45)	28 (96.55)	-	Reference
Education								
No formal education	12(27.91)	31(72.09)	-	Reference	4 (9.3)	39 (90.70)	-	Reference
Basic education	47(38.84)	74(61.16)	0.2	1.64 (0.76-3.50)	14(11.57)	107 (88.43)	0.68	1.27(0.39 - 4.11)
High education	35(49.30)	36(50.70)	0.02	2.51 (1.11 - 5.66)	10(14.88)	61 (85.92)	0.45	1.59 (0.46 - 5.45)
Years of Experience								
0-5 years	36(37.5)	60 (62.5%)	-	Reference	13(13.54)	83 (86.46)	-	Reference
6-10 years	19(35.85)	34 (64.15%)	0.84	0.93(0.46-1.87)	5(9.43)	48 (90.57)	0.46	0.66 (0.22 - 1.97)
>10 years	39(45.35)	47 (54.65%)	0.28	1.38(0.76 - 2.50)	10 (11.63)	76 (88.37)	0.69	0.84 (0.34 - 2.02)
Food Safety Training								
Yes	12(54.5%)	10(45.5%)	0.14	1.91(0.79 - 4.63)	3(13.64)	19(86.36)	0.79	1.18 (0.32-4.30)
No	82 (38.5%)	131(61.5%)	-	Reference	25(11.74)	188(88.26)		Reference
Food Safety License								
Yes	11(68.8%)	5(31.3%)	0.02	3.60 (1.20 - 10.74)	4(25.00)	12(75.00)	0.106	2.7(0.80 - 9.06)
No	83(37.9%)	136(62.1%)	-	Reference	24(10.96)	195(89.04)		Reference

Note: Pearson correlation coefficient (r) for knowledge and practice is 0.278*

878 – A Blueprint for Fostering a One Health Culture: The ICBAS Governance Model for Science Communication and Public Engagement

Adriano A. BORDALO (1,2), **Begoña PEREZ-CABEZAS** (1,3,4), Dalila VEIGA (1,5), João R. MESQUITA (1,6,7), Sofia A. COSTA LIMA (1,8)

1: ICBAS - School of Medicine and Biomedical Sciences, University of Porto, Rua Jorge Viterbo Ferreira 228, 4050-313, Porto, Portugal; 2: CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Novo Edifício do Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos S/N, 4450-208, Matosinhos, Portugal; 3: EPIUnit - Institute of Public Health, University of Porto, Rua das Taipas 135, 4050-600, Porto, Portugal; 4: Laboratory for Integrative and Translational Research in Population Health (ITR), Porto, Portugal; 5: Department of Anaesthesiology, Multidisciplinary Chronic Pain Unit, Centro Hospitalar Universitário Do Porto, Unidade Local de Saúde de Santo António, Largo Professor Abel Salazar, 4099-001, Porto, Portugal; 6: Centro de Estudos de Ciência Animal (CECA), Instituto de Ciências, Tecnologias e Agroambiente (ICETA), University of Porto, 4051-401, Porto, Portugal; 7: Associate Laboratory for Animal and Veterinary Science (AL4AnimalS), 1300-477, Lisboa, Portugal; 8: LAQV-REQUIMTE, Praça Coronel Pacheco, 15 6º, 4050-453 Porto, Portugal

The School of Medicine and Biomedical Sciences (ICBAS), University of Porto (Portugal), has brought together human, animal, and environmental health since its foundation in 1975, anticipating the One Health approach within the academic landscape. However, fully embedding this integrated vision required an institutional structure capable of guiding, coordinating, and strengthening it. In 2021, the One

Health Office was created at ICBAS as a governance mechanism to align strategies, support internal adoption, and promote a shared commitment to One Health across the school.

Composed of Professors and researchers from medicine, veterinary and environmental sciences, the Office has developed an internal policy rooted in strategic communication, literacy, and active participation. Through regular initiatives such as the “One Health Talks” and the “One Health PhD Forum”, it fosters interdisciplinary dialogue and embeds One Health thinking within academic practice, contributing to a more integrated organisational culture.

In parallel, it coordinates external public engagement activities that reinforce the institution’s social responsibility by translating One Health principles into accessible and participatory experiences. Events such as the Expo One Health, the One Health in Schools programme, and cultural or editorial initiatives serve as collaborative governance tools linking the university with the civil society, policymakers, and multigenerational audiences.

The ICBAS model demonstrates how dedicated structures, clear policies, and participatory communication strategies can consolidate a genuine One Health culture. It offers a replicable governance approach for institutions seeking to strengthen interdisciplinarity and enhance societal impact.

890 – Integrated One Health surveillance of human, canine and sand fly Leishmania infantum transmission in Sicily, southern Italy

Federica BRUNO (1), Eugenia OLIVERI (1), Francesco LA RUSSA (1), Maria Liliana DI PASQUALE (1), Maria Paola MAURELLI (2), Gaetano OLIVA (2), Giuseppe PISTONE (3), Fabrizio VITALE (1), **Germano CASTELLI** (1)

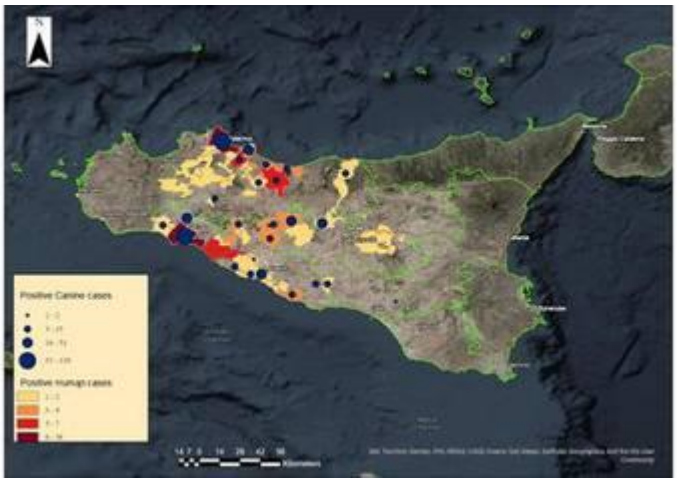
1: Istituto Zooprofilattico Sperimentale della Sicila, Italy; 2: Department of Veterinary Medicine and Animal Production, University of Naples Federico II, 80137 Naples, Italy.; 3: UOC di Dermatologia e MTS, Azienda Ospedaliera Universitaria Policlinico Paolo Giaccone, 90127 Palermo, Italy.

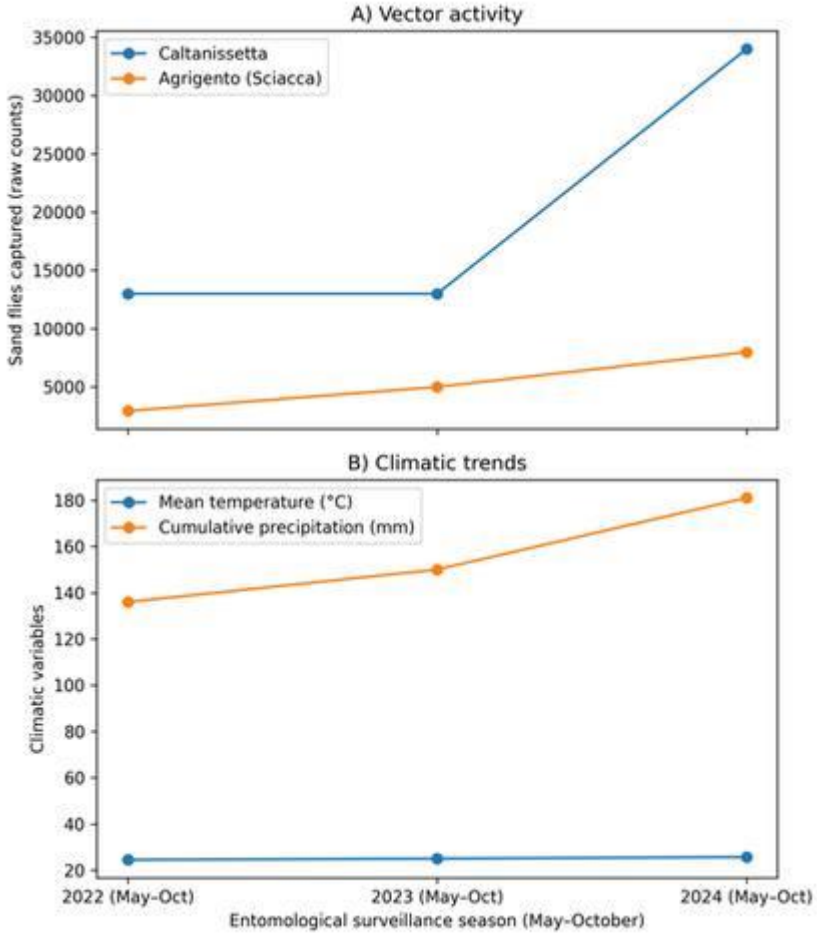
Background: In Mediterranean endemic areas, human leishmaniasis risk emerges from the convergence of infected reservoirs, permissive vector ecology, and environmental conditions. In Sicily, *Leishmania infantum* circulates widely, but the extent to which human detections co-occur in space and time with canine infection and sand fly abundance—under local microclimates—remains insufficiently characterized to guide targeted prevention.

Methods: We developed a One Health surveillance framework in Sicily (2022–2024) integrating clinical, veterinary, entomological and meteorological information across three provinces (Palermo, Agrigento, Caltanissetta). Suspected human visceral/cutaneous leishmaniasis cases were captured through hospital-based pathways (infectious diseases/dermatology) and confirmed by PCR and/or IFAT; structured questionnaires collected demographic and exposure variables. Following human detections, canine serosurveys were conducted in the same municipalities in owned and shelter dogs using IFAT (positive threshold ≥1:160). During May–October, peri-domestic CDC light traps were used for sand fly monitoring and male specimens were identified morphologically to species. Monthly temperature and precipitation from the regional agrometeorological network (SIAS) were descriptively aligned with seasonal vector patterns.

Results: Of 561 human clinical samples, 65 were confirmed positive (11.59%): 50 cutaneous (76.9%) and 15 visceral (23.1%). Most confirmed cases occurred in Palermo (44/65; 67.7%) and Agrigento (20/65; 30.8%). Positivity was more frequent among individuals aged 51–70 years (p=0.002). Outdoor occupational exposure was strongly associated with infection (p0.001), and smoking was associated with PCR positivity (p=0.039). In dogs (n=3,046), seroprevalence varied between 12% and 34% across municipalities, with spatial concordance between higher canine positivity and human case clusters. Entomological monitoring collected 75,376 sand flies (16,309 in 2022; 17,212 in 2023; 42,355 in 2024), with pronounced geographic heterogeneity: Caltanissetta accounted for 80.6% of captured specimens. *Phlebotomus perniciosus* was predominant, while *Ph. papatasi* was documented in Agrigento. Peak vector activity occurred during months averaging ~20–28 °C and following moderate rainfall; the highest densities coincided with the warmest/wettest surveillance season (2024).

Conclusions: Linking human diagnostics, canine sentinel data, vector monitoring and local climate highlighted consistent “risk convergence” zones and seasons for *L. infantum* transmission in Sicily. This integrated One Health approach can strengthen early warning, prioritize geographically focused interventions, and support climate-informed preparedness in endemic Mediterranean settings.





897 – Building up One Health Exploratories in the African tropics

Oby Zéphirin WAYORO (1,2,3), Kathrin NOWAK (1), Franziska STOEK (1), Filipe DIAS (1), Léonce KOUADIO (1,4,5), Niklas FLOSS (1,6), Yanthe NOBEL (1), Frédéric SINGHA (1,7), Dominic BLÄSING (1), Markus ULRICH (1), Elangwe Milo SARAH-MATIO (1), Larin GIERSE (1), Vincent ACHI (2,3), Stéphane YOUFEINA (7), Inza KONÉ (4), Emmanuel NAKOUNE (8), Fabian LEENDERTZ (1), Fee ZIMMERMANN (1)

1: Helmholtz Institute for One Health, Greifswald, Germany; 2: Centre Hospitalier et Universitaire de Bouaké, Côte d'Ivoire; 3: Université Alassane Ouattara de Bouaké, Bouaké, Côte d´Ivoire; 4: Centre Suisse de Recherches Scientifiques, Abidjan, Côte d´Ivoire; 5: Peleforo Gon Coulibaly University Korhogo, Korhogo, Côte d'Ivoire; 6: University Medicine Greifswald, Greifswald, Germany; 7: World Wide Fund for Nature, Central African Republic; 8: Institut Pasteur de Bangui, Bangui, Central African Republic

The African tropics are a hotspot for emergence of zoonotic diseases and AMR, with high biodiversity, a large degree of ecological change and often-insufficient health infrastructures. This leads to an increased risk for the emergence of novel pathogens at the human/animal/environment interface. Therefore, surveillance and research approaches with a focus on One Health are of particular importance in this setting. The Helmholtz Institute for One Health (HIOH) and its partners are dedicated to addressing the interdependence of human, animal, and ecosystem health and how they are affected by climate change.

Similar to weather stations that record various parameters over many years, we systematically collect and analyze a broad spectrum of samples and data at high resolution in defined indicator regions, so called One Health Exploratories (OHE). The OHEs focus on a range of topics, including human and animal health, vectors, climate and biodiversity. The first two OHEs are placed in Côte d'Ivoire (CIV) and Central African Republic (CAR), both in and around rain forest areas. OHEs are always built up in collaboration with local partners. HIOH has stable long-term partnerships with collaborators in Côte d'Ivoire (over 25 years) and Central African Republic (over 10 years). These ties include research institutes, hospitals, communities, NGOs and authorities.

The following data is included in the OHE setup: To determine which pathogens are relevant for the population in the OHE regions, we are collaborating with local health centers and providing on-site diagnostics. We are running veterinary programs to detect wildlife diseases in CIV and CAR using non-invasive methods such as the analysis of urine and fecal samples, as well as necropsies of wild animals found dead. Currently we are setting up cohort studies with healthy human volunteers whose health we will follow over the course of many years. In addition, we will systematically survey associated livestock, vectors, biodiversity and micro - and macroclimate.

Integration of this data from multiple disciplines will provide important information for stakeholders and contribute to the development of efficient measures for pandemic prevention and preparedness. The OHEs can be a blueprint to be copied and multiplied around the world for a healthier future for humans, animals, and the environment. Moreover, they foster interdisciplinary cooperation beyond health research. With a commitment to sustainable development of structures and skills among the local population, OHEs will train the next generation of a global One Health workforce and strengthen regional and national research infrastructure.

904 – Prioritization of interventions to reduce antimicrobial use in dairy cows: a multicriteria decision analysis

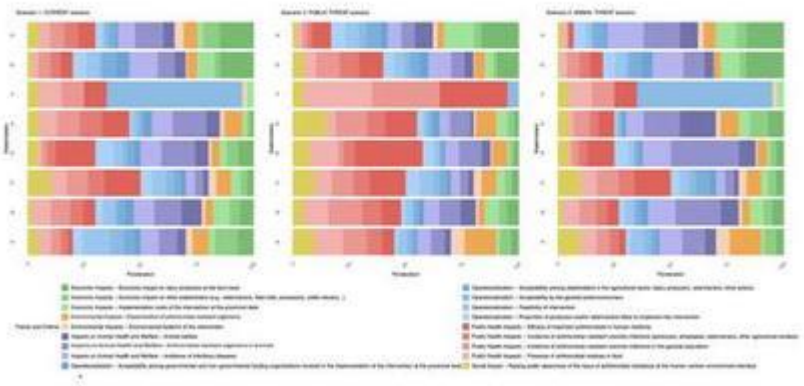
Nikky MILLAR (1,2,3,4,6), Simon DUFOUR (1,2,4), Jean-Philippe ROY (1,4,5), Maud DE LAGARDE (1,4,7,8), Juan Carlos ARANGO-SABOGAL (1,2,4), Catherine BELLOC (6), Cécile AENISHAENSLIN (1,2,3)

1: Department of Pathology and Microbiology, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada; 2: Groupe de recherche en épidémiologie des zoonoses et santé publique (GREZOSP), Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, CanadaBiologie, Épidémiologie et Analyses de risque en santé animale (BIOEPAR), ONIRIS-INRAE, Nantes, France; 3: Centre de recherche en santé publique, Université de Montréal et Centre intégré de santé et de services sociaux du Québec du Centre-Sud-de-l'Île-de-Montréal, Montréal, QC, Canada; 4: Regroupement FRQ Op+lait, Saint-Hyacinthe, QC, Canada; 5: Department of Clinical Sciences, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada; 6: iologie, Épidémiologie et Analyses de risque en santé animale (BIOEPAR), ONIRIS-INRAE, Nantes, France; 7: World Organization for Animal Health (WOAH) Reference Laboratory for Escherichia coli, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, J2S 2M2, Canada; 8: Swine and Poultry Infectious Research Center (CRIPA-FQRNT), Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, J2S 2M2, Canada

Background: Antimicrobial resistance (AMR) is a global health challenge affecting humans, animals, and the environment, making it a central One Health concern. Addressing AMR requires coordinated cross-sectoral actions that protect public health while maintaining animal health, welfare, and sustainable food production. In the province of Québec (Canada), a 2019 regulation restricted the use of Category I AMs in livestock, as defined by Health Canada (including third- and fourth-generation cephalosporins, polymyxins, and fluoroquinolones). This policy shift aimed to preserve AMs critical for human medicine. However, regulation alone cannot fully prevent AMR spread, highlighting the need for complementary, context-adapted, and evidence-based interventions acceptable to stakeholders.Objectives: This study developed a participatory Multi-Criteria Decision Analysis (MCDA) model to identify and prioritize interventions limiting the dissemination of antimicrobial-resistant microorganisms originating from dairy herds in the province of Québec while supporting animal health and farm viability.Methods: The MCDA model was co-constructed with stakeholders from agricultural, veterinary, public health, governmental,

and consumer sectors. Twenty-two interventions were evaluated across 18 criteria covering public health, animal welfare, environmental, economic, social, and operational dimensions. Stakeholders weighted criteria under three AMR scenarios: (1) CURRENT, reflecting the existing situation; (2) PUBLIC THREAT, reflecting increased human AMR infections; and (3) ANIMAL THREAT, reflecting increased AMR infections in dairies. Intervention performance was informed by literature review and expert elicitation. Sensitivity analyses assessed ranking robustness.Results: Across scenarios, three interventions consistently ranked highest: (i) producer education, particularly mandatory AM stewardship training; (ii) financial support for preventive veterinary activities, such as herd health monitoring subsidies; and (iii) strengthened disease surveillance through mandatory reporting systems. These interventions were considered effective for reducing AMU and limiting resistance spread while maintaining animal welfare, feasibility, and social acceptability. In contrast, stricter regulations on AMU and sales ranked lowest. Stakeholders raised concerns about economic uncertainty, limited impact on resistance spread, unintended animal welfare consequences, and lower professional acceptability, despite recognizing their theoretical potential.Discussion: The participatory MCDA improved transparency, encouraged cross-sector dialogue, and helped stakeholders find common ground. By combining scientific evidence with practical experience, this decision model made the One Health approach more actionable for AMR decision-making. The prioritization of educational, preventive, and surveillance interventions reflects a preference for upstream multidisciplinary strategies that address root causes of AMU rather than relying mainly on restrictive interventions. These preventive approaches promote coordination across sectors and support sustainable AM stewardship while balancing public health, animal welfare, environmental concerns, and farm-level feasibility.Conclusions: Although tailored to the province of Québec's dairy sector, this adaptable model provides a transferable foundation for prioritizing AMR mitigation strategies across livestock systems and regions. Participatory MCDA offers a practical tool to align policy decisions with One Health principles while ensuring feasibility, acceptability, and long-term sustainability.

Stakeholders' weightings across the CURRENT scenario, the PUBLIC THREAT scenario and the ANIMAL THREAT scenario, grouped by theme and criterion, included in the multicriteria decision analysis (MCDA) tool designed to limit the dissemination of antimicrobial-resistant organisms from dairy herds in the province of Québec, Canada.



910 – Operationalizing One Health at the local level: a Theory of Action and Reflection tool

Syed ABBAS (1), Manish KAKKAR (2), Pushpa WIJESINGHE (2), Tim SHORTEN (3)

1: Institute of Development Studies, United Kingdom; 2: World Health Organization Regional Office for South East Asia, India; 3: Independent consultant

Background

Zoonotic influenzas continue to pose a major global health threat due to their pandemic potential and the complex, multisectoral nature of their prevention and control. Despite long-standing advocacy for One Health and other multisector partnerships (MSPs), countries frequently struggle to operationalize such approaches at national and subnational levels. Existing guidance tends to overlook the social, political, ecological, and institutional dynamics that shape collaboration, contributing to a persistent gap between policy aspirations and implementation realities. To address these challenges, this study sought to develop a practical framework that characterizes the functioning of MSPs for zoonotic influenza and

provides structured guidance to support programme managers in designing and adapting collaborative arrangements suited to local contexts.

Methods

The study synthesized insights from a prior critical review of academic and programmatic literature on intergovernmental and multisector collaborations, alongside iterative consultations with researchers and programme managers engaged in zoonotic influenza preparedness and response. Drawing on these sources, the authors developed a Theory of Action (ToA) that aligns with and elaborates components of the One Health Quadripartite's Theory of Change. The ToA was then used to construct a structured reflection tool aimed at helping country-level programme managers identify MSP characteristics, understand partner expectations, and strengthen collaborative processes. Additional programmatic attributes were developed to support the systematic categorization of MSPs according to varying 'levels' of strength.

Results

The study produced a Theory of Action comprising five interlinked elements—**Starting Conditions**, **Characterization**, **Collaborative Process**, **Outputs**, and **Responsiveness**—that explain how multisector partnerships can be activated and sustained for zoonotic influenza prevention and control. A key contribution is the development of a set of **'additional attributes'**—Information, Interaction, Activities, Outputs, Resources, and Governance—which enable managers to **categorize MSPs by their level of strength** across 11 possible configurations. This provides a nuanced, non-normative typology that recognizes the diverse institutional realities within which MSPs operate. The accompanying Reflection tool translates the ToA into a practical instrument for eliciting MSP characteristics, clarifying motivations, examining governance arrangements, and identifying strategies to enhance collaboration.

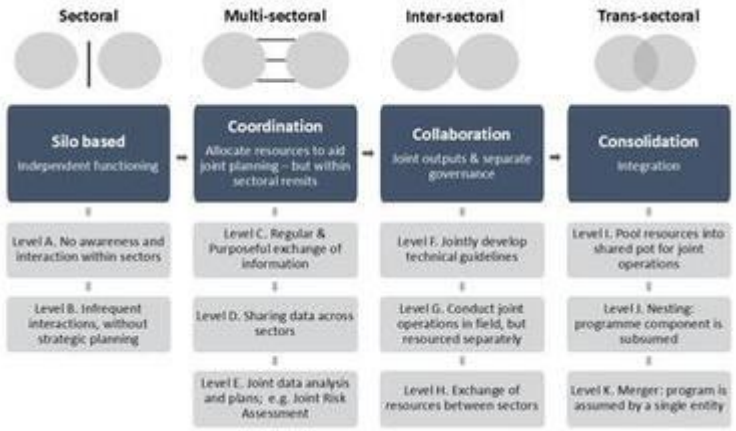
Conclusions

This study offers the first detailed programmatically oriented characterization of multisector partnerships for zoonotic influenza. By making explicit the processes, attributes, and assumptions underlying MSP functioning, the Theory of Action and Reflection tool help bridge persistent gaps between high-level multisectoral aspirations and day-to-day operational realities. The Reflection tool can be used by programme designers and evaluators to better design and assess **locally appropriate One Health MSPs**, strengthening both preparedness and response capacities for zoonotic influenza and other complex multisector challenges.

Figure 1: Theory of Action for operationalising One Health partnerships

Figure 2 Additional attributes of multisector One Health programmes

Figure 3: 'Levels' of MSPs with varying strengths



913 – Applying Programme Theory for the Design and Evaluation of Local, Multisector One Health Partnerships

Syed ABBAS (1), Manish KAKKAR (2), Tim SHORTEN (3), Pushpa WIJESINGHE (2)

1: Institute of Development Studies, United Kingdom; 2: World Health Organization Regional Office for South East Asia, India; 3: Independent consultant

Background

Despite an abundance of toolkits, it remains difficult to operationalise One Health (OH) at local level. A key challenge lies in adapting high-level frameworks to the complex institutional, political, and multisector realities that shape zoonotic disease preparedness and response. Recent work on OH Theory of Action (ToA) and Reflection tools offers a new, practical pathway for translating multisector collaboration aspirations into actionable programme design and evaluation.

Importance & Relevance

This workshop introduces an innovative, programme-theory-driven approach that moves beyond generic OH toolkits. By equipping participants with a structured ToA and a set of programmatic attributes - such as scale, scope, formality, and strength - it enables nuanced characterisation of multisector partnerships. Participants will learn how to diagnose weaknesses, identify partner expectations, and adapt governance and collaboration processes to their own national contexts. The session is relevant for practitioners seeking to enhance responsiveness, sustainability, and pandemic preparedness through more locally attuned OH partnerships.

Educational Outcomes

By the end of the session, participants will be able to:

These skills will directly benefit managers, advisors, and evaluators responsible for designing or improving national OH initiatives.

Workshop Format and Methodology (90 minutes)

The workshop is fully participatory, combining short presentations with structured exercises, small-group work, and applied problem-solving. With **3–4 facilitators** supporting **15–30 participants**, the facilitator-to-delegate ratio (1:5–1:10) ensures interactive support.

Proposed Structure:

Hands-On Introduction to Theory of Action & Reflection Tool (35 minutes)

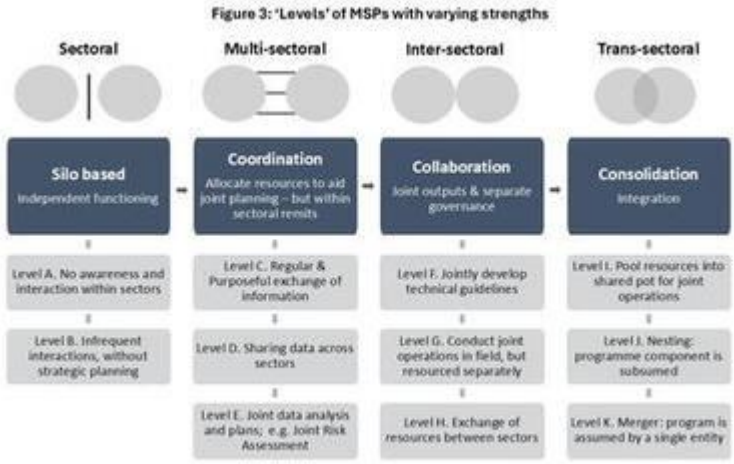
Applied Problem-Solving on Strengthening Collaboration (30 minutes)

Reflection & Feedback (10 minutes)

All materials - including worksheets, ToA diagrams, attribute scoring sheets, and H-form templates - will be provided. Participants will leave with practical, ready-to-apply tools.

Figure 1: Theory of Action for operationalising One Health partnerships

Figure 2 Additional attributes of multisector One Health programmes



919 – Strengthening One Health Governance through Transparent and Systematic Evidence-Informed Policy-Making: Lessons from Croatia, Ghana and Nigeria

Francis Sena NUVEY (1), Fadi EL-JARDALI (2), Pavle JELIČIĆ (3), Barbara BEKAVAC (3), John AMUASI (4,5), Leslie Mawuli AGLANU (4,5), Daniel OPOKU (4), Jesse UNEKE (6), Onyedikachi CHUKWU (6), Traore TIEBLE (7), Marge REINAP (7), Patrick AVEVOR (7), Laxmikant CHAVAN (7), Tanja KUCHENMÜLLER (7), Davi ROMÃO (7), Anna FAHRION (1)

1: Friedrich-Loeffler-Institut, Germany; 2: Knowledge to Policy Center, American University of Beirut, Lebanon; 3: Croatian Institute of Public Health, Croatia; 4: Kumasi Centre for Collaborative Research, Kwame Nkrumah University of Science and Technology, Ghana; 5: Bernhard Nocht Institute of Tropical Medicine, Hamburg, Germany; 6: African Institute for Health Policy & Health Systems II, David Umahi Federal University of Health Sciences, Uburu, Ebonyi State, Nigeria; 7: World Health Organization

Background: Global health threats, including recent pandemics, antimicrobial resistance, emerging and re-emerging zoonoses, environmental spillover risks and the climate crisis, underscore the fundamental interdependence of human, animal and environmental health, and the need for cross-sectoral collaboration to effectively address these threats. Despite growing recognition of the value of the One Health approach, gathering and translating evidence into coherent policies and governance mechanisms, with active contribution of relevant stakeholders remains a persistent challenge. The Evidence-Informed Policy Approaches for One Health (OH-EVI) project was therefore designed to strengthen knowledge translation and support evidence-informed policymaking for challenges which could benefit from a One Health approach across diverse country contexts.

Methods: OH-EVI implemented a participatory, multisectoral approach in Croatia, Ghana and Nigeria. The project applied the structured four-stage WHO EVIPNet methodology to address complex policy challenges from a One Health perspective. In each country, cross-disciplinary stakeholders from sectors linked to human, animal and environmental health conducted situational analyses to identify priority One Health policy problems. Systematic searches of peer-reviewed and grey literature were undertaken to assess the magnitude, drivers and policy responses to the selected health or health system-related problems, drawing on literature database sources including Health Systems Evidence, Cochrane, PubMed and Epistemonikos. The evidence was then synthesized into Evidence Briefs for Policy (EBPs), which outlined feasible intervention options and implementation considerations for decision-makers. Subsequently, multi-stakeholder dialogues involving policymakers, researchers, practitioners, development partners and civil society were convened to deliberate on the evidence, contextualize intervention options and assess feasibility within national governance and health system structures.

Results: Strengthening zoonotic disease surveillance in Croatia, integrating disease surveillance and preparedness systems in Ghana, and mitigating antimicrobial resistance through a One Health approach in Nigeria, were addressed as priority policy challenges. Across all three contexts, fragmented governance structures, weak multisectoral coordination and siloed data systems were identified as major barriers to effective One Health implementation. Evidence-informed intervention options converged around four core policy domains: (1) establishing or strengthening formal One Health governance and multisectoral coordination mechanisms; (2) developing integrated surveillance and data-sharing systems across

human, animal and environmental health sectors; (3) strengthening workforce capacity, collaborative education and public engagement to promote responsible health practices; and (4) securing sustainable financing, stewardship programmes and accountability frameworks to support long-term implementation. The discussions generated consensus on context-specific priorities and actionable steps for operationalizing these interventions within national policy environments.

Conclusions: The OH-EVI project demonstrates how structured stakeholder engagement, and evidence synthesis, combined with inclusive dialogue can strengthen governance innovations and ultimately support the translation of One Health evidence into policy and practice. By fostering collaboration across disciplines and sectors, the initiative has helped identify feasible governance reforms and intervention options tailored to addressing prioritized health problems within specific national contexts.

925 – Safety in the Game Meat Chain – A European Network

Anneluise MADER (1), Peter PAULSEN (2), Maciej DURKALEC (3), Tersia KOKOSKOVA (4), Arja Helena KAUTTO (5), Eugenio DEMARTINI (6), Rafael MATEO (7), Gunita DEKSNE (8), Jana RUPP (1), Selene RUBIOLA (9), Daniel BURES (10), Riikka LAUKKANEN-NINIOS (11), Daniel VECCIATO (12), Mark TAGGART (13), Madalena VIEIRA-PINTO (14), Rafael Hernan MATEUS VARGAS (15), Members of the COST ACTION CA22166 (16)

1: German Federal Institute for Risk Assessment, Germany; 2: University of Veterinary Medicine Vienna; 3: National Veterinary Research Institute Puławy; 4: Czech University of Life Sciences Prague; 5: Swedish University of Agricultural Sciences; 6: Università degli Studi di Milano; 7: Institute of Environmental Assessment and Water Research; 8: University of Latvia; 9: University of Turin; 10: Czech University of Life Sciences Prague; 11: University of Helsinki; 12: University of Padua; 13: Environmental Research Institute; 14: University Trás-os-Montes e Alto Douro; 15: University of Göttingen; 16: www.safegamemeat.eu

Background

With an estimated seven million hunters in the EU alone, hunting is a popular activity in most European countries. However, scientific knowledge on the food safety and the production chain for game meat in Europe is limited. Although the game meat market is small compared to the livestock meat market, a notification concerning game meat or products thereof in the European Rapid Alert System for Food and Feed arises almost monthly.

Methods

A transnational and multidisciplinary One-Health approach was adopted for the establishment of the COST Action “Safety in the Game Meat Chain”. The aim was facilitating the exchange of experiences and concepts through networking, thereby promoting the strengthening and harmonization of food safety standards within the expanding European game meat market. The COST Action is running from September 2023 to September 2027 with a budget of about 700 000 Euro and focuses on the following scientific topics:

Results

The network currently consists of all relevant stakeholders along the game meat supply chain. In total, around 250 members are supporting it, including the 38 members of the Management Committee. For around three quarters of the members, this is their first COST Action — an important indicator that underlines the novelty of the project.

The differences and similarities in hunting practices, training of hunters, game meat processing, trade, legislation, controls and consumption between European countries were determined by investigating all stages of the supply chain, from wild animals to consumers, or 'from forest to fork'. Particular focus was given to identifying and assessing known and emerging chemical and biological risks of regional, national or global importance that pose a hazard to human health when consuming game meat. This resulted in several scientific reports and peer-reviewed publications (Ayaz et al. 2026, Mateus-Vargas et al. 2025, Kautto et al. 2025, Durkalec et al. 2025, Pain et al. 2025, Demartini et al. 2025). Further results are expected.

Conclusion

Overall, the network promotes informed decision-making in regional, national and international risk assessment, management and communication regarding game meat safety. It does this by creating a

comprehensive knowledge base and providing concrete recommendations for action. The gain in knowledge will help to strengthen food safety and consumer protection across Europe.

Acknowledgement

This article is based upon work from COST Action Safety in the Game Meat Chain (SafeGameMeat, CA22166), supported by COST (European Cooperation in Science and Technology). We, the members of the Core Group, would like to express our heartfelt thanks to all members who are actively involved in this COST Action for their excellent and fruitful collaboration.

For forther information and references, please email safegame@bfr.bund.de or visit our website: www.safegamemeat.eu.

937 – Operationalising One Health for National Action: Singapore's Approach to developing its second National Strategic Action Plan on AMR and Setting Measurable Targets

Yueh Nuo LIN (1), **Gabriel Fang Yih LIM** (1), Ann GOMEZ (1), Shuzhen SIM (2), Shin Giek GOH (2), Han Bin PEK (2), Diana CHEE (3), Shi Yun TOH (3), Yong Ping CHEN (3), Chee Meng PANG (4), Siao Yun CHANG (4), Jessica Jie Ying ONG (4), Joanna KHOO (5), Lina SABRINA (5), Kyaw Thu AUNG (5), Jeffery CUTTER (1), Li Yang HSU (6), Yee Sin LEO (7), Oon Tek NG (1)

1: Communicable Diseases Agency, Singapore; 2: National Environment Agency, Singapore; 3: National Parks Board, Singapore; 4: PUB, Singapore's National Water Agency, Singapore; 5: Singapore Food Agency, Singapore; 6: National University Hospital, Singapore; 7: National Centre for Infectious Diseases, Singapore

Antimicrobial resistance (AMR) is a complex, cross-sectoral threat that undermines human and animal health, food safety, and environmental sustainability. Following the implementation of its first National Strategic Action Plan on AMR (NSAP), Singapore recognised the need to develop a second plan (NSAPv2) that was outcome oriented, evidence-informed and aligned with global expectations, including the 2024 United Nations General Assembly Political Declaration on AMR. A key challenge was translating heterogenous sectoral objectives into coherent national priorities and measurable targets while addressing the gaps from the first plan, and ensuring a common vision, cross-agency ownership and feasibility. This abstract describes Singapore's One Health approach to developing the NSAPv2 and establishing ambitious but realistic national targets to achieve by 2030.

We adopted Singapore's One Health governance framework involving the human health, animal health, food security and safety, water, and environment authorities. The development process began with an internal review by the multisectoral AMR Workgroup, followed by a qualitative evaluation, with focus group discussions led by a local university to understand the strengths and weaknesses of the first NSAP. We then took an outcome-driven approach by crafting a mission statement, and identifying goals and specific targets to achieve. Within pre-determined parameters, potential targets and monitoring indicators were brainstormed at a multi-sectoral workshop. These were then shortlisted using an adaptation of the Delphi method, by scoring for ambition (targets only), relevance and specificity, while ensuring representation across sectors. Shortlisted targets were further refined through a combination of baseline trend analysis, international benchmarking, policy relevance screening and feasibility-vs-ambitiousness assessment. Monitoring indicators were aligned with existing surveillance systems to minimise reporting burden.

This process resulted in the development of vision, mission and 13 strategic goal statements across the core pillars of NSAPv2, along with eight specific targets to be achieved by 2030 (Table 1). The targets were applicable to the human (3 targets), animal and agricultural (2 targets), water and environment (2 targets) and One Health (1 target) sectors. The goals and targets provided the scaffold around which the NSAPv2 initiatives were developed. These were supplemented by recommendations from the internal review and academic evaluation. Twenty indicators were selected for monitoring under the NSAPv2 Monitoring and Evaluation (M&E) Framework. Detailed technical sheets were established for each indicator to provide the definition, purpose, method of estimation, and data sources. The NSAPv2 and its M&E Framework were launched on 12 November 2025 and is available on WHO's library of national action plans.

The One Health process enabled a shift from activity-based planning in the first NSAP to outcome-oriented strategic planning in NSAPv2. Singapore's experience demonstrates how a structured One Health approach can be operationalised to develop a coherent national strategy and set meaningful, context-appropriate targets that drive concrete actions.

Table 1. List of targets

Target	Sector
1. Reliable estimates of deaths associated with AMR in sentinel healthcare facilities are obtained and reported.	Human (Impact)
2. Antimicrobial stewardship programmes are implemented in all acute hospitals.	Human
3. Antibiotic prescribing guidelines for at least 7 common primary care infectious disease conditions are developed and disseminated.	Human
4. The quantity (kg) of sales of fluoroquinolones to farms is reduced.	Animal & Food
5. A regulatory framework for antimicrobial use in the animal sector is established, including regulatory levers to ensure antimicrobials used are safe, effective, and only supplied through prescription.	Animal & Food
6. Baseline levels of relevant antimicrobial resistant bacteria (ARBs) and antimicrobial resistance genes (ARGs) in sentinel environmental sites and water bodies are established.	Water & Environment
7. Levels of relevant ARBs and ARGs in the sentinel environmental sites and water bodies are reported at least yearly.	Water & Environment
8. Data from surveillance of priority drug-resistant organisms in the human, animal, food and environment sectors are integrated and correlated.	One Health

940 – Global genomic epidemiology and transmission dynamics of methicillin-resistant Staphylococcus aureus (MRSA): A One Health perspective

Ha NGUYEN NGAN, Nam LE TRUNG, Phuong NGUYEN UYEN, Pei Yee WOH
College of Health Sciences, VinUniversity, Hanoi, Vietnam

Methicillin-resistant Staphylococcus aureus (MRSA) remains a leading cause of antimicrobial-resistant (AMR) infections worldwide. While MRSA is traditionally viewed through a clinical lens, the emergence of MRSA in livestock and the environment has shifted the paradigm toward a One Health perspective. Our aim is to systematically review and synthesize global evidence to understand the genomic epidemiology and transmission dynamics of MRSA across sectors.

Following the PRISMA framework, we conducted a comprehensive literature search across PubMed, Scopus, and Embase for peer-reviewed English articles published from 2000 to 2025. Studies were included if MRSA were epidemiologically assessed through whole genome sequencing (WGS), PCR, or other molecular typing methods. Studies were required to involve MRSA from at least two out of three One Health domains: human (clinical or community), animal (livestock, wildlife, or veterinary), or environment (wastewater, food products, or water systems). Research must provide data on the

transmission of MRSA strains, clones, or genetic elements between these interfaces. Data extraction and risk of bias assessment were performed using JBI-guided protocols.

Out of 1,926 screened records, we included and analyzed 190 studies that showed a clear genomic bridge between human, animal, and environmental reservoirs. The human–animal domain accounts for 49.5% of the research, while 50.0% of studies integrate environmental data. Conventional PCR (46.3%) and WGS (45.8%) were the frequently used genomic methods. We observed a strong concentration of specific lineages of MRSA associated with livestock where ST398 was the most dominant sequence type identified. Pigs were the most common animal reservoirs, followed by dairy cattle and companion animals like dogs and cats. The mecA genes remained the primary determinant of methicillin-resistant phenotype across most samples. Although evidence of MRSA transmission were cited as zoonotic (n=63) and zooanthroponotic (n=26), nearly half of the studies described the transmission as ambiguous or mutual, suggesting a complex, multi-directional circulation of MRSA within shared environments.

The evidence of transmission between people, livestock, and the shared environment demonstrated that MRSA evolution is not confined to clinical settings. The adaptation of specific lineages across diverse hosts signifies the need for integrated surveillance to track emerging clones and global resistance.

944 – Canine leptospirosis in a flood-prone region of Southern Brazil: dogs as One Health sentinels

Cintia JUPPA (1), Ana SIEGLOCH (2), Bruna SILVA (3)

1: Universidade do Planalto Catarinense, Postgraduate Program in Environment and Health, Brazil; 2: Universidade do Planalto Catarinense, Postgraduate Program in Environment and Health, Brazil; 3: Universidade do Planalto Catarinense, Postgraduate Program in Environment and Health, Brazil

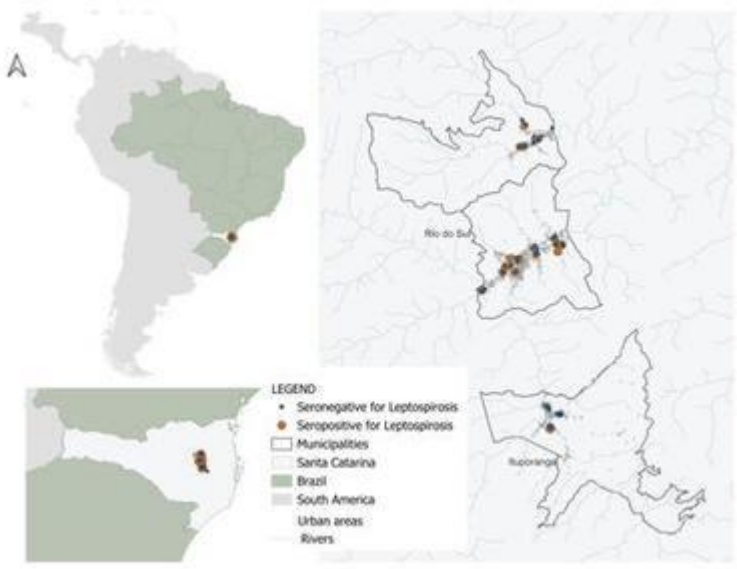
Background: Leptospirosis is a globally distributed zoonosis whose transmission is strongly influenced by environmental conditions, particularly in regions vulnerable to hydrological disasters. In these scenarios, dogs play a strategic role as sentinels for *Leptospira* spp. circulation due to their close contact with the shared environment. This study aimed to estimate the seroprevalence of anti-*Leptospira* spp. antibodies in domiciled dogs from the Alto Vale do Itajaí region, southern Brazil, an area characterized by recurrent flooding, identify circulating serovars, and analyze factors associated with seropositivity.

Methods: A cross-sectional observational study was conducted between January and October 2025 in the municipalities of Rio do Sul, Ituporanga, and Presidente Getúlio, Santa Catarina, Brazil. A total of 188 dogs were evaluated through owner epidemiological questionnaires, clinical examinations, and serological testing using the Microscopic Agglutination Test (MAT) with a panel of 18 serovars (cut-off ≥1:100). Statistical associations between seropositivity and explanatory variables were assessed using Pearson's chi-square or Fisher's exact tests ($p \leq 0.05$).

Results: Overall seroprevalence was 12.2% (23/188). The most frequent serovars were Icterohaemorrhagiae (43.5%), Wolffi (34.8%), and Canicola (21.7%). Antibody titers ranged from 1:100 to 1:400, and no dog reacted simultaneously to more than one serovar. Significant associations were found between seropositivity and contact with floodwater or mud ($p = 0.024$), interaction with stray dogs ($p = 0.043$), and animal density per household ($p = 0.049$). In addition, 49.5% of the dogs had never been vaccinated against leptospirosis, and only 21,8% were within the recommended immunization interval, highlighting critical gaps in canine immunoprophylaxis.

Conclusions: These findings demonstrate active circulation of *Leptospira* spp. in domiciled dogs from a region chronically affected by flooding and support the role of the dog as an epidemiological sentinel in climate-vulnerable territories. The predominance of Icterohaemorrhagiae highlights relevant zoonotic risk, while low vaccine coverage may contribute to pathogen persistence in the peridomicile. Integrated One Health strategies combining environmental management, urban drainage improvements, and systematic canine vaccination are essential to reduce shared risk at the human-animal-environment interface.

Acknowledgments: The authors gratefully acknowledge the research financial support provided by Fundação de Amparo à Pesquisa e Inovação do Estado de Santa Catarina (FAPESC) under grant numbers TO2024TR002584 (Universal 21/2024). Cintia Cavilha Juppa acknowledges financial support from the Programa Institucional de Bolsas de Pós-Graduação – PIBPG (CNPq Nº 69/2022).



949 – Changing antimicrobial resistance patterns in Salmonella Kentucky in Canada – the power of integrated surveillance

Melissa C. MACKINNON (1), Kathryn MCDONALD (1), Hailey SILVER (1), Ketna MISTRY (2), Audrey CHARLEBOIS (2), Agnes AGUNOS (1), Ashley KEARNEY (2), Jennifer CAMPBELL (2), Sara CHRISTIANSON (2), Celine NADON (2), David C. ALEXANDER (3,4), Sadjia BEKAL (5,6), Linda CHUI (7,8), Ian DAVIS (9), Xiaofeng DING (10), Tanis C. DINGLE (11,12), Gabriel GIROUARD (13), Jennifer GRANT (14), Camille HAMULA (15), Linda HOANG (14), Samir PATEL (16), Robert TAYLOR (17), Antoine CORBEIL (16), Amrita BHARAT (2), Richard J. REID-SMITH (1), Carolee A. CARSON (1)

1: Infectious Disease and Vaccination Programs Branch, Public Health Agency of Canada, Canada; 2: National Microbiology Laboratory Branch, Public Health Agency of Canada, Canada; 3: Cadham Provincial Laboratory, Diagnostic Services, Shared Health, Winnipeg, MB, Canada; 4: Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, Canada; 5: Laboratoire de santé publique du Québec, Sainte-Anne-de-Bellevue, QC, Canada; 6: Département de Microbiologie, Infectiologie et Immunologie, Université de Montréal, Montréal, QC, Canada; 7: Alberta Precision Laboratories, Public Health Laboratory, Edmonton, AB, Canada; 8: Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, Canada; 9: Department of Pathology and Laboratory Medicine, Queen Elizabeth II Health Sciences Centre, Halifax, NS, Canada; 10: Provincial Laboratory Services, Queen Elizabeth Hospital, Charlottetown, PE, Canada; 11: Alberta Precision Laboratories, Public Health Laboratory, Calgary, AB, Canada; 12: Department of Pathology and Laboratory Medicine, University of Calgary, Calgary, AB, Canada; 13: Centre hospitalier universitaire Dr-Georges-L.-Dumont, Réseau de santé Vitalité, Moncton, NB, Canada; 14: Public Health Laboratory, British Columbia Center for Disease Control, Vancouver, BC, Canada; 15: Department of Laboratory Medicine and Pathology, University of Saskatchewan College of Medicine, Saskatoon, SK, Canada; 16: Public Health Ontario Laboratory, Public Health Ontario, Toronto, ON, Canada; 17: Department of Pathology and Laboratory Medicine, Newfoundland and Labrador Public Health and Microbiology Laboratory, St. John's, NL, Canada

Background: In Canada, *Salmonella enterica* serovar Kentucky (*S.* Kentucky) sequence type (ST) 152 is commonly recovered from chickens. Whereas, *S.* Kentucky isolated from human clinical samples are generally ST198 and often linked to travel and imported foods. Although ciprofloxacin-resistant ST198 was identified in Canada, azithromycin resistance and extended-spectrum beta-lactamases have not been reported yet.

The Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) detected increased ceftriaxone resistance *S.* Kentucky in 2024 across human and chicken sources, and investigated isolate relatedness and resistance patterns.

Methods: *Salmonella* Kentucky from human clinical cases and chickens (clinical cases, farm, abattoir and retail) from 2018 to 2024 were included. Whole genome sequencing was performed with *Salmonella in silico* Typing Resource used to determine the serovar and Staramr used to determine the multilocus sequence typing (MLST) scheme. Resistance determination for 15 antimicrobials was predicted using Staramr for the human isolates and broth microdilution for the chicken isolates. Whole-genome MLST was used to assess isolate relatedness, with clusters defined as isolates differing by 0 to 10 alleles. Antimicrobial resistance percent differences compared 2024 to 2018 unless otherwise noted.

Results: Of the 205 human isolates, 80% were ST198. Nationally, ceftriaxone and azithromycin resistance increased 31% and 20%, respectively (Figure 1). Ciprofloxacin resistance was variable and was 89% in 2024. The substantial increase in ceftriaxone resistance was driven by a cluster of 11 ST198 isolates in 2023-2024 that were resistant to ceftriaxone (*bla*CTX-M-55), ampicillin, ciprofloxacin, nalidixic acid and tetracycline. The substantial increase in azithromycin resistance was driven by a cluster of 6 ST198 isolates in 2024 that included resistance to at least azithromycin (*mphA*), ciprofloxacin, gentamicin, nalidixic acid, trimethoprim-sulfamethoxazole and tetracycline. This cluster included two extensively drug-resistant isolates with resistance to ampicillin, azithromycin, ciprofloxacin, ceftriaxone (*bla*CMY-4), trimethoprim-sulfamethoxazole, and 5 additional antimicrobials.

Of the 1809 isolates from chicken samples, 92% were ST152 and none were ST198. Ceftriaxone resistance increased 16%, 16% and 3% since 2023 in chicken clinical cases, chickens at abattoir and retail chicken, respectively, however, it decreased 8% in broiler chickens on farm. Ciprofloxacin resistance increased 18% since 2023 in retail chicken, whereas it decreased in all other chicken sources. There was no azithromycin resistance in chicken isolates. Genotypic analysis of the chicken isolates is underway.

Conclusions: Emerging resistance patterns in Canadians with*S.*Kentucky show multidrug resistance that may complicate treatment when required. These infections involve a sequence type distinct from domestic poultry, suggesting travel-related or imported food sources. This rapid and robust analysis confirmed that human and chicken isolates are unrelated, underscoring the value of integrated surveillance and genomic analysis. We are preparing to share these findings publicly through an integrated story on our interactive data platform, pairing the data with epidemiologic intelligence.

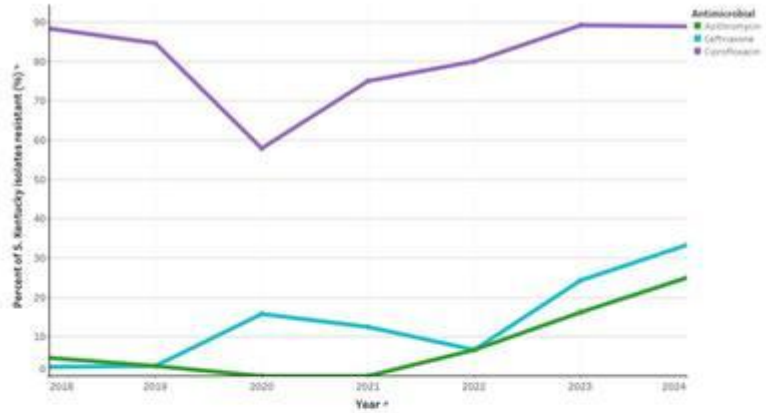


Figure 1 – Frequency of resistance to azithromycin, ceftriaxone and ciprofloxacin in human *Salmonella* Kentucky isolates from Canada.

957 – Evolutionary dynamics and molecular adaptation of Rift Valley fever virus across human and non-human outbreaks in Africa

Isaac Emmanuel OMARA (1), John JUMA (2), Derek TSHIABUILA (1), Graeme DOR (1), Eduan WILKINSON (1), Cheryl BAXTER (1,3), Houriiyah TEGALLY (1), **Monika MOIR** (1), Samuel O. OYOLA (2), Tulio de OLIVEIRA (1,3,4)

1: Centre for Epidemic Response and Innovation (CERI), School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa; 2: International Livestock Research Institute (ILRI), Old Naivasha Road, Nairobi, Kenya; 3: Centre for the AIDS Programme of Research in South Africa (CAPRISA), South Africa; 4: KwaZulu-Natal Research and Innovation Sequencing Platform (KRISP), University of KwaZulu-Natal, Durban, South Africa

Abstract

Background: Rift Valley fever virus (RVFV) remains one of Africa's most important climate-sensitive zoonotic arboviruses, causing recurrent outbreaks in human, livestock and wildlife with major public health and economic consequences. Although past genomic studies focused on outbreak response and lineage classification, the molecular mechanisms driving viral persistence and adaptation remain poorly understood. This study aimed to identify RVFV protein-coding mutations and adaptive signatures across multiple epidemics and epizootics in Africa.

Methods: This retrospective genomic analysis examined 596 complete genomes of the three RVFV segments from the NCBI virus database, including L (n =173), M (n=196) and S (n =227) from 13 African countries across both human and non-human hosts (1940 – 2020). Protein-coding mutations were identified using Genome Detective and custom scripts. Phylogenetic reconstruction was performed with IQ-TREE, host-state reconstruction was conducted to infer cross-species transmission patterns and selection pressure analysis conducted using codon-based models implemented in the Datamonkey platform. All data analysis and visualizations were performed using R software.

Results: A total of 7,339 protein-coding mutations were identified, ranging from 2 - 20 per isolate. RVFV isolates collected in South Africa, Kenya and Madagascar exhibited the highest genomic diversity. Comparative analysis of the genome revealed higher mutation in L and S segments than in M and broader diversity among non-human hosts. Phylogenetic reconstruction showed human isolates formed sub clusters nested within livestock and vector lineages, consistent with transmission bottlenecks. We identified seven critical amino acid mutations across the genome: N277S, N277D and S278N in the polymerase (L); I442S, I442V, V659A in the glycoproteins (M) and N133S in the NSs protein (S). Positive selection at the corresponding codon sites, particularly within the polymerase and glycoprotein regions of human isolates, which suggests adaptive evolution linked to replication efficiency and immune evasion.

Conclusion: RVFV evolution across Africa is shaped by both purifying and diversifying selection. Host-specific pressures drive adaptive substitutions that may fine tune polymerase function, alter glycoprotein antigenicity and enhance immune escape. These findings reveal molecular mechanisms of viral persistence and support the design of cross protective vaccines.

970 – Wastewater-Based Epidemiology Reveals Pathogen Circulation at the Human–Animal–Environment Interface in Rural Mozambique

Filomena MANJATE (1,2), Percina CHIRINDA (1), Valdemiro NOVELA (1), Augusto MESSA JR. (1), Marcelino GARRINE (1), Valeriano CHICHAVA (1,2), Mónica NUNES (3), Delfino VUBIL (1), Sergio MASSORA (1), Martin NYAGA (4), Ricardo PARREIRA (2), Sofia Santos COSTA (2), Sofia G. SEABRA (2), Inácio MANDOMANDO (1,2,5,6)

1: Centro de Investigação em Saúde de Manhiça, Mozambique; 2: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisboa, Portugal; 3: cE3c—Centre for Ecology, Evolution and Environmental Changes & CHANGE—Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, Campo Grande, Portugal; 4: Next Generation Sequencing Unit and Division of Virology, Faculty of Health Sciences, University of the Free State, Bloemfontein, South Africa; 5: Instituto Nacional de Saúde (INS), Marracuene, Maputo, Mozambique; 6: Institut de Salut Global de Barcelona (ISGlobal), Spain

Background: Sewage systems contain infectious agents discharged by infected individuals, allowing pathogen detection through wastewater based epidemiology (WBE), which serves as a complementary tool to clinical surveillance. WBE is important within the One Health framework, mainly in settings with risk of pathogen spillover into humans, where diseases transmission is driven by inadequate sanitation, environmental conditions and poor healthcare infrastructures. Mozambique, as a low-income country,

bears a high burden of infectious and zoonotic diseases, due to high/close human-animal interaction and by the fact that agriculture is the main source of living (approximately 81% of the country labor force). WBE integrated within One Health framework may enhance infectious diseases traceability across larger populations, although its implementation remains limited in Mozambique. We propose a WBE integrated One Health framework to monitor infectious agents circulation in Manhiça District, Southern Mozambique to contribute with data and address this gap.

Methods: Due to absence of centralized sewage infrastructure in the study setting, community septic tanks were used as environmental sampling points, with households randomly selected within the Health and Demographic Surveillances of Manhiça Health Research Center to collect raw sewage, alongside fecal samples from domestic animals (turkey, goose, goat, pig, duck and chicken) and bats. Additionally, for comparisons were collected wastewaters from Manhiça district hospital (adult ward, children's ward and outpatient visits). Wastewaters were processed using organic flocculation, QIAamp® DNA Mini Kit and screened using the TaqMan Array cards RT-qPCR panels, for targeted enteric (28 targets) and respiratory (39 targets) pathogens. Stool samples, were processed using QIAamp Fast DNA Stool Mini Kit and tested with the same RT-qPCR enteric panel.

Results: Several pathogens were detected in the enteric panel in both hospital and community. While others were exclusively identified in hospital (*Cryptosporidium parvum* and *Mycobacterium tuberculosis)* or in community *(Giardia* spp., Shiga-like toxin 2 and sapovirus). In animal stools were detected *Aeromonas* spp., *Enterococcus faecalis, Enterococcus faecium, Campylobacter jejuni, enteroaggregative E. coli (aaiC)* and heat-stable-harboring/producing enterotoxigenic *E. coli.* Five out of the six pathogens were identified in the stool sample of duck (Fig. 1). On the other hand, in the respiratory panel, *Adenovirus* and *Klebsiella pneumoniae* were identified in both community andhospital, while the remaining pathogens (*Acinetobacter baumannii*, *Ureaplasma parvum*, *Chlamydia trachomatis*, *Bordetella parapertussis, Bordetella bronchiseptica* and Group B *Streptococcus*) were found in community only (Fig. 1).

Conclusions: This preliminary analysis identified highly pathogenic agents, including strains known to possess resistant genes to commonly used antibiotics, some that cause opportunistic infections and are difficult to control. The data may demonstrate a pathway of infectious disease transmission and proves the utility of WBE integrated One Health in Mozambican context and alerts for continuous surveillance, to track diseases outbreaks and provide guidelines for their rapid containment.

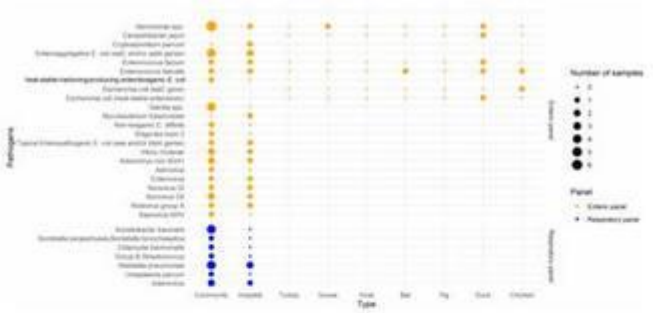


Figure 1. Pathogens profile in six septic tanks, wastewater from Manhiça District Hospital (one in adult ward, one in children's ward and one in outpatient visits) and animal (one from each) stools collected in the households of Manhiça community from 4 Jan-4 March 2026.

973 – One Health Initiatives: Best Practices and Lessons Learned for Future Implementation

Tequam WORKU (1), Elmoubasher FARAG (2), Samira MUBAREKA (3), Wondwossen GEBREYES (4), Desalegne M. DEGEFAW (1)

1: One Health Global Alliance, United States of America; 2: United Nations; 3: University of Toronto; 4: Ohio State University

Background: The growing complexity of global health challenges—including emerging infectious diseases, antimicrobial resistance, climate change, biodiversity loss, urbanization, and ecosystem degradation—has reinforced the need for integrated One Health (OH) approaches. Yet translating OH principles into coordinated, locally responsive, and sustainable action remains challenging. Fragmentation across disciplines and institutions, limited access to expertise and partnerships, and gaps between strategy and implementation can constrain impact and scalability. The One Health Global Alliance (OHGA) offers one innovative approach through its On-Demand Global Catalyst, a collaborative platform connecting institutions, professionals, learners, and partners across human, animal, and environmental health with expertise, knowledge, resources, and opportunities for action. Complementing this platform is Ohio State Global One Health, the nonprofit implementation wing, which has advanced One Health through initiatives addressing antimicrobial resistance, food safety, laboratory and workforce capacity, and other complex health challenges.

Methods: This poster presents the OHGA On-Demand Global Catalyst as an emerging model for operationalizing One Health collaboration and connecting global expertise to locally identified needs. The model is examined alongside implementation experience from Ohio State Global One Health to

illustrate how a global collaboration platform can complement nonprofit, field-based One Health implementation. Examples across diverse geographic and institutional contexts are used to examine pathways for mobilizing multidisciplinary expertise, building partnerships, strengthening capacity, and translating knowledge into action. Key dimensions include demand-driven collaboration, cross-sector partnerships, knowledge exchange, implementation support, and approaches to sustainability. Together, these experiences demonstrate a continuum from collaboration to implementation and sustained impact, offering an innovative framework for strengthening the operationalization of One Health.

Results:

· The OHGA On-Demand Global Catalyst provides a mechanism for connecting multidisciplinary expertise, and institutions, to emerging and locally defined One Health needs.

· Ohio State One Health Global demonstrates how implementation can translate cross-sector collaboration into practical initiatives across diverse One Health priorities.

· Together, the models highlight an integrated pathway from global connection and knowledge exchange to locally grounded implementation, capacity strengthening, and sustainable impact.

---

982 – AI-Driven Clinical Decision Support Systems for Antimicrobial Stewardship in the Asia-Pacific: A Scoping Review and Regional Maturity Roadmap

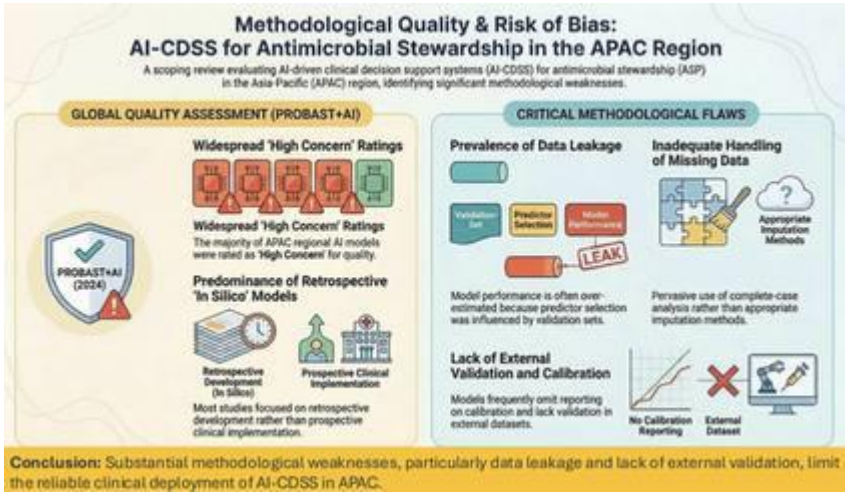
Huy HO VU NHAT, Thu LE ANH, Yee WOH PEI
College of Health Sciences, VinUniversity, Hanoi, Vietnam

Background: Antimicrobial resistance (AMR) is a critical public health threat in the Asia-Pacific (APAC) region, where diverse healthcare infrastructures complicate standardized antimicrobial stewardship (ASP). Artificial intelligence-driven clinical decision support systems (AI-CDSS) offer promising solutions for optimizing prescribing; however, their implementation landscape remains poorly characterized. This scoping review systematically maps the scope, technological maturity, implementation determinants, and reported impacts of AI-CDSS for ASP within the APAC region to inform a regional maturity roadmap.

Methods: Guided by JBI methodology and PRISMA-ScR guidelines, we searched five major databases (PubMed, Embase, IEEE, ACM, and Scopus) from 2000 to 2025. Studies were eligible if they focused on AI-CDSS for ASP in APAC healthcare settings. Data were mapped to the Consolidated Framework for Implementation Research (CFIR 2022) for determinants and the RE-AIM framework for public health impact. Methodological quality and technical robustness were appraised using the Mixed Methods Appraisal Tool (MMAT 2018) and the PROBAST+AI (2024) tool.

Results: We identified a predominance of retrospective model development studies (in silico) over prospective clinical implementations. Predominant architectures include machine learning (XGBoost, Random Forest) for predicting resistance and vancomycin dosing. Key implementation barriers identified through CFIR include fragmented IT infrastructure and low clinician trust in "black-box" models. Mapping to RE-AIM reveals a significant gap in "maintenance" and "economic impact" data, with most studies focusing on technical "effectiveness". PROBAST+AI appraisal highlights a widespread lack of external validation and high risks of bias due to data leakage in regional models.

Conclusions: While AI-CDSS for stewardship is an expanding field in APAC, there is a critical disconnect between technical development and clinical integration. Future research must prioritize external validation, explainable AI (XAI) to build clinician trust, and long-term sustainability assessments. We propose a tiered maturity roadmap: Tier 1 (Scale-up validated dosing tools), Tier 2 (Bridge diagnostic evidence gaps with trials), and Tier 3 (Prioritize foundational IT infrastructure in low-income sub-regions).


Methodological Quality & Risk of Bias:
AI-CDSS for Antimicrobial Stewardship in the APAC Region
A scoping review evaluating AI-driven clinical decision support systems (AI-CDSS) for antimicrobial stewardship (ASP) in the Asia-Pacific (APAC) region, identifying significant methodological weaknesses.
GLOBAL QUALITY ASSESSMENT (PROBAST+AI)
PROBAST+AI (2024)
Widespread 'High Concern' Ratings
Widespread 'High Concern' Ratings
The majority of APAC regional AI models were rated as 'High Concern' for quality.
Predominance of Retrospective 'In Silico' Models
Retrospective Development (In Silico)
Prospective Clinical Implementation
Most studies focused on retrospective development rather than prospective clinical implementation.
CRITICAL METHODOLOGICAL FLAWS
Prevalence of Data Leakage
Validation Set
Predictor Selection
Model Performance
LEAK
Model performance is often over-estimated because predictor selection was influenced by validation sets.
Inadequate Handling of Missing Data
Appropriate Imputation Methods
Pervasive use of complete-case analysis rather than appropriate imputation methods.
Lack of External Validation and Calibration
Models frequently omit reporting on calibration and lack validation in external datasets.
No Calibration Reporting
External Dataset
Conclusion: Substantial methodological weaknesses, particularly data leakage and lack of external validation, limit the reliable clinical deployment of AI-CDSS in APAC.

AI-CDSS for Antimicrobial Stewardship:
The APAC Regional Roadmap
Regional Maturity Roadmap
Critical Research Gaps
1
2
3
Tier 1: Implementation-Ready (Dosing Optimization)
Tools focused on Vancomycin and Aminoglycoside dosing are currently the most mature and ready for immediate clinical integration in APAC healthcare settings.
Tier 2: Evidence Gap Bridging (Diagnostic Support)
Functions such as blood culture outcome prediction and MRSA genotyping require prospective trials to bridge the gap between retrospective success and live clinical utility.
Tier 3: Infrastructure Priorities (Low-Income Settings)
Functions such as blood culture outcome prediction and MBSA genotyping require prospective trials to bridge the gap between retrospective success and live clinical utility.
In low-resource settings, the priority must shift to establishing basic IT standards, data registries, and policy frameworks before AI integration can occur.
Implementation Determinants (CFIR Framework)
Innovation Complexity
The success of AI implementation is highly dependent on 'Innovation Adaptability' - the degree to which a tool can be refined to fit local hospital workflows.
Outer Setting Pressures
External factors such as national policies, professional guidelines, and 'Performance Measurement Pressure' are key drivers for hospitals to adopt AI-CDSS.
Mind the Gap
Methodological Risk of Bias
Functions such as blood culture outcome prediction and MRSA genotyping require prospective trials to bridge the gap between retrospective success and live clinical utility.
The Lack of External Validation
Most tools are developed and tested within a single center, there is a critical shortage of multi-center validation to ensure models work across different hospital systems.
The 'Implementation Cliff'
This phenomenon describes the failure of AI tools to move from a "silent" or retrospective testing mode into live, real-time clinical environments where they can impact patient care.
Neglected Clinical Areas
Research is currently heavily skewed toward adult bacterial infections, leaving massive gaps in pediatric stewardship and antifungal stewardship.

988 – Youth as Knowledge Holders in Zoonotic Disease Prevention: Co-Producing a One Health Education Framework

Camille BARKER (1), Mia PERRY (1), Lwitiko SIKANA (2), Kennedy LUSHASI (2)

1: University of Glasgow, United Kingdom; 2: Ifakara Health Institute, Tanzania

Background

Rabies remains a preventable yet deadly zoonotic disease, with children accounting for nearly 40% of deaths. Despite this disproportionate burden, youth are rarely engaged as knowledge holders in rabies prevention efforts. Within many One Health education initiatives, community members are positioned as recipients of expert knowledge rather than contributors to locally grounded prevention. In this model participation is typically framed as behavior change, limiting the role of community perspectives in shaping prevention strategies. Although education and community engagement are recognized priorities in zoonotic disease prevention, limited guidance creates a methodological gap in translating community knowledge into effective health education. We address this gap by learning from youth to co-produce One Health education materials that reflect their lived realities.

MethodsThis qualitative participatory study integrates two components: immersive ethnographic fieldwork embedded within community life and a youth-centered participatory workshop series. Ethnographic fieldwork documented everyday health learning and decision-making related to dog bites and care-seeking. Youths participated within two workshops, in rabies endemic areas of Tanzania, involving a series of activities grounded in culturally responsive pedagogy. Activities included story circles about bite experiences, visual risk representation through drawing, and group discussions to surface experiential and tacit knowledge about human-dog relationships. Data was analyzed to identify how cultural norms and household dynamics shape youth interpretations of rabies risk and responses to dog bites. The next stage of work involves the contribution of youth to the interpretation of workshop findings and shaping of educational messages shared during community engagement activities.

ResultsFindings are informing the development of a co-produced One Health education framework and implementation guidelines for youth-engaged rabies prevention adaptable to other zoonotic diseases. Analyses highlight how everyday responsibilities for animal care, fear of punishment after dog bites, and reliance on family decision-makers influence whether children report bites or seek care. Findings indicate that youth have a unique perspective on human-dog interactions and barriers to bite reporting. Participatory mapping and visual risk representation surface how lived experiences and local interpretations of illness shape their responses. These youth-generated insights will directly inform the design of culturally grounded educational materials and strategies embedded within this framework which includes; principles for youth-centered learning and participatory tools for integrating youth perspectives into One Health education programs.

ConclusionsThis research demonstrates how participatory engagement with youth can generate locally grounded insights that strengthen rabies prevention strategies. The study aims to empower youth as stakeholders in zoonotic disease prevention. The participatory methods developed here offer a transferable model for community-engaged education addressing zoonotic diseases where everyday human animal interactions shape risk. As such, this work contributes to broader One Health efforts to advance community-engaged research and strengthen health education.

1000 – An inventory of Information and Communication Technologies and tools for One Health to enhance visibility and support countries in strategic tool selection

Kaushi KANANKEGE (1), Lina AWADA (1), Fernanda DOREA (1), Paolo TIZZANI (2), Ismaila SECK (1), Madhur DHINGRA (1), Julie FONTAINE (3), On Ki LI (4), Simon RÜEGG (5), Barbara HAN (6), Valeriia YUSTYNIUK (7), Chinenye Mary EMELIFE (8), **Elizabeth COOK** (9), Alejandro DORDO GARCIA (1), Fairouz LARFAOUI (1), Zelalem TADESSE (1), Junxia SONG (1)

1: Animal Production and Health Division, Food and Agriculture Organization, Rome, Italy.; 2: Data Integration and Analytics Department, World Organisation of Animal Health, Paris, France.; 3: WHO Hub for Pandemic and Epidemic Intelligence, World Health Organization. Berlin, Germany.; 4: Centre for Agriculture and Bioscience International, Oxfordshire, United Kingdom.; 5: University of Zürich, Zürich. Switzerland.; 6: Cary Institute of Ecosystem Studies, New York, USA.; 7: Center for Animal Health and Food Safety, University of Minnesota, St Paul, USA.; 8: Africa Centres for Disease Control and Prevention, Addis Ababa, Ethiopia.; 9: International Livestock Research Institute, Nairobi, Kenya.

Background: The growing complexity of One Health (OH) threats at the human–animal–plant–ecosystem+ interface requires digital systems that support integrated surveillance, risk assessment, early warning, and coordinated response. In line with Pathway 3 of the One Health Joint Plan of Action, which prioritizes strengthening One Health intelligence through improved data sharing and digitalization, numerous Information and Communication Technologies and tools (ICT) have emerged to facilitate OH data and information flow across sectors. However, fragmented digital landscapes, limited interoperability, and duplicated data entry have caused digital fatigue, particularly among frontline staff. To address this, the FAO Community of Practice on ICT for One Health (ICT CoP), a multisectoral platform connecting practitioners and experts, developed an Inventory of ICTs for One Health to support countries in select context-appropriate minimal set of ICTs.

Methods: The inventory compiles ICT used in country-level One Health programs, including digital platforms, software, mobile apps, databases, and decision-support tools enabling cross-sectoral data collection, analysis, reporting, prediction, risk management, risk communication, and knowledge sharing for workforce capacity building. Developed through an inclusive, participatory process, ICT CoP coordinators convened a 14-member advisory Core Group representing diverse OH sectors to define Inventory's scope, inclusion, and merit criteria. The team engaged end users and tool developers, collected standardized information via a structured submission form, established a regular update cycle for both the tools and the inventory, and incorporated practitioner feedback to ensure their continued relevance and usability. The Inventory organizes ICTs by functional domain, sectoral relevance, technical features, and interoperability. Inclusion criteria require ICTs to be freely available for non-profit use with clear licensing; developed or governed by Quadripartite, public, academic, or non-profit entities; demonstrate One Health relevance; support standard data exchange and interoperability; enable cross-sector integration; be suitable for national or subnational implementation in low-resource settings; and show documented country-level use. Merit criteria further assess multi-data and functional capacity, cross-issue applicability, open-source flexibility, adherence to data governance and security standards, scalability and adaptability, technical support, and long-term sustainability, especially in low-resource settings.

Results: As of March 2026, 28 ICT tools meeting these criteria have been included in the inventory, collected with active CoP member engagement in the process. The Inventory serves as a decision-support tool for informed ICT selection, utilizing a structured framework to compare tools by scalability, integration capacity, and cross-sector utility. By highlighting cross-sector use, the inventory promotes harmonization, allows comparison of tools by purpose, scalability, integration, and context, and identifies functional gaps to guide ICT investments. Simultaneously, the ICT CoP hosts webinars showcasing country use, and multisectoral applications.

Conclusion: By combining a structured, multisectoral, and participatory approach with tool visibility, the Inventory of ICT for OH strengthens knowledge, collaboration, coordination, and investment alignment, fostering efficient and sustainable digital ecosystems.

1003 – One-health approach to determine and tackle antimicrobial resistance in the human dairy interface: A case of non-typhoidal Salmonella and lactose-fermenting Enterobacteriaceae

Achenef MELAKU BEYENE (1), Mucheye GIZACHEW (1), Ahmed E. YOUSEF (2), Baye GELAW (1)

1: Department of Medical Microbiology, School of Biomedical and Laboratory Sciences, College of Medicine and Health Sciences, University of Gondar, Gondar, Ethiopia; 2: Department of Food Science and Technology, Ohio State University, Ohio, Columbus, United States of America

Background: Antimicrobial resistance (AMR) is among the top public health concerns globally. Determining the susceptibility pattern of pathogens is important in designing strategies to combat AMR. Thus, this study was designed to determine the AMR pattern of non-typhoidal *Salmonella* (NTS) and lactose-fermenting Enterobacteriaceae (LFE) isolated from the human-dairy interface in the northwestern part of Ethiopia, where such information is lacking.

Methods: The study analysed 362 samples collected from humans, animals, food (milk) and the environment (sewage). The bacteria were isolated from the samples using standardized bacteriological methods. The antimicrobial susceptibility patterns and extended-spectrum beta-lactamase (ESBL) production ability were screened and confirmed by using the Kirby-Bauer disk diffusion method. The isolates were further characterized genotypically using multiplex polymerase chain reaction targeting the three ESBL-encoding genes.

Results: A total of 28 and 375 NTS and LFE bacterial isolates were identified. Isolates were more resistant to ampicillin and tetracycline. Forty-six point four and 70.7% of NTS and LFE were multidrug resistant (MDR), respectively. None of NTS and 21.3% of LFE were ESBL-producing. Genotypically, the majority of the isolates (97.5%), which were positive on the phenotypic test, were carrying one or more ESBL encoding genes. In conclusion, a high proportion of the bacterial isolates were resistant to commonly used antimicrobials, MDR, and were positive for ESBL production.

Conclusion: The findings provide evidence that the human-dairy interface is one of the important reservoirs of AMR traits and intervention points to reduce AMR. Therefore, the implementation of AMR mitigation strategies in a one-health approach is highly needed in the area.

1009 – Social-Ecological System Health: rooting One Health in territories

Alexandre CARON (1), **Michel DE GARINE-WICHATITSKY** (2), Raphaël DUBOZ (3), Aurélie BINOT (4)

1: CIRAD ASTRE - ILRI, ILRI, Nairobi, Kenya; 2: CIRAD, UMR ASTRE, Montpellier, France; 3: CIRAD, UMR ASTRE, Dakar, Senegal; 4: CIRAD, UMR ASTRE, Harare, Zimbabwe

Background: Social-Ecological System Health (SESH) is an approach intersecting the SES and One Health (OH) approaches. The OH approach has been redefined recently as a systemic, intersectoral and transdisciplinary approach aiming at "Healthy ecosystems with healthy people and animals". To deliver this ambitious and place-based objective, OH initiatives need to move beyond institutionalization towards a methodology that connect top-down ambitions with demand-driven bottom-up operationalization.

Methods: We have been involved in testing SESH methodology through applied research and development projects for the past ten years and we have drafted this presentation and manuscript following numerous brainstorming and exchanges, notably recently through the creation of SESH group within the SocSES (Society for SES).

Results: While One Health has invested heavily in data infrastructures, surveillance systems, and integrative knowledge platforms, their contribution to action at territorial level remains limited. We argue that SESH explicitly addresses this gap by conceptualising intermediation as a core condition for translating One Health knowledge into locally relevant and collectively negotiated interventions. We propose defining SESH as a necessarily subjective, contextual and changing construct based on the health of its constituent elements and their relationships. Local multi-stakeholder approaches, (e.g., living labs) can be understood not only as spaces for co-production of interventions, but also as key infrastructures of intermediation or socio-technical interfaces that enable One Health information to be mobilised in ways that are meaningful, legitimate, and actionable at the territorial scale.

Beyond SES properties, e.g., resilience, robustness, sustainability, intermediation capacities are seen as an emergent function of a healthy SES, enabling the system to navigate complexity, uncertainty, and competing health objectives across scales. From a SESH perspective, the quality of intermediation may constitute a critical indicator of a system's capacity to sustain healthy trajectories. We identify the design and analysis of intermediation-ready One Health infrastructures as a key frontier for future SES research.

Conclusion: Advancing this agenda requires closer dialogue between SES science, information systems research, and practice-oriented One Health communities.

1013 – Mycotoxins in Pork-Based Meat Products: A Systematic Review

Melissa ALVES RODRIGUES (1), Lais FREITAS (1,2,3), Claudemar OLIVEIRA (2,3), Letícia ESTEVINHO (2,3), Rosa CAPITA (4,5), Alexandra ESTEVES (6,7,8)

1: Doctoral School, University of León (ULE), Campus de Vegazana, 24007 León, Spain; 2: Centro de Investigação de Montanha (CIMO), Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-252 Bragança, Portugal; 3: Laboratório para a Sustentabilidade e Tecnologia em Regiões de Montanha, Instituto Politécnico de Bragança, Campus de Santa Apolónia, 5300-253 Bragança, Portugal; 4: Department of Food Hygiene and Technology, Veterinary Faculty, University of León, E-24071, León, Spain; 5: Institute of Food Science and Technology, University of León, E-24071, León, Spain; 6: Al4AnimalS Associated Laboratory for Animal and Veterinary Science, 5000-801 Vila Real, Portugal; 7: Department of Veterinary Science, School of Agrarian and Veterinary Science (ECAV), University of Trás-os-Montes e Alto Douro (UTAD), 5000-801 Vila Real, Portugal; 8: Veterinary and Animal Research Center (CECAV), University of Trás-os-Montes e Alto Douro (UTAD), 5000-801 Vila Real, Portugal

Background: Mycotoxins, such as Aflatoxin B_1 (AFB_1) and Ochratoxin A (OTA), are fungal toxins with carcinogenic and genotoxic potential. This study was based on data previously published on the occurrence of mycotoxins in pork-derived products, reinforcing the importance of a One Health approach linking feed contamination, ingredient contamination during meat product manufacturing, animal health, and food safety.

Methods: A review of studies published between 1990 and 2025 on fungi and mycotoxins in meat and meat products was conducted according to Preferred Reporting Items for Systematic Reviews and Meta-

Analyses (PRISMA) principles. Initially, 3,374 records (PubMed and Google Scholar) were screened. In this work, only the results related to mycotoxins are presented, covering the stages of slaughter, meat processing, and commercialisation. Only 10 studies reported the proportion of positive samples relative to the total number of samples, the limit of detection in µg/kg, the concentrations of mycotoxins in µg/kg, and described the analytical method used, of which 7 focused on pork and pork-derived products.

Results: Studies conducted at the slaughterhouse stage did not meet the inclusion criteria. From the included studies, four studies reported data from the pork meat processing stage, and three from the pork meat marketing stage. The occurrence of AFB_1 has been reported in *Slavonski kulen* (Croatia) and other traditional Croatian meat products. OTA was detected in *Slavonski kulen* and other Croatian cured products, in dry-cured pork hams (Portugal), on the surface of Iberian ham (Spain), in artisanal and industrial dry sausages (Italy), and in typical salamis from several Italian regions. The highest mean OTA concentration (16.13 ± 3.32 µg/kg) was recorded in *Slavonski kulen* samples after 12 months of production under controlled conditions.

Conclusions: The European Union does not establish maximum limits for mycotoxins in meat and meat products, although some countries, such as Italy, recommend a maximum level of 1 µg OTA/kg for pork and pork-derived products. Several pork products included in this review were found to exceed this recommended level. Mycotoxin contamination may occur through different pathways along the meat production chain, including contaminated spices and other raw materials used in meat product manufacturing, mycotoxin-producing moulds present on the surface of dry-cured meat products, and the carry-over effect from farm animals exposed to contaminated feed, leading to the accumulation of mycotoxins in tissues such as liver, kidneys, muscles, and fat. These findings highlight the need for an integrated One Health approach, recognising the interconnection between feed safety, animal health, food processing practices, and public health. Strengthening feed control, monitoring raw materials and ingredients, and implementing good manufacturing and storage practices are essential to reducing mycotoxin contamination throughout the pork production chain and protecting both animal and human health.

1021 – From “hidden” biodiversity to zoonotic risk – links between iDNA biodiversity and small mammal zoonoses in different forest management regimes in Sweden

Anna JONSSON SUNDBERG (1), Hussein KHALIL (1), Jörgen SJÖGREN (1), Frauke ECKE (1,2), Yonas MEHERETU (1)
1: Swedish University of Agricultural Science, Sweden; 2: University of Helsinki, Finland

Introduction:

The dilution effect hypothesis predicts that higher biodiversity will suppress enzootic pathogen transmission, implying that biodiversity conservation could help mitigate zoonotic disease risks. However, empirical evidence remains mixed, and the mechanisms are poorly understood. Swedish boreal production forests provide an ideal system to study these dynamics. Current forestry practices often simplify forest structure, reducing biodiversity and potentially favouring zoonotic reservoirs like the bank vole (*Clethrionomys glareolus*). Bank voles are the principal host of Puumala orthohantavirus (PUUV), a pathogen that is endemic in Sweden and causes thousands of human cases of nephropathia epidemica annually. Here, we examine links between PUUV infection in bank voles and mammal community diversity, taking advantage of recent advances in environmental DNA (eDNA) and invertebrate-derived DNA (iDNA) that enable non-invasive detection of vertebrates, including elusive species often missed by traditional monitoring.

Methods: In 2025, we conducted field sampling across 12 forest plots in Hälsingland, Sweden, representing three forest management strategies: retention forestry, in which patches of living trees are left standing during harvesting, clear-cutting, and set-asides not managed for production (>90 years). We collected eDNA from vegetation swabs, and iDNA from >1,300 *Diptera* blow flies captured using mosquito-net pyramid traps over bait, pooling samples from each site and metabarcoding to detect mammal DNA. We live-trapped and euthanized 71 bank voles across all sites for PUUV screening by enzyme-linked immunosorbent assay (ELISA) to detect anti-PUUV IgG antibodies and identify sero-positive individuals.

Results: iDNA analyses detected 12 mammal species (five Carnivora, two Cetartiodactyla, one Eulipotyphla, four Rodentia) across all sites, with between two and eight species detected per site. Small mammal trapping confirmed the presence of bank voles, the primary host for PUUV. Ongoing analyses will

evaluate the relationship between PUUV infection in the captured animals and forest patch-level biodiversity estimates by iDNA and eDNA mammal detection.

Conclusions:

This study contributes to a growing literature on biodiversity and zoonotic disease risk, exploring the relevance of the dilution effect hypothesis in Swedish forest ecosystems. First results show variation in mammal species richness and confirm the presence of bank voles, primary reservoirs of PUUV, in Swedish boreal forests managed for restoration. Ongoing analyses and additional data collection, including camera traps, sound recorders, and remote sensing, will further clarify how forest management influences biodiversity and PUUV infection risk. This research, as part of the RESTOREID project, has significant implications for OneHealth, highlighting the potential for ecosystem-based disease mitigation through targeted biodiversity conservation and habitat restoration strategies.

1033 – Biosecurity, Zoonoses, and the Wildlife Trade: A New Approach to Safeguarding Public Health through Injurious Wildlife Listing in the United States

Cadhla FIRTH, Amanda LIEW, Grant CONNETTE, Jane ANDERSON, Jonathan KOLBY
Smithsonian Institution, United States of America

Background:

The COVID-19 pandemic increased global awareness of the potential zoonotic disease risks associated with the movement and trade of animals and animal products. In the United States, The U.S. Fish and Wildlife Service (USFWS) has the authority to classify wildlife species as 'injurious', thereby prohibiting international importation without permit. In 2021, The U.S. Congress instructed USFWS to evaluate wildlife species associated with zoonotic disease risk for injurious listing. To support USFWS in their decision-making process, we were engaged to develop a risk prioritization framework to identify bird, mammal, and reptile species likely to pose zoonotic disease risk if imported into the U.S..

Methods:

We created a database of all pathogens characterized as zoonotic in scientific literature and applied a step-wise filter to include only those meeting our definition of a zoonotic threat to the U.S.. Using variables designed to characterize the potential impact on public health, we then calculated a 'risk score' associated with the theoretical introduction of each pathogen. Separately, we generated a database of all bird, mammal, and reptile hosts associated with each pathogen and identified their occurrence status in the U.S. and whether live animals or animal products have been imported in the last decade. Finally, we assigned relative risk scores to each host species based on occurrence status, confirmed presence in trade, strength and number of pathogen associations, and concomitant pathogen risk scores.

Results:

From our initial database of ~1,200 pathogens, we identified ~300 that may pose a threat to the U.S. if introduced through trade. Notably, we were unable to find evidence of both human and animal infection for ~14% of pathogens that were referred to as zoonotic in the literature. Mammalian species were most commonly identified as hosts of the pathogens in our dataset, while several pathogens were not associated with any bird, mammal (excluding human), or reptile species. Approximately 16% of hosts were native or established in the U.S., while ~66% were documented as recently imported. Hosts associated with higher zoonotic disease risk included species not commonly perceived as wildlife, such as companion animals and livestock.

Conclusions:

To our knowledge, this study is the first to use an evidence-based approach to quantify the zoonotic disease risks associated with animal import at the host species level, rather than by pathogen. Our results suggest that these risks cannot be siloed based on host taxonomy or the nature of the relationship between a host species and humans. Instead, effective management of zoonotic disease risks requires a One Health approach that begins with governance. We expect the databases and risk prioritization framework presented here to be foundational for future evidence-based biosecurity risk assessments that are agnostic to the species of either pathogen or host.

1038 – Digitalization of One Health Surveillance Response (OHSR): The case study of Somali Regional State of Ethiopia

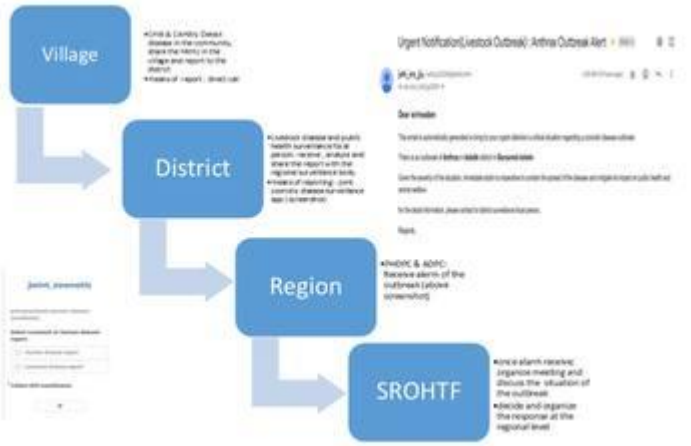
Yahya OSMAN (1), Jakob ZINSSTAG (2), Rea TSCHOPP (3)
1: Jigjiga University,Ethiopia; 2: Basel university; 3: Basel university

Background: - Ethiopia has a large livestock population and ranks second among the human population in Africa. More than 80% of the citizens depend on agriculture, where livestock plays a significant role in the livelihood of the communities and there is close contact between humans and animals. This could put communities at risk for zoonotic diseases. Furthermore, a recent cross-sectional study in the Somali region revealed exposure of both humans and livestock to Rift Valley Fever (RVF), brucellosis, and Q-fever, highlighting the importance of collaboration between human and animal health sectors in controlling zoonotic diseases. The evaluation conducted by the International Health Regulations (IHR) in 2016 indicated that in Ethiopia, communication and collaboration between animals and the public health sector is very weak and occurs on an ad hoc basis.

Methods: -Given the identified challenges, a study was conducted to assessed the feasibility of operationalizing a OHSRS in Adadle, Shinile and Gode districts of SRS between February 2020 to June 2024. The aim of the study to were to improve the weak collaboration in disease surveillance-response between the human and animal sectors. We set up a community-based health surveillance system using existing surveillance systems where the staff of both human and animal health sectors were linked and the Human and animal health information (HAHI) communicated at all levels from the village (community) to the national level. The reporting at the village level were direct call to one health surveillance and response unit (OHSRU) where both human and animal health surveillance focal points sit together, verify and then share (HAHI to regional surveillance level using joint pririotized zoonotic disease surveillance platform. This system is designed to produce alert notification for both public and Livestock disease surveillance directorates.

Result: - During the study period, anthrax , rabies, suspected RVF (mass abortion), food borne illness and unknown disease outbreaks were detected and shared among the sectors at the different level of surveillance points. Joint responses were organized and conducted by the sectors through the Somali Region One Health task force to mitigate the impact of the zoonotic outbreaks. The linkage of both health staff and mobile technology applications contributes to the early detection and response to zoonotic diseases.

Conclusion: - We believe this system will help to operationalize OHSR in SRS and to subsequently to the countries as the system is designed to be implemented using the existing surveillance system. Joint database or application used during the pilot study can be validated and endorsed through a broad consultative workshop, in which all relevant stakeholders are involved and then used for the implementation of OHSR. However, technical and institutional should be addressed to successfully implement OHSR in Ethiopia



1042 – One Health Knowledge Nexus: Communities of Practice fostering cross-sector knowledge exchange, collaborative learning, and One Health implementation

Lina AWADA (1), Kaushi KANANKEGE (1), Alessandra ALVITI (1), Danny SHEATH (1), Marion SELOSSE (1), Kassahun WONDIM (1), Rosie CLEAR HILL (2), Maria DE LA PUENTE AREVALO (1), Ludovica GRIMALDI (1), Hui YIN (1), Francesca LATRONICO (1), Laetitia LEMPEREUR (1), Damian TAGO PACHECO (1), Chadia WANNOUS (3), Mauro DE ROSA (3), Marie-Isabelle PEYRE (4), Yoeri BOOIJINK (4), Katie WOOLASTON (5), Emily Michelle RONIS (5), Cheng LIANG (6), Sinaia NETANYAHU (6), Fazil DUSUNCELI (2), Barbara HÄSLER (1), Fairouz LARFAOUI (1), Zelalem TADESSE (1), Junxia SONG (1)

1: Animal Production and Health Division, Food and Agriculture Organization of the United Nations (FAO), Rome, Italy.; 2: Plant Production and Protection Division, Food and Agriculture Organization of the United Nations (FAO), Rome, Italy.; 3: One Health Department, World Organisation for Animal Health (WOAH), Paris, France.; 4: Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), Montpellier, France; 5: United Nations Environment Programme (UNEP), Nairobi, Kenya.; 6: World Health Organization (WHO), Geneve, Switzerland.

One Health (OH) recognizes the interconnected nature of human, animal, plant, and ecosystem health, while acknowledging persistent challenges such as fragmented knowledge systems, limited cross-sector coordination, and shortage of workforce capacity trained in transdisciplinary. Despite growing global commitment, practical mechanisms to connect professionals across sectors and regions remain underdeveloped.

Launched in 2023 under the leadership of the Food and Agriculture Organization of the United Nations (FAO) and powered by the Quadripartite collaboration, the One Health Knowledge Nexus (OHKN) was established to address these gaps and support implementation of the OH Joint Plan of Action. The OHKN serves as a global learning and exchange platform advancing knowledge generation, sharing, policy translation, and community engagement.

Today, the OHKN connects over 3,000 stakeholders from more than 170 countries and territories through eight Communities of Practice (CoPs), spanning OH governance, biosecurity, antimicrobial resistance, tick control and acaricide resistance, emerging pest and disease drivers, Information and Communication Technologies, and return on OH investment. Participants include stakeholders from governments, academia, NGOs, international organizations, communities, and the private sector fostering peer learning, and evidence-informed decision-making.

Hosted on FAO Virtual Learning Centers, the CoPs, supported through multiple technical and financial partnerships, facilitate structured knowledge exchange, discussion and learning through webinars,

workshops, dialogues, discussion forums, resource repositories, training sessions, co-creation of outputs, and sharing of country experiences. Impact is measured through participation analytics, co-developed resources, and qualitative feedback from forums, interviews and surveys, to assess contributions to workforce competencies and collaborative learning.

Through these collaborative processes, the OHKN has co-developed several practical tools and resources. These include the FARM 5G Checklist/Guide to support prudent antimicrobial use at farms, inventories of ICT tools for One Health and OH policies and regulations, the Guidelines for Sustainable Tick Control and Acaricide Resistance Management in Livestock, and the Return on Investment (ROI) framework. The ROI CoP has also developed a training course to strengthen professionals' capacity to assess the value of OH investments. Other activities include "ask-the-expert" sessions, cross-CoP collaborations, and professional subgroups such as veterinary training alumni and laboratory networks that promote peer exchange and early-career engagement.

By the end of 2025, survey results from some of these CoPs indicated that 74% participants reported improved OH coordination through stronger cross-sector and cross-border collaboration and access to practical tools, 54% improved communication including more effective messaging, expanded professional networks, and greater harmonization of terminology, 64% better alignment of activities with clearer roles and responsibilities, increased adoption of common standards, and strengthened cross-sector policy dialogue, and 79–93% across CoPs reporting increased knowledge through activities.

Overall, the OHKN demonstrates how a globally connected platform can strengthen collaborative learning and workforce capacity, supporting the translation of One Health principles into coordinated national and international action.

1045 – Bridging the surveillance gap: an integrated one health risk assessment of Crimean-Congo Hemorrhagic Fever outbreak occurrence in Cameroon

Lorraine FOKOU KUIGNOU MATCHIO (1,2,3), Loïc NCHANKOU KOUOTOU (2), Félicité DJUIKWO TEUKENG (3)

1: University of Yaoundé I, Cameroon; 2: Molecular Parasitology and Diseases Vector Research Laboratory; 3: Université des Montagnes

Background

In the face of increasing zoonotic threats, proactive risk assessment has become a strategic imperative for global health security. Crimean-Congo Hemorrhagic Fever (CCHF) is a severe viral zoonosis with a case fatality rate of 10-40 %. In Cameroon, evidence of viral circulation has been reported in livestock, humans and tick vectors; however the surveillance system remains predominantly passive. Given the country's ecological diversity, the potential risk of a CCHF outbreak remains poorly estimated and likely varies geographically. This study aims to evaluate the risk of CCHF outbreak occurrence across Cameroon by integrating available data to strengthen public health preparedness.

Methods

We conducted a systematic review and meta-analysis following PRISMA guidelines. Data were searched across PubMed, Web of Science, African Journals OnLine, and the African Index Medicus without time restrictions. Statistical analyses were conducted using R software (version 4.4.1), with a p-value 0.05 considered statistically significant. The risk of emergence was categorized across Cameroon's ten regions by integrating these findings into an adapted framework. This framework combined the AFSSA method to estimate the probability of occurrence (based on human/animal seroprevalence, vector density, and urbanization rates) with the Tripartite (WHO/FAO/WOAH) joint risk assessment tool to quantify impact severity (based on clinical outcomes and socio-economic consequences) and risk levels. This approach was chosen because, unlike the AFSSA method which relies on criteria-based weighting to estimate consequences, the Tripartite method directly evaluates the severity of an event's consequences. This is more suitable for vector-borne diseases, where the simultaneous presence of both virus and vector is essential for the hazard to occur.

Results

A total of 8 studies were included in the study. Meta-analysis reveals that CCHF is actively circulating among ruminants. Out of 3,094 livestock samples, the pooled prevalence was 34% (95% CI [14–59]; $I2$=

99.4%, *p 0.0001*). Sub-group analysis showed a significant higher prevalence in cattle compared to small ruminants (*p = 0.0364*). In humans, data remains scarce but indicates a pooled seroprevalence of 4% among 662 individuals tested (95% CI: [1-8]; I2 = 71.4%, *p = 0.0303*). While specific viral prevalence in ticks was not reported, the presence of vectors was documented in five regions, with the highest density observed in the North. The risk assessment identifies the northern regions (Far North, North and Adamawa) as high risk zones, driven by intense agro-pastoral activities, high tick vector density and established livestock trade routes.

Conclusion

The risk of CCHF outbreak in Cameroon is high, particularly at the human-animal interface in northern pastoral communities. To mitigate this threat, we recommend shifting from passive to active integrated surveillance. Implementing a One Health sentinel system in high-risk slaughterhouses and pastoral zones is critical for early detection and preventing zoonotic spillover.

1058 – Health management practices, antimicrobial use and the adoption of alternatives among Nigerian fish farmers: a mixed-methods study

Ismail Ayoade ODETOKUN (1), Jadesola Juliana AJAO (2), Rodiat Olabisi OMOTOSO (3), Afisu BASIRU (4), Mutiat Adenike ADETONA (1), Wasiu Adeyemi JIMOH (5), Somrat ABDULSALAMI (5), Abdulfatai AREMU (6), Mutiat Olaitan MOHAMMED (7), Samira SARIH (8), Enric GISBERT (8), Maria Dolores Furones NOZAL (8), Silvia TORRECILLAS (8), **Mahmoud ELTHOLTH** (2,9)

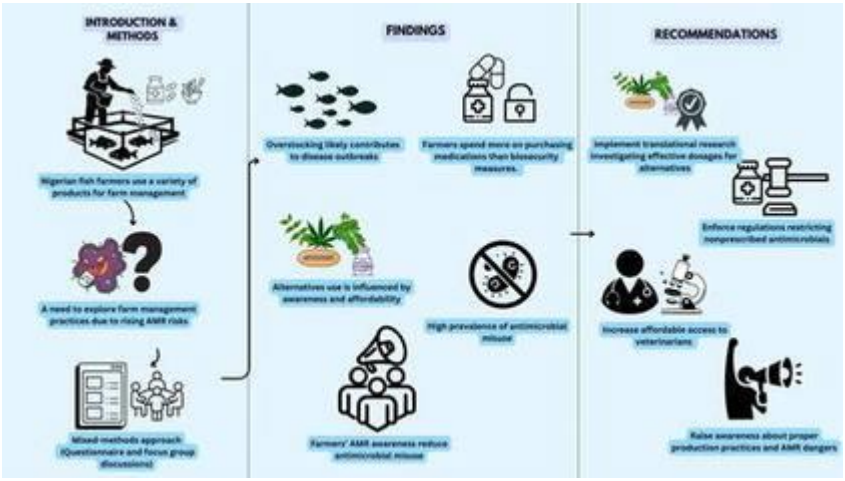
1: Department of Veterinary Public Health and Preventive Medicine, University of Ilorin, 240003, Ilorin, Nigeria; 2: Department of Health Studies, Royal Holloway University of London, Egham TW20 0EX, UK; 3: Department of Statistics, University of Ilorin, 240003, Ilorin, Nigeria; 4: Department of Veterinary Physiology and Biochemistry, University of Ilorin, 240003, Ilorin, Nigeria; 5: Department of Aquaculture and Fisheries, University of Ilorin, Ilorin 240003, Nigeria; 6: Department of Veterinary Pharmacology and Toxicology, University of Ilorin, 240003, Ilorin, Nigeria; 7: Department of Biological Sciences, Summit University, Offa, Nigeria; 8: Aquaculture Program, Institut de Recerca i Tecnología Agroalimentaries (IRTA), La Rápita, Spain; 9: Hygiene and Preventive Medicine Department, Faculty of Veterinary Medicine, Kafrelsheikh University, Kafr el-sheikh, Egypt

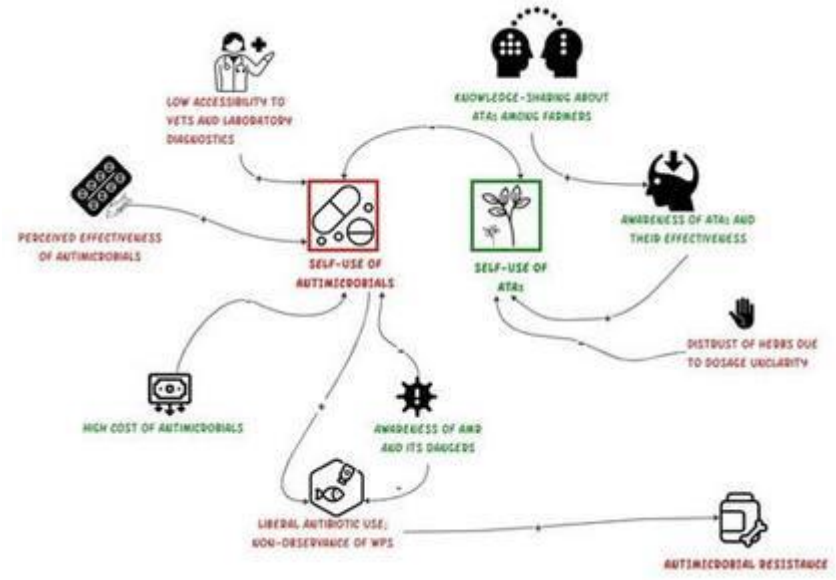
Background: The intensification of fish production via aquaculture in Nigeria has led to an increase in antimicrobial use for health management, potentially contributing to antimicrobial resistance (AMR), a global health problem intersecting fish farming, human health, and the wider environment. Preventive management and antimicrobial alternatives (ATAs) offer an AMR-risk-free pathway for fish production; however, several factors have been identified as restricting their adoption by fish farmers globally. In our study, we sought to identify the influence of prevalent production practices on disease outbreaks and health management, and to examine factors shaping Nigerian farmers' choices between antimicrobials and ATAs.

Methods: A mixed-methods approach was employed, comprising questionnaire surveys (n = 330) and focus group discussions in Lagos and Kwara State, Nigeria.

Results: 69.7% of farmers raised catfish alone; 89% of farmers stocked fish at densities exceeding those deemed safe by existing research. Most farmers spent 100% of their health expenses on medication only, rather than biosecurity or water quality management. Tilapia farmers were more likely to spend on water management than catfish farmers (OR: 3.3, 95% CI: 1.4-7.4, p: 0.004). 27% of farmers experienced up to 50% mortality over the last production cycle. Perceived effectiveness promoted farmers' antimicrobial use, while high cost and AMR awareness limited their use. Farmers used a variety of ATAs, including herbal plants, vitamins, and salt, for disease prevention and treatment. Adoption of ATAs was influenced by farmers' awareness and cost affordability, while uncertainty about the correct dosage formulations prevented greater adoption. ATAs were considered less effective than antimicrobials. Farmers reported regularly using antimicrobials, particularly during severe disease outbreaks.

Conclusions: We recommend that pharmaceutical and translational studies be embarked on to determine effective dosage formulations for ATAs currently in use. AMR awareness should be increased among farmers, and affordable access to veterinary care should be improved.





1061 – Operationalising One Health in fragile settings: a systems assessment of priority zoonotic disease preparedness in Somalia using the OH-SAPZ tool

Mohamed Abdelrahman MOHAMED, Kamaludin Rage ALI, Abdinasir Yusuf OSMAN
One Health Unit, Ministry of Health and Human Services, Mogadishu, Somalia

Background

Zoonotic diseases account for approximately 60–75% of emerging human pathogens and represent a major driver of global pandemic risk, particularly in fragile and conflict-affected settings. Somalia faces heightened zoonotic vulnerability due to pastoral production systems, recurrent climatic shocks, population displacement, and fragmented federal governance structures that challenge surveillance, detection, and response capacities. While the One Health approach is widely recognized as a critical framework for zoonotic disease preparedness and response, empirical evidence on how One Health systems function operationally in fragile contexts remains limited. This study aimed to characterize the functional architecture of Somalia's One Health system for priority zoonotic diseases and identify structural determinants affecting operational preparedness using the One Health Systems Assessment for Priority Zoonoses (OH-SAPZ) tool.

Methods

A mixed-methods One Health systems assessment was conducted between April and June 2025 in Mogadishu, Somalia. The OH-SAPZ survey tool was administered to 23 multisectoral stakeholders

representing human, animal, and environmental health sectors during a national validation workshop. Scenario-based discussions were used to simulate suspected zoonotic events and evaluate system performance across the detection-to-response continuum. Five nationally prioritized zoonotic diseases: Rift Valley fever, Middle East respiratory syndrome coronavirus (MERS-CoV), Anthrax, Brucellosis, and Zoonotic enteric parasites were used as tracer conditions to assess surveillance, laboratory, coordination, response, and recovery functions across community, district, state, and national levels. Systems mapping and cross-sectoral reviews were conducted iteratively to triangulate findings and enhance internal validity.

Results

Core One Health functions were identified for all priority zoonotic diseases; however, these functions were largely organized within sector-specific vertical systems with limited cross-sectoral integration. Formal multisectoral coordination mechanisms existed mainly at the national level through the One Health Unit and the National One Health Technical Working Group. Institutionalized coordination structures were largely absent at district and state levels where zoonotic exposure risks are highest. Surveillance and laboratory systems operated in parallel across sectors without integrated data management platforms, while environmental surveillance and diagnostic capacities remained weakly integrated into zoonotic preparedness frameworks. Response activities depended largely on informal cross-sectoral communication, and structured mechanisms for recovery, evaluation, and post-outbreak learning were not identified.

Conclusions

Somalia's One Health system demonstrates foundational multisectoral capacity for zoonotic disease preparedness but remains constrained by vertical sectoral structures, limited subnational coordination, and weak environmental health integration. Strengthening operational One Health capacity will require institutionalizing coordination mechanisms at decentralized levels, integrating surveillance and laboratory information systems across sectors, and embedding environmental health within zoonotic preparedness frameworks. These findings provide critical insights for operationalizing One Health systems in fragile and conflict-affected settings and may inform broader regional strategies for zoonotic disease preparedness in similar contexts.

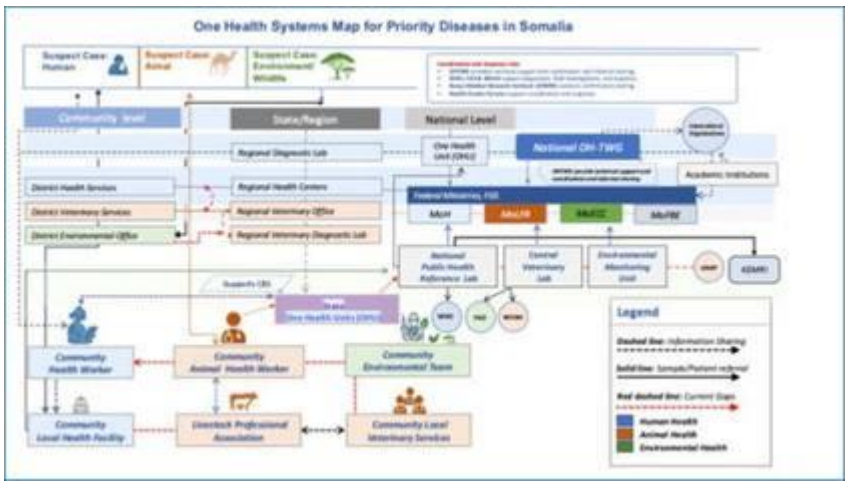


Table1: Prioritised Zoonotic Diseases – OHZDP & OH-SAPZ Analysis

Analytical Category	n. of Diseases Prioritised (OHZDP)	Prioritised Diseases	Included in OH-SAPZ Analysis
Viral Haemorrhagic Fevers	4	• Rift Valley Fever	• Rift Valley Fever
		• Ebola Virus Disease	
		• CCHF	
		• Yellow Fever	
Respiratory Zoonotic Viruses	2	• Middle East respiratory syndrome	• MERS-CoV
		• *Zoonotic Influenza Viruses*	
Bacterial Zoonoses	10	• Anthrax	• Anthrax
		• *Bovine Tuberculosis*	
		• Brucellosis	• Brucellosis
		• *Leptospirosis*	
		• *Q Fever*	
		• *Rickettsioses*	
		• *Campylobacteriosis*	
		• *Salmonellosis*	
		• *Listeriosis*	
		• *Escherichia coli*	
Zoonotic Enteric Parasites	6	• Giardiasis	• Giardiasis
		• *Fasciolíasis*	
		• Cryptosporidiosis	• Cryptosporidiosis
		• *Echinococcosis*	
		• *Schistosomiasis*	
		• *Cysticercosis/Taeniasis*	
Other Zoonoses	11	• Not included in OH-SAPZ analysis	—

Note: "-" indicates diseases not included in OH-SAPZ analysis. OH-SAPZ-included diseases are highlighted in green.

1068 – Seroprevalence and Associated Risk Factors of Toxoplasma gondii in Small Ruminants from Northeastern Portugal: Preliminary Findings from a One Health Study

Tifany PEREIRA (1,3), Hélder QUINTAS (1), Ana LOPES (3), Maria CALDEIRA (1,4), Carina RODRIGUES (2)

1: Mountain Research Center (CIMO), Collaborative Laboratory for Mountains of Tomorrow (SusTEC), Instituto Politécnico de Bragança (IPB), Portugal., Portugal; 2: LiveWell, Research Center for Active Living and Wellbeing ,Instituto Politécnico de Bragança, Portugal; 3: University of Trás-os-Montes and Alto Douro (UTAD), Vila Real, Portugal; 4: School of Medicine and Biomedical Sciences Abel Salazar (ICBAS), University of Porto, Portugal

Context*Toxoplasma gondii* is a globally distributed zoonotic protozoan parasite infecting a wide range of warm-blooded animals, including humans. Small ruminants play a key role in the epidemiology of toxoplasmosis, as infection causes reproductive losses and represents a source of human exposure through ingestion of infected meat. The parasite persists in the environment via oocysts, highlighting the relevance of environmental and management factors. In Portugal, epidemiological data on *T. gondii* infection in livestock remain scarce, particularly in the Northeast, where small ruminant farming is prevalent and interactions between humans, animals and the environment are frequent. Within a One Health framework, updated information is essential to understand *T. gondii* circulation and support integrated surveillance. This study estimated the seroprevalence of *T. gondii* in small ruminants from Northeastern Portugal and identified biological, environmental, management and farmer-related factors associated with infection.

Methods A cross-sectional study was conducted on farms with small ruminants in Northeastern Portugal between 2020 and 2022. A total of 1104 samples (881 sheep and 223 goats) from 61 farms were analysed.

Farms and animals were selected using a random sampling approach. Serum samples were analysed using a commercial indirect ELISA (ID Screen® Toxoplasmosis Indirect Multi-species, IDVet, Grabels, France) for detection of IgG antibodies to *T. gondii*. Epidemiological data were collected through farmer questionnaires on animal characteristics, management practices, environmental exposure, and biosecurity. Associations between seropositivity and variables were evaluated using chi-square tests, and spatial differences were assessed across municipalities and localities.

Results Among 1104 samples, the apparent seroprevalence of antibodies to *T. gondii* was 17.8% (197/1104; 95% CI: 15.6–20.2). No significant differences were observed between species or sex. However, animal age was significantly associated with seropositivity (p 0.001), with a higher prevalence in animals older than 2 years (23.0%) than in those aged 6 months to 2 years (9.6%) or younger than 6 months (8.7%). Farmer-related variables were also associated with infection. Lower seroprevalence was observed among farmers who reported livestock production training (p 0.001) and higher education (p = 0.011). Regarding management, housing type was significantly associated with seropositivity (p = 0.002), with higher prevalence in precarious housing (23.0%). Contact with domestic species was also significantly associated (p = 0.020). Spatial analysis revealed significant differences between municipalities (p = 0.0017) and localities (p 0.001), suggesting heterogeneous environmental exposure.

Conclusions These findings provide preliminary evidence of *T. gondii* circulation in small ruminants from Northeastern Portugal, highlighting the influence of age, management and farmer-related factors. Additional studies with larger sample sizes are warranted to strengthen the robustness and representativeness of these findings and to enable a more comprehensive evaluation of risk factors. These results emphasise the importance of integrated surveillance and prevention within a One Health framework.

1077 – Developing a national database for recording Environmental Incidents of Public Health concern in Ireland

Mairead MADIGAN, Patricia GARVEY, Angeline MCINTYRE, Aoife COLGAN, Ina KELLY
Health Protection Surveillance Centre, Ireland

BackgroundEnvironmental hazards are recognised threats to health, and numerous environmental factors have been linked to adverse health outcomes. In Ireland, advice on Environmental Incidents is sought from Departments of Public Health from various sources; however, this information was not previously collated at national level. A review of regional data from 2023 showed variation in datasets and inclusion criteria, with no standardised system for logging incidents.

Our aim was to develop a national database to support the collection, monitoring, and reporting of environmental incidents in Ireland, enabling a clearer understanding of their impact on public health and to protect the Irish population against harm from any environmentalhazards.

MethodsBetween September 2024 and January 2025, consultations were held with regional colleagues to identify relevant incident types and key variables required for surveillance. Additional meetings took place to gather feedback on experience with the tool. A national Excel-based database was developed and distributed to regional departments for data entry. Data were analysed using RStudio, and quarterly reporting was agreed as the standard frequency for data collation and dissemination.

Results

Agreement was reached to capture data on nine different environmental incident types. A core suite of surveillance variables was established including: key data on the incident recognition, health and health service impact of the incident, actions taken, and recommendations arising.

In a pilot between 1st April to 30th September, advice was sought from public health departments on 234 Environmental Incidents. Drinking water (DW) accounted for 69% (n=162) of requests. Most incidents (60%) were linked to the public water supply. Bathing water (BW) accounted for a quarter of all incidents, 79% of which were associated with sea/salt water. Less than 3% of incidents related to Legionella detections, Air quality and other incidents. Advice was issued to the public in 80% of all incidents, including 43 boil water notices, and 40 bathing prohibition notices.

Conclusions

For the first time in Ireland, information on public health responses to environmental incidents is collated in a single repository in a standardised way, which will allow us to describe the type, volume and impact of environmental incidents in Ireland, monitor progress on public health recommendations, and highlight gaps.

1088 – An Ethical Framework for Zoonotic Disease Emergency Management, Enabling a One Health Strategy – Developing an approach informed by perspectives from US Animal Health Professionals

Raymond ANTHONY (1), Kate MILLAR (2)

1: University of Alaska Anchorage, United States of America; 2: University of Nottingham, United Kingdom

Background:

The overarching goal of this multidisciplinary and collaborative co-designed research study is to strengthen the ethical aspects of animal disease management, such as hazard identification and risk assessment management, by enabling a One Health strategy. This study is a collaboration between bioethicists, veterinarians and public health officials. Results from the first phases of a National Institute of Food and Agriculture funded project (# ALKW-2023-10957) are discussed. Anchored in One Health, the study identifies, maps and assesses conflicts at the heart of disease outbreaks to provide decision-making support by developing strategies and ethical decision-making tools to strengthen food system governance and professional resilience of veterinarians, public health officials, animal caregivers, farmers and ranchers, disease responders and related interest-holders. This research focuses on examining emerging infectious disease (zoonoses) and public health preparedness resources through the lens of interspecies social-ethical determinants of health-welfare, which is informed by new understanding across health-agriculture-veterinary professionals. It explores the ethical foundations of zoonotic disease management and how values-awareness and ethical analysis strengthen One Health approaches.

Methods:

A systematic literature review mapped how ethical frameworks, decision trees and concepts have been utilized in disease outbreaks and what approaches guide decisions in animal disease management and preparedness response. Key themes in zoonotic/pandemic planning and response were identified to support a one-day multidisciplinary collaborative, co-production, workshop of national professionals with first-hand working knowledge of pandemic and zoonotic disease preparedness. The collaborators identified impediments and themes.

Results:

Thematic insights around multispecies, multivariant public health ethics and zoonosis management, and future capacity needs emerged. The dialogue revealed how values, relationships and norms influence ethical behavior and action within zoonotic disease management are typically identified, characterized and analyzed. An overarching frame that emerged around One Health Animal Disease Management is that of a “moral ecology,” referring to Anchoring Values, Ethics Dimensions in Risk Management, and the role of Professional Practice and Governance Structures, respectively, in disease preparedness, mitigation, response and recovery. This frame informs capacity building and investment opportunities, around ethics-related training, and highlights the need for further work on (i) ethical decision-making for disaster management, (ii) interspecies vulnerabilities and animal welfare issues, and (iii) professional resilience and mental health and wellness.

Conclusions:

This project addresses the need for further work on One Health Animal Disease Management by taking a multisectoral approach to strengthen ethical governance of global health security at the human-animal interface.

The results will have implications for US food security by exploring the ethical nature of preparedness and response, and improving knowledge transfer and understanding of human-animal relations during a crisis.

1098 – A Community Competence Index to estimate pathogens transmission risk in the context of the diversity-disease risk relationship: the effect of land use on West Nile virus

María José TOLSÁ-GARCÍA (1), Paulina PONTIFES (1), Omar GARCÍA-SUÁREZ (1), Magdalena L. WEHMEYER (2), Ana Laura VIGUERAS-GALVÁN (3), Paola MARTÍNEZ-DUQUE (1), Marie-Marie OLIVE (4), Gilbert LE GOFF (3), Roger ARANA (1), Stanislas TALAGA (5), Tatiana SULESCO (2), Leif RAUHÖFT (2), Felix Gregor SAUER (2), Víctor RODRÍGUEZ-VALENCIA (3), Alhelí FLORES-FERRER (1), Audrey ARNAL (3), Rosa Elena SARMIENTO (1), Renke LÜHKEN (2), Benjamin ROCHE (3), Gerardo SUZÁN (1), David ROIZ (3)

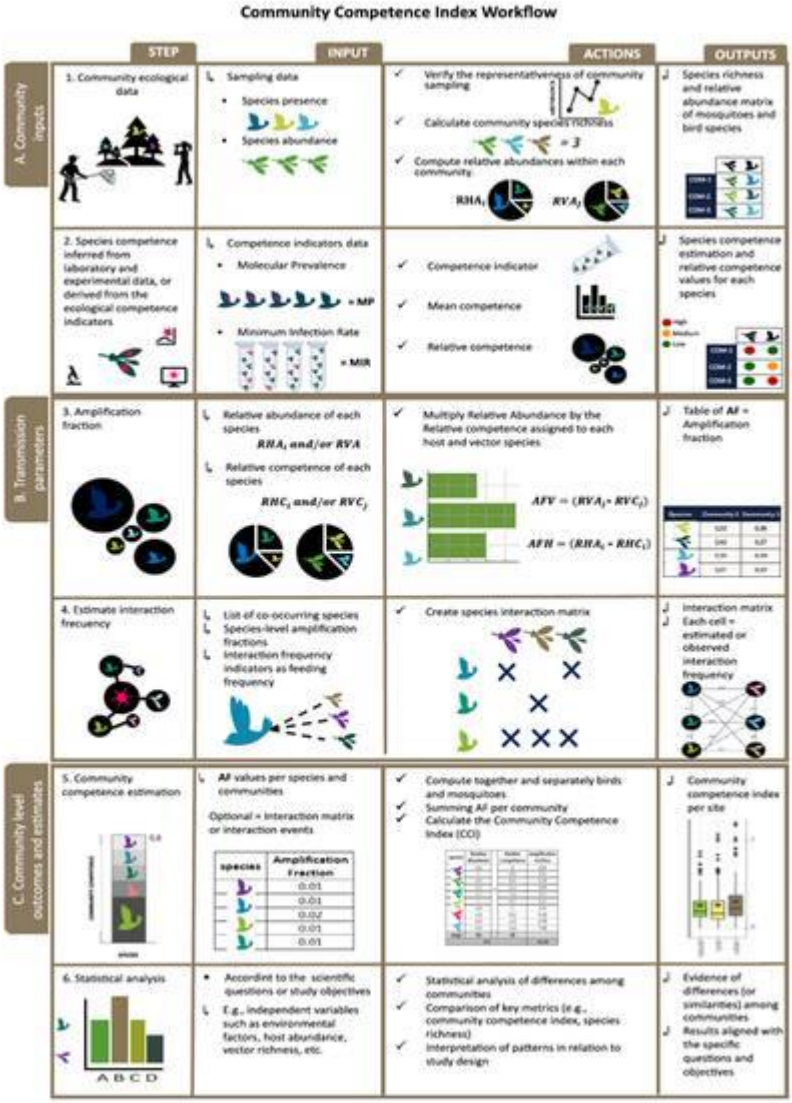
1: Faculty of Veterinary Medicine, National Autonomous University of Mexico., Mexico; 2: Bernhard Nocht Institute for Tropical Medicine, WHO Collaborating Centre for Arbovirus and Hemorrhagic Fever Reference and Research, Hamburg, Germany; 3: MIVEGEC, Univ. Montpellier, IRD, CNRS, Montpellier, France; 4: ASTRE, Univ. Montpellier, Cirad, INRAE, Montpellier, France; 5: Unité d'Entomologie Médicale, Institut Pasteur de la Guyane, Cayenne, French Guiana.

Background. Host competence refers to a species' ability to acquire a pathogen and support its replication. The Amplification Fraction (AF) framework integrates host competence with species abundances to assess disease risk. In vector-borne pathogen systems, interactions between vector feeding preferences andhost competence play a key role in shaping transmission dynamics. To better capture this complexity within a community context, we propose a Community Competence Index (CCI), and we applied this index to the West Nile virus (WNV) system, using data on avian and mosquito communities collected in France, Germany, and Mexico, across various land-use types.

Methods. The index was constructed by integrating (i) species-level competence values, (ii) species abundances, and (iii) mosquito-feeding preferences. Using this index, we assessed how AF, CCI, and species interactions vary across urban, rural, and natural land-use types to examine the influence of ecological context on community competence. Additionally, we evaluated what proportion of a community's total species richness and abundance is attributable to competent vs. non-competent species.

Results. Species richness was consistently higher in natural habitats compared to rural and urban land-use types. However, rural and urban areas hosted higher presence, and abundances of competent species than natural habitats. Our results showed that urban, and in some cases rural, areas exhibited significantly higher AF and CCI values compared to natural habitats. This pattern suggests that the lower diversity typically found in urban environments is associated with higher average community competence. These results support the diversity-disease riskdilution effect hypothesis, which posits that greater species richness can dilute in some cases pathogen transmission.

Conclusions. The CCI provides a versatile and integrative tool for estimating pathogen transmission capacity at the community level, complementing existing strategies for the early prevention, surveillance, and risk assessment of zoonotic diseases.



1101 – Serological survey of Bioko Island, Equatorial Guinea suggests shifting vector-borne and zoonotic pathogens

Graham MATULIS (1,2,3), Kellie GOODNIGHT (1,2,3), Evan TEAL (1,2,3), David GALICK (4), Teresa Ayingono ONDO MIFUMU (4), Crisantos Nsue ABESO (4), Wonder P PHIRI (4), Nicole CHEN (2,3), Allison SCHMID (2,3), Nora G CLEARY (1,2,3), Keats REDICK (2,3), Dawood AZIEZ (2,3), Abigail A LILAK (1,2,3), Carlos A GUERRA (5), Guillermo A GARCIA (5), Michael E VON FRICKEN (1,2,3)

1: Department of Environmental and Global Health, University of Florida, Gainesville, Florida, United States of America; 2: Emerging Pathogens Institute, University of Florida, Gainesville, Florida, United States of America; 3: One Health Center of Excellence, University of Florida, Gainesville, Florida, United States of America; 4: MCD Global Health, Malabo, Equatorial Guinea; 5: MCD Global Health, Silver Spring, Maryland, United States of America

Background: For the past 22 years, Bioko Island, Equatorial Guinea has been the site of numerous interventions aimed at reducing the burden of malaria. Despite the significant reductions in malaria prevalence, population exposure to other vector-borne and zoonotic pathogens of public health concern remains poorly characterized. Here, we used dried blood spots (DBS) collected in 2021 and a MagPix multiplex assay to assess serological evidence of exposure to pathogens from seven viral groups.

Methods: Three thousand DBS were collected on Whatman 903 Protein Saver cards during the 2021 malaria indicators survey from a representative sample of the general population of Bioko Island and stored at room temperature until processing in 2025-2026. Five 2mm discs were cut out of the blood spots

and eluted in 200ul PBS overnight at 4°C with shaking. Eluates were analyzed using a MagPix multiplex assay which detects the presence of IgG reactive against Rift Valley Fever virus (RVFV), Alphaviruses, Flaviviruses, Ebola virus (EBOV), Marburg virus (MARV), Lassa virus (LASV), and Crimean-Congo Hemorrhagic Fever virus (CCHFV). A signal-to-noise ratio threshold of 20 was used to define seropositivity.

Results: We found evidence of past exposure to RVFV (13, 0.43%), Alphavirus (1,226, 40.87%), Flavivirus (221, 7.37%), EBOV (1, 0.03%), and CCHFV (1, 0.03%). No evidence of past exposure was noted for either MARV or LASV. These findings are considered preliminary, with efforts currently underway to confirm independently with commercial ELISAs. Additionally, specification of Alphavirus and Flavivirus seropositivity is currently underway using commercial ELISAs for IgGs against Chikungunya (CHIKV), Dengue (DENV), Yellow fever (YFV), and Zika (ZIKV).

Conclusions: These results represent the first serological survey of vector-borne and zoonotic virus exposure targeting the population of Bioko Island in almost 40 years. Compared to serological studies conducted in 1985-1987, seroprevalence for certain high-consequence pathogens (EBOV, MARV, CCHFV, LASV) has decreased, while exposure to non-*Anopheline*-vectored pathogens (RVFV) appears to have increased. Most notably, Alphavirus seroprevalence was 40.87%, the first such estimate for this population which suggests a substantial and previously uncharacterized exposure burden, similar to that seen elsewhere in West Africa, that warrants further investigation.

1115 – One Health Investigation: Resurgence of Human A/H5N1 Cases in Cambodia and Continued Zoonotic Transmission of a Novel Reassortant Clade 2.3.2.1e Virus at Human–Animal Interfaces

Jurre SIEGERS (1), Ruopeng XIE (2,3), Alexander M. BYRNE (4), **Kimberly M. EDWARDS** (2,3), Shu HU (2,3), Sokhoun YANN (1), Sarath SIN (1), Songha TOK (1), Kimlay HORM (1), Sreyviseth HORM (1), Chenthearath RITH (1), Seangmai KEO (1), Leakhena PUM (1), Veasna DUONG (1), Heidi AUERSWALD (1,5), Yisuong PHOU (1), Sonita KOL (1), Andre SPIEGEL (6), Ruth HARVEY (4), Sothyra TUM (7), San SORN (8), Bunnary SENG (7), Yi SENGDOEURN (9), Chau DARAPHEAK (10), Chin SAVUTH (10), Makara HAK (11), Vanra LENG (12), Sarika PATEL (12), Peter THIELEN (13), Filip F. CLAES (14), Nicola S. LEWIS (4), Ly SOVANN (9), Erik A. KARLSSON (1), Vijaykrishna DHANASEKARAN (2,3)

1: Virology Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia.; 2: School of Public Health, LKS Faculty of Medicine, The University of Hong Kong, Hong Kong.; 3: HKU-Pasteur Research Pole, LKS Faculty of Medicine, The University of Hong Kong, Hong Kong.; 4: Worldwide Influenza Centre, The Francis Crick Institute, London, United Kingdom.; 5: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise Giuseppe Caporale, Teramo, Italy.; 6: Administration, Institut Pasteur du Cambodge, Phnom Penh, Cambodia.; 7: National Animal Health and Production Research Institute, Phnom Penh, Cambodia.; 8: General Directorate of Animal Health and Production, Phnom Penh, Cambodia.; 9: Communicable Disease Control Department, Ministry of Health, Phnom Penh, Cambodia.; 10: National Institute of Public Health, Ministry of Health, Phnom Penh, Cambodia.; 11: Emergency Centre for Transboundary Animal Diseases, Food and Agriculture Organization of the United Nations, Phnom Penh, Cambodia.; 12: World Health Organization, Phnom Penh, Cambodia.; 13: Applied Physics Laboratory, Johns Hopkins University, Laurel, MD, United States.; 14: Emergency Centre for Transboundary Animal Diseases, Food and Agriculture Organization of the United Nations, Bangkok, Thailand.

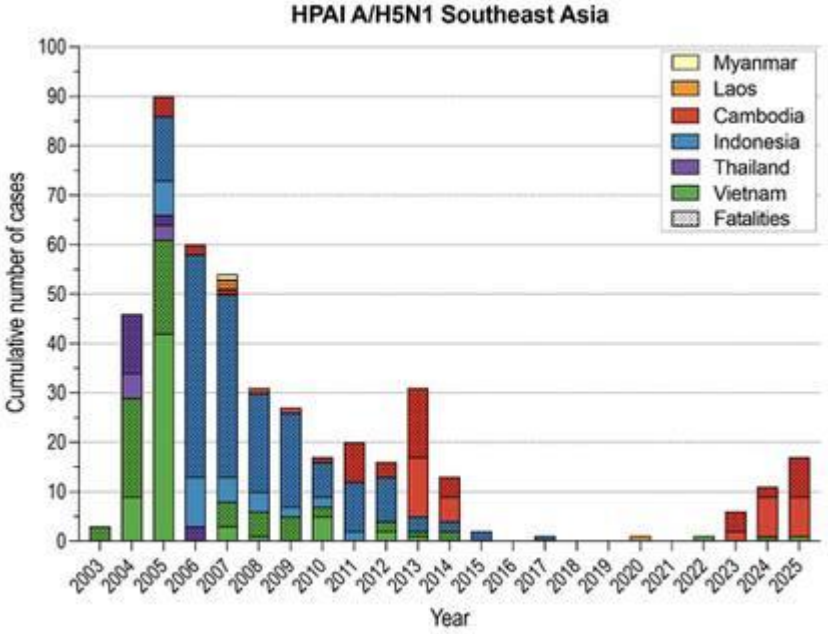
Background: Cambodia has experienced endemic circulation of highly pathogenic avian influenza (HPAI) A/H5N1 in poultry since 2004, with sporadic zoonotic transmission to humans. After nearly a decade without reported human infections, Cambodia has recorded a resurgence in human H5N1 cases since February 2023, highlighting persistent risks at the human-animal-environment interface (Fig. 1). We investigated the drivers of this resurgence using a One Health framework integrating outbreak response, poultry and live bird market surveillance, and genomic epidemiology to characterize viral emergence, transmission pathways, and implications for cross-sector preparedness.

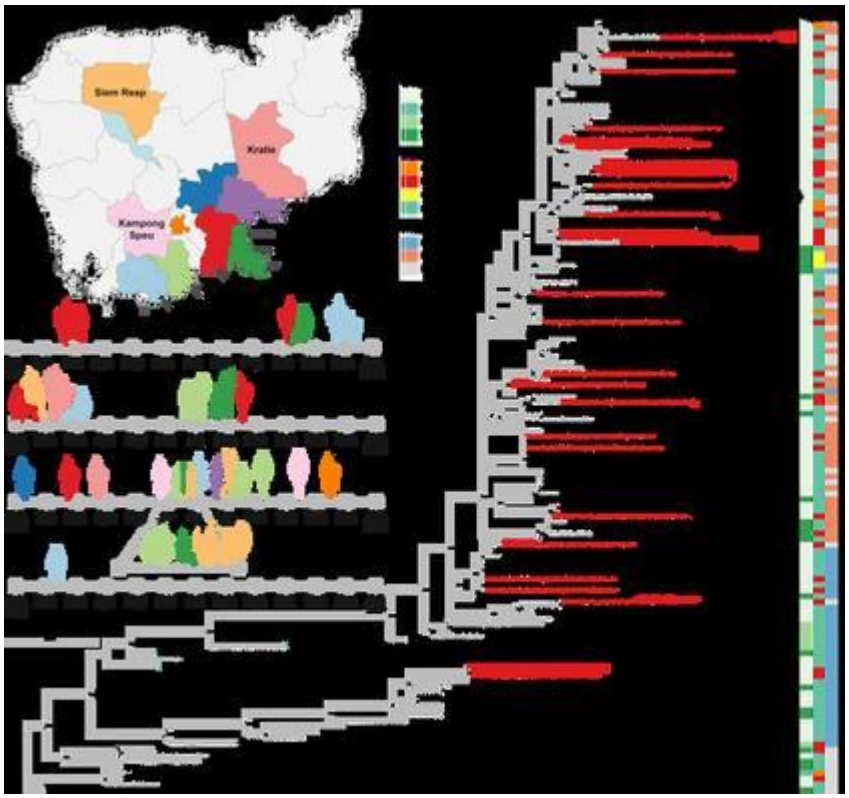
Methods: Samples were collected through One Health outbreak investigations associated with human H5N1 cases and through ongoing active surveillance at live bird markets across multiple provinces in Cambodia. Viruses were detected by qRT-PCR, isolated, and sequenced using Oxford Nanopore GridION. Genomic epidemiology, phylogenetic reconstruction, and reassortment analyses were used to characterize viral diversity and evolution. Epidemiological information from case investigations was used to assess exposure histories and link human infections with poultry-associated transmission contexts.

Results: Since February 2023, Cambodia has confirmed 35 human H5N1 infections (case fatality rate approximately 43%, Fig. 2). Early cases (n=2) were associated with the long-circulating clade 2.3.2.1e virus previously endemic in Cambodian poultry. However, the resurgence in cases from October 2023 onward was associated with a novel reassortant A/H5N1 genotype. Genomic analyses indicate that this virus

emerged through at least two reassortment events in which the endemic clade 2.3.2.1e backbone acquired gene segments from clade 2.3.4.4b and low pathogenic avian influenza viruses likely introduced through wild bird-associated regional viral movement. This reassortant genotype subsequently spread into poultry systems across Cambodia and Vietnam displacing previously circulating endemic strains. Most viruses from human cases and contemporary poultry viruses contained the mammalian-adaptive and host-range-associated marker PB2 E627K (Fig 2). Additional markers of mammalian adaptation such as HA T156A, and PB1 H99Y were also observed, increasing zoonotic concern. All human cases were epidemiologically and/or genetically linked to prior poultry exposure or to poultry viruses detected at outbreak locations (Fig 2). However, limited wild bird data from Cambodia, Laos, and Vietnam constrain assessment of transmission dynamics along the East Asian-Australasian Flyway to detect transboundary introductions, and disentangle wild bird and poultry transmission pathways.

Conclusions: The resurgence of human H5N1 cases in Cambodia reflects a One Health problem driven by viral evolution across cross-border poultry systems, market networks, human exposure settings, and regional ecological interfaces. Integrated surveillance linking outbreak investigations, poultry and market monitoring, wild bird surveillance, and genomics is critical for early warning, risk assessment, and coordinated interventions to reduce zoonotic spillover and strengthen regional and global preparedness.





1121 – Iceland as a Transcontinental Outpost for Early Detection of Emerging HPAI H5 Genotypes

Ann Kathrin AHRENS (1), Stefán Ragnar JÓNSSON (2), Heiða SIGURÐARDÓTTIR (2), Brigitte BRUGGER (3), Vilhjálmur SVANSSON (2), Timm HARDER (1), Martin BEER (1), Anne POHLMANN (1)

1: Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Greifswald-Insel Riems, Germany; 2: Institute for Experimental Pathology at Keldur, University of Iceland, Reykjavík, Iceland; 3: The Icelandic Food and Veterinary Authority (MAST), Selfoss, Iceland

High pathogenicity avian influenza (HPAI) subtype H5 viruses rapidly reassorting with local low pathogenicity (LP) AIV, have evolved into a globally persistent, threat to both animal and human health. Their capacity for long-distance spread via migratory birds, poultry trade and spillover into mammals underscores the need for geographically strategic early warning systems. Early detection of newly emerging genotypes is crucial for effective outbreak prevention and pandemic preparedness. Iceland's unique geographic location between Europe and North America makes it a natural strategic sentinel for monitoring and forecasting transatlantic virus movement.

Since 2021, targeted sampling of avian species and mammals has been conducted in Iceland. However, passive surveillance has been ongoing since 2004/2005. Samples were analyzed using influenza A-specific PCR, followed by sequencing with Oxford Nanopore Technology (ONT). The sequence data were then compared with contemporary European and North American sequences, enabling near real-time monitoring of viral genotypes and the early identification of putative transcontinental spread.

Our results demonstrate the predictive value of Iceland as an outpost for virus traffic across the North Atlantic. Since the first emergence of HPAI in Iceland in 2021, we have detected six distinct H5 HPAI genotypes (Genin designation: C1, C2, AB, BB, I, DI.2.1) in wild and domestic birds and mammals. All of these genotypes had previously been identified in Europe, and three of them (C1, C2, I) subsequently became established in North America (GenoFlu designation: A2, A5, A6).

The European genotype H5N1 C, detected between 2021 and 2022 in Iceland, was the first genotype that was confirmed in 2021 in Newfoundland, Canada, and subsequently spread across the entire American continent, undergoing continued reassortments. Between 2023 and 2025, H5N5 genotype I was dominating in Iceland and was detected in Atlantic Canada in 2023, marking their first entry and subsequent

establishment in North American avian populations. Most recently, H5N1 of the European genotype DI.2.1, detected on the continent since autumn 2025, was found in Iceland.

Together, our longitudinal genomic surveillance provides empirical evidence that Iceland functions as an early transatlantic predictor of HPAI genotype spread where emerging European genotypes can be detected prior to broader establishment in the Americas. Integrating strategically located regions into coordinated international surveillance networks enhances preparedness and strengthens One Health responses to evolving HPAI threats across wildlife, agriculture and public health sectors.

1129 – Pastoralist Local Ecological Knowledge Provides Insights into Tick-Borne Disease Risk in Sub- Saharan Africa

Madison HEWITSON (1,2,3), David Redding REDDING (1), Eric FEVRE (3), Kate JONES (2), James HASSELL (4)

1: The Natural History Museum, London, United Kingdom; 2: University College London; 3: The International Livestock Research Institute; 4: Smithsonian

Background Tick-borne diseases (TBDs) impose a significant but underestimated burden on livestock productivity and human health across Sub-Saharan Africa's arid and semi-arid lands (ASALs), where conventional surveillance infrastructure remains sparse. Pastoralist communities possess rich Local Ecological Knowledge (LEK) accumulated through generations of close environmental observation, yet this knowledge remains largely absent from formal disease surveillance frameworks. This study investigates whether Samburu pastoralist LEK in northern Kenya provides valid, actionable insights into TBD risk, and examines how its integration could strengthen equitable One Health surveillance strategies in ASAL regions.

Methods This qualitative study was conducted across four ecologically distinct habitat zones in Samburu County, Kenya—riverine, semi-arid, arid, and afro-montane. Data were collected through gender-stratified focus group discussions (FGDs), key informant interviews with herders, elders, and ethnoveterinary practitioners, and community-led participatory mapping exercises. FGDs were specifically designed to elicit longitudinal risk perception, capturing how communities understand changes in tick burden, disease occurrence, and habitat risk across seasons and over time, including in relation to shifting rainfall patterns and long-term ecological change. Thematic analysis was applied to qualitative data, while participatory maps were digitised and integrated with concurrent entomological and geospatial field data to assess convergence between LEK and biomedical findings.

Results Samburu pastoralists demonstrated detailed, spatially specific knowledge of tick seasonality, habitat associations, and livestock health indicators consistent with TBD exposure. Herders identified riverine corridors and dense bush margins as sites of elevated risk, particularly during transitional rainfall periods. FGDs revealed temporally granular accounts of tick risk fluctuating across the Samburu seasonal calendar, with communities describing shifts in tick activity in relation to vegetation state, livestock condition, and migration timing. Livestock movement decisions were explicitly calibrated to minimise tick exposure, representing sophisticated risk mitigation embedded within seasonal resource management systems, but also highlighted challenges on conservancy-guided grazing plans in specific communities. Gender-stratified analysis revealed differentiated knowledge profiles and risk, with women managing young ruminants demonstrating distinct and complementary risk awareness compared to male herders. Participatory maps showed strong spatial convergence with entomological sampling sites of highest tick density. Structural barriers—including geographic remoteness and cost—were consistently identified as limiting healthcare access, compounding TBD vulnerability.

Conclusions Samburu pastoralist LEK reflects ecological specificity that closely parallels concurrent biomedical findings, supporting its validity as an epidemiological resource rather than a supplementary narrative. The temporal richness captured through FGDs demonstrates particular promise for informing seasonal early warning systems and longitudinal risk modelling in data-sparse ASAL environments. Realising this potential requires a shift toward decolonial, CARE-aligned research methodologies that centre pastoralist communities as co-producers of knowledge and prioritise data sovereignty and equitable benefit-sharing.

1140 – Genomic epidemiology and antimicrobial resistance of non-typhoidal Salmonella in humans and chickens in Vietnam: an integrated one health analysis

Vinh Trung NGUYEN (1), Van Tuat CHU (2), Thu Thuy NGUYEN (2), Thanh Vinh NGUYEN (1), Xuan Truong NGUYEN (1), Xuan Yen HUYNH (1), Le Kim Yen PHUNG (1), Diem Phuc HO (1), Truc Linh VO (1), Thi Hue LE (2), Thi Phuong Loan NGUYEN (2), Thi Hue PHAN (2), Thi Kim Chung NGUYEN (2), Thi Trang PHAM (2), Ramon MALUPING (3), Thomas CHISNALL (3), Alistair DAVIES (3), Jazmin CONWAY (3), Thi Trang Dai VO (4), Hoang Vu NGUYEN (4), Nguyen Huy Man DINH (5), Minh Hien VO (6), Hoai Phuong HOANG (7), Minh Tuan HUYNH (8), Minh Hong NGUYEN (9), Juan CARRIQUE-MAS (9), Vu Trung NGUYEN (4), Pawin PADUNGTOD (9), Roderick CARD (3), Thi Hoa NGO (1,10,11)

1: Oxford University Clinical Research Unit, Vietnam; 2: Department of Animal Health and Production, Viet Nam; 3: UK FAO Reference Centre for AMR at the Animal and Plant Health Agency, UK; 4: Ho Chi Minh City Pasteur Institute, Ho Chi Minh City, Vietnam; 5: Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam; 6: City Children's Hospital, Ho Chi Minh City, Vietnam; 7: Institute of Public Health Ho Chi Minh, Ho Chi Minh City, Vietnam; 8: University Medical Center, Ho Chi Minh City, Vietnam; 9: Food and Agriculture Organization of the United Nations, Viet Nam; 10: Centre for Tropical Medicine, Nuffield Department of Medicine, University of Oxford, UK; 11: Tropical Medicine Research Center for Talaromycosis, Centre for Biomedical Research, Pham Ngoc Thach University of Medicine, Ho Chi Minh City, Vietnam

Background

Non-typhoidal *Salmonella* (NTS) is a leading cause of bacterial gastroenteritis and invasive infections worldwide. Poultry and livestock are major reservoirs that contribute to foodborne transmission and antimicrobial resistance (AMR). This study aimed to characterize the serovar distribution, genomic diversity, and AMR profiles of NTS isolated from both humans and poultry to investigate potential zoonotic transmission within a One-Health framework.

Methods

A total of 470 non-typhoidal *Salmonella* isolates collected between 2017 and 2025 were included, comprising 259 clinical isolates from five institutions, 200 poultry-derived isolates, and 11 food-derived isolates in Vietnam. Antimicrobial susceptibility testing was conducted using broth microdilution and interpreted according to EUCAST breakpoints. All isolates underwent whole-genome sequencing to analyze genomic relatedness and explore the animal-human interface of NTS in Vietnam.

Results

Among 470 *Salmonella* isolates from humans and poultry, 55 distinct serovars were identified, indicating high diversity. In chickens, the predominant serovars were *S.* Infantis (26.5%), *S.* Agona (11.0%), and *S.* Kentucky (11.0%). In humans, *S.* Enteritidis predominated (42.2%), followed by monophasic *S.* I 1,4,[5],12:i:- (9.3%) and *S.* Weltevreden (8.9%). All 11 NTS isolates from food were *S.* Enteritidis. Overall, 289/470 isolates (61.5%) belonged to 21 serovars shared between humans and chickens, demonstrating significant overlap at the human-animal interface.

Phenotypically, the prevalence of ciprofloxacin resistance in NTS was high in chickens, food, and humans(>60%). Genomic analysis identified 67 AMR genes, with strong agreement between resistance genotypes and phenotypes. Overall, chicken NTS isolates carried more AMR genes than human NTS isolates.

Core genome phylogeny revealed strong serovar-specific clustering. *S.* Enteritidis formed a predominantly human-associated clade, while *S.* Infantis, *S.* Typhimurium, *S.* Newport, and *S.* Weltevreden showed intermixing of human and chicken isolates, indicating shared reservoirs or cross-host transmission. Pairwise SNP analysis further supported zoonotic links by identifying mixed human-animal clusters, especially for *S.* Agona and *S.* Kentucky.

Conclusions

This study indicates that chickens serve as a reservoir for genetically diverse, antimicrobial-resistant NTS strains that significantly contribute to human infections. The detection of multiple *Salmonella* serovars in isolates from both humans and chickens suggests potential zoonotic transmission, emphasizing the urgent need for integrated One-Health surveillance and control strategies.

Figure 1: Circular maximum-likelihood core-gene phylogenetic tree of *Salmonella* isolated from chickens and humans in Vietnam. The phylogenetic tree was reconstructed based on 179,269 SNPs in the core genomes of 470 *Salmonella* isolates. The inner ring designates the serovars of the isolates (the 8 most common serovars). The outer ring designates the host.

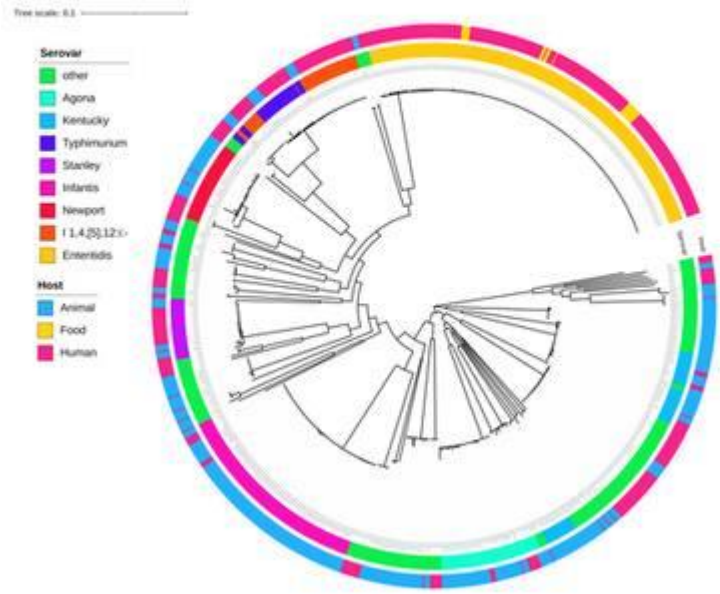
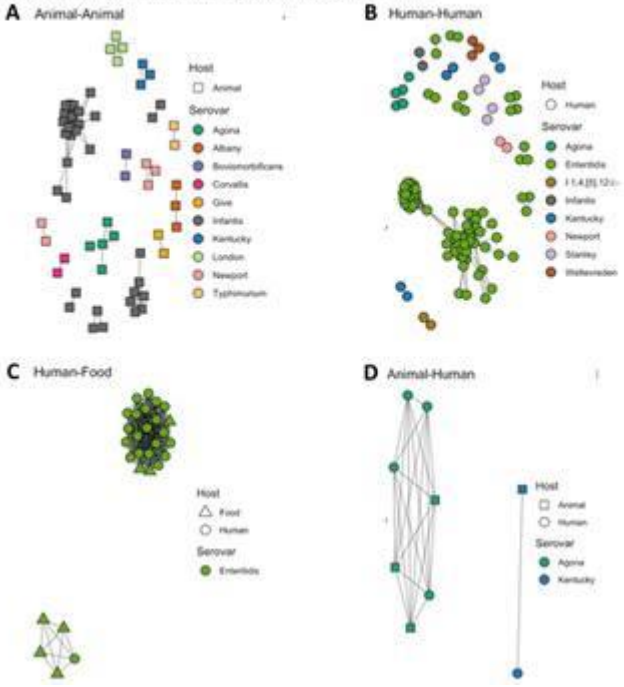


Figure 2: Network analysis of non-typhoidal *Salmonella* isolates from chickens and humans in Vietnam. The results shown include only pairs identified in pairwise comparisons that differ by ≤5 SNPs in the core genome. (A) Network analysis of *Salmonella* strains within the animal population (B) Network analysis of *Salmonella* strains within the human population (C) Network analysis of outbreak-associated *Salmonella* from human and food sources (D) Network analysis of *Salmonella* from animals and humans



1144 – Building a Regional One Health Community of Practice in Biosafety Through Multisector Biorisk Management Training

Teresa LIMM (1), Renata POLOTNIANKA (1), Chris MORRISSY (2), Phoebe READFORD (1)

1: Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australian Centre for Disease Preparedness (ACDP), Geelong, Australia; 2: Laboratory Technical Expert (Consultant)

Background

Effective biosafety and biorisk management is essential for laboratories handling infectious agents, especially zoonotic pathogens with dual-use or high-consequence potential. As emerging infectious diseases increasingly arise at the human, animal, and environmental interface, strengthening biorisk management is critical for both laboratory safety .and global One Health security. In our region, access to structured biorisk training and cross-sector collaboration is limited, highlighting the need for cross-sectoral training and professional networks that support leadership and sustained improvements in biorisk management.

Methods

The Australian Centre for Disease Preparedness (ACDP) Regional Biorisk Management Training project, funded by the Department of Foreign Affairs and Trade's Partnerships for a Healthy Region initiative, delivers biorisk training across Southeast Asia and the Pacific, using a One Health and gender-equity approach. The project develops a regional community of biorisk practitioners and leaders who strengthen their institution's biorisk management systems, while ensuring safe work with zoonotic and public health pathogens.

Participants are drawn from human, animal and environmental health sectors, as well as research and education institutions. Bringing together professionals from different sectors promotes dialogue and shared learning around biosafety and biosecurity challenges common across One Health systems, including safe handling of pathogens with epidemic potential, dual-use risks and infectious disease research.

Training is delivered through two linked streams: Introduction and Leadership. The Introduction project provides foundational biosafety and biorisk management knowledge and practical skills. Alumni with biosafety responsibilities within their institutions may then be selected to participate in the Leadership project.

During the Leadership project the Food and Agriculture Organization's (FAO) Laboratory Mapping Tools (LMT) help participants to identify gaps, prioritise improvements, and assess progress. Participants apply the tools within their institutions, while engaging in cross-sector discussions with peers from other One Health disciplines.

Results

To date, 98 participants from 14 countries have completed the Introduction project, representing 58 institutions. Participants were 55% female and 45% male, with representation across the animal, human, and environment/other sectors of 57%, 34%, and 9% respectively. Within this cohort, 48 participants have also completed the Leadership project, with sector representation of approximately 48%, 38%, and 14%.

Recent Leadership participants demonstrated up to 13.4% improvement in LMT-Safety scores over a 12-month period. Selected participant experiences and LMT data will be explored to illustrate how cross-sector learning supports practical biorisk management improvements.

Conclusions

Through sustained engagement, peer learning, and extensive mentoring, the R-BMT project fosters a One Health community of practice in biorisk management across the region while supporting female participants in developing leadership roles. The project strengthens institutional biorisk management, encourages collaboration across sectors, enhances preparedness for emerging infectious diseases, including zoonotic and high-consequence pathogens, and contributes to regional laboratory capacity and global health security.

1148 – Food insecurity in Mexico, zoonotic diseases and climate change

Valeria Jazmín RODRIGUEZ VILLAVICENCIO, Linda Guiliana BAUTISTA GÓMEZ
Universidad Autónoma del Estado de México, Mexico

Introduction. Historically, Mexico has faced various challenges due to climate change, with droughts being the most significant challenge in recent years, a phenomenon that has led to food insecurity and the emergence of various zoonotic diseases. In terms of agriculture, droughts mainly affect it in the following ways: reduced crop yields; increased food prices due to decreased supply; reduced animal feed production, leading to lower production of animal-based foods; and increased malnutrition and food insecurity caused by a lack of affordable food. As a result, in human health, the main problems caused by food insecurity are poor nutrient intake, leading to malnutrition, which increases the risk of serious diseases, some of which are zoonotic in origin. Among the diseases that are frequently reported are: infectious diarrhoea, due to poor hygiene and lack of sanitation services due to the limited availability of drinking water; and respiratory and skin infections, caused by overcrowding and poor hygiene practices. From a One Health perspective, we must ask: What impact does food insecurity have on malnutrition and the increase in zoonotic diseases in communities affected by drought? Therefore, the objective of this study is to identify the zoonotic risks caused by food insecurity in Mexico due to droughts.

Method. Using meta-search engines, a search was conducted for studies, reports, and data collected by climate monitoring agencies, focusing on climate change and the animal health risks it poses to food security.

Results. National Water Commission and the National Meteorological Service reported that in recent years, 83% of crops have suffered from an alarming lack of water, which has repercussions not only on agriculture but also on the general population, since, according to statistics, more than 500 localities in the country have suffered extreme drought, and the National Institute of Public Health reports that as a result of this phenomenon, six out of 10 Mexican households are experiencing food insecurity, a situation that encourages the spread of various zoonotic diseases such as hepatitis E, malaria, cholera, avian influenza, diphtheria, and the most commonly reported, salmonellosis.

Conclusion. Food insecurity caused by extreme droughts in Mexico generates significant economic losses due to low agricultural productivity, which leads to price increases due to low supply, and due to the costs incurred by the spread of infectious diseases (of zoonotic origin) and as collateral damage from poor nutrition and poor hygiene among the human population

1157 – Bridging the Knowledge-Practice Gap: Assessing Zoonotic Risks and Pet Waste Management Among Malaysian Cat and Dog Owners

Nur Indah AHMAD (1), Jia Qi YU (1), Syamira Syazuana ZAINI (1), Sharifah Norkhadijah SYED ISMAIL (2)

1: Faculty of Veterinary Medicine, Universiti Putra Malaysia, Malaysia; 2: Faculty of Medical and Health Sciences, Universiti Putra Malaysia

Background and Objectives: The human–animal bond has strengthened significantly in recent years, leading to a global surge in pet ownership. While this bond offers numerous psychosocial benefits, it also presents unique challenges in urban health, particularly concerning the management of pet waste. Improper disposal of animal feces can serve as a primary pathway for the transmission of zoonotic pathogens, including toxocariasis, ancylostomiasis, and salmonellosis, posing significant public health

risks. In Malaysia, empirical research regarding pet owner behaviors and their understanding of these risks remains scarce. This study aimed to evaluate the knowledge, practices, and risk perceptions of Malaysian pet owners regarding pet waste management and its associated zoonotic threats, with the ultimate goal of generating evidence-based insights to improve community health outcomes and veterinary care protocols.

Methods: A cross-sectional online survey was conducted using a validated questionnaire distributed to cat and dog owners across Malaysia. Over a three-week period, 215 complete responses were collected. The survey instrument assessed four primary domains: participant demographics, specific knowledge of zoonotic diseases, current waste disposal practices, and subjective risk perception. Data were analyzed using descriptive statistics, alongside non-parametric Mann–Whitney U and Kruskal–Wallis tests to identify significant differences between demographic groups. Spearman's correlation was utilized to determine the relationship between knowledge, practice, and perception scores.

Results: The study revealed mean scores for knowledge, practices, and risk perception of 77.10%, 85.42%, and 84.61%, respectively. Statistical analysis indicated significant correlations (p 0.01) between knowledge and risk perception, as well as between practice and risk perception. However, no significant association (p > 0.01) was observed between knowledge and actual practice, suggesting that awareness alone does not always translate into behavioral change. Respondents with higher education levels were significantly associated (p 0.05) with superior knowledge and heightened risk perception. Interestingly, while a longer duration of pet ownership correlated with higher knowledge (p 0.05), it did not necessarily result in safer disposal practices. Furthermore, the source of information played a critical role; individuals who received guidance from veterinarians were significantly linked to safer waste management practices (p 0.05), highlighting the veterinarian's role as a key One Health advocate.

Conclusion: Malaysian pet owners generally demonstrate moderate knowledge and high risk perception but exhibit gaps in translating that knowledge into consistent practice. These findings underscore the necessity of a transdisciplinary One Health approach to community education. Strengthening tailored awareness programs and leveraging the influence of veterinary professionals are essential strategies to promote responsible pet ownership. Such interventions are vital to mitigating zoonotic disease transmission at the human-animal-environment interface within urban Malaysian settings.

1160 – Extending One Health concepts and approaches to schools: The Ethiopian Model

Yordanos Tadesse KIDANEMARIAM (1), Balako Gumi DONDE (1), Fufa Abunna KURRA (1), Argaw Ambelu BAYIH (1), Roba Argaw TESSEMA (12), Selamawit Fantahun ALI (10), Behailu korma OSRO (11), Alemselam ZEBDIOS (9), Tadesse Guadu DELELE (8), Lechisa Assefa BISHILA (7), Theodore KNIGHT-JONES (4), Alfoalem Abera ABIYE (1), Berhanu Abera TEGEGN (1), Kisanet Tesfaye WELDEAREGAY (6), Siobhan M. MOR (2,3), Seid Tiku MERETA (5), **Mirgissa Kaba SERBESSA** (1)

1: Addis Ababa University, Ethiopia; 2: International Livestock Research Institute, Nairobi, Kenya; 3: Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Leahurst Campus, Neston CH64 7TE, UK; 4: International Livestock Research Institute, Addis Ababa, Ethiopia; 5: Jimma University,Ethiopia; 6: Mekelle University,Ethiopia; 7: Bule Hora Univeristy ,Ethiopia; 8: University of Gondar,Ethiopia; 9: Hawassa University,Ethiopia; 10: Wollo University ,Ethiopia; 11: FDRE Ministry of Education,Ethiopia; 12: Haramaya University,Ethiopia

Background: One Health (OH) is now widely recognized as the solution for the complex problem the world is facing. More than ever, public health threats are associated to what happens in the ecosystem. The continuous interaction between animals, humans, and the environment and its constituencies challenged the health of those interacting. Despite such realties, education sector in Ethiopia has failed to build the competencies of future workforces. The educational system remains on conventional discipline focused instruction that the future generation remains naïve to what is evolving. COHESA project in Ethiopia has taken bold measure to initiate an extra-curricular but more robust OH initiative at school level to ensure school children are informed of the vivid challenges and could contribute to mitigation measures.

Methods: COHESA worked with eight universities in Ethiopia. Leveraging engagement with universities and knowing their role in community engagement and service, the COHESA team and COHESA instituted university OH focal persons developed strategy to reach out to schools found within the university's operational domain. Each university selected five schools and engaged students, teachers, school leaders, and education administrators from local government and school management structures. Two workshops were organized at each site for students, teachers, and management. These helped them

understand public health problems at the human-animal-environment interface and the role of OH in preventing or reducing such challenges. At the end of the workshops, students developed plans to establish OH clubs, while teachers, school leaders, and local education administrators prepared action plans to support implementation in schools and their communities.

Results: The model was designed to reach five selected schools within each university's operational site and support the university's mandate for community engagement and service. Accordingly, 40 schools were included in the initiative to expand OH activities through extracurricular platforms. Student clubs are expected to play a key role in educating the wider student population, while teachers and school management provide support and guidance. University teams, in turn, provide mentorship to schools and share current evidence, tools, and learning materials on OH. As a result, a total of 160 students are now engaged in OH clubs, while 200 teachers and 40 school administrators and managers are providing continued guidance and support. University teams claims to have good opportunity now to extend its responsibility to the community per the moto of universities to engage and serve the community.

Conclusions: The COHESA model of extending OH into school functions has served an important purpose by engaging students, teachers, managers, and local education administrators in implementation. To sustain the initiative and ensure continuous support, alignment with local universities has been strengthened. Additional technical support and guidance from OH experts could further enhance sustainability and institutionalization within Ethiopia's school system.

1167 – Prevalence of Unregistered, Substandard, and Falsified Veterinary Antimicrobials in Ethiopia: A National Post-Market Quality Surveillance Study

Tenaw Andualem TADEGE (1), **Ayenew Ashenef ALEMU** (2), Belachew Tefera ZERIHUN (3), Belachew BACHA (3), Nardos Tefera1 KEBEDE (3)

1: FAO of UN, Ethiopia; 2: Addis Ababa University, Ethiopia; 3: Animal products and inputs quality testing center, Ethiopian Agriculture Authority

Background: The proliferation of unregistered, substandard, and falsified (SF) veterinary pharmaceuticals represents a critical global threat to animal health, food security, and environmental conservation. In sub-Saharan Africa, these products exacerbate the emergence of antimicrobial resistance (AMR), potentially accelerating the transition toward a "post-antibiotic" era. Despite Ethiopia's relatively developed regulatory framework compared to neighboring states, vulnerabilities such as inadequate diagnostic facilities, porous supply chains, and limited post-marketing enforcement persist.

Objective: This descriptive study was conducted to determine the prevalence and quality profile of selected veterinary antimicrobials including antibacterials, anthelmintics, and antiprotozoals circulating in the Ethiopian market.

Methods: Post-market quality surveillance (PMS) study was conducted across five administrative regions. A total of 142 samples were collected and evaluated through three distinct regulatory tiers: verification of Ethiopian Agricultural Authority (EAA) registration status, standardized visual/physical screening, and official pharmacopeial (compendial) laboratory testing.

Results: The majority of sampled products (**95.7%**) were imported, predominantly from China (**75.7%**) and India (**15.0%**). Primary sampling sites included veterinary retail outlets (**50.7%**) and clinics (**22.9%**). Regulatory analysis revealed that **17.9% (*n*=25)** of samples were unregistered. Visual screening identified an administrative substandard prevalence of **24.3%** among registered products. Of the 44 samples subjected to compendial laboratory analysis, **22.7% (*n*=10)** failed to meet established pharmacopeial specifications. While suspected falsified products were identified through labeling discrepancies, laboratory confirmation of falsification is ongoing.

Conclusions: A significant proportion of unregistered and substandard veterinary medicines are circulating in the Ethiopian supply chain, posing severe risks to animal health and contributing to the regional AMR crisis. These findings necessitate urgent, concerted efforts from stakeholders to strengthen the national regulatory system, enhance EAA laboratory capacity, and secure the pharmaceutical supply chain through targeted post-marketing enforcement.

1174 – Bridging interdisciplinary methods on multispecies networks and disease emergence

Hellena DEBELTS (1), **Santiago Rayment GOMEZ** (2), Almudena MARI SAEZ (3), Jose Gabriel Nino BARREAT (4), Johanna HANEFELD (1), David REDDING (4), Senzor CONSORTIUM (1,2,3,4)

1: Robert Koch Institut, Germany; 2: London School of Hygiene and Tropical Medicine, England; 3: Institut de recherche pour le développement, France; 4: Natural History Museum London, England

Background

Spillover events are often attributed to interspecies contact, yet little is known about the types and frequencies of interactions that drive pathogen transmission. Taking contact as a proxy for potential transmission, this work brings together interdisciplinary perspectives to examine multi-species contact networks. Anthropological approaches conceptualize networks as dynamic relations among human and non-human actors, shaped by practices such as touch, grazing, and spatial overlap. Modelling approaches can be applied to both anthropological and social network data to examine their relationships and identify underlying patterns. Social network analysis bridges these approaches by identifying patterns and key actors, highlighting how integrating relational and quantitative perspectives can deepen understanding of spillover dynamics.

Methods

To investigate how human-livestock contacts may shape spillover dynamics, we combine anthropological insights, social network analysis, telemetry data and mathematical modeling to analyze interaction networks. Important contact types (n = 18) identified through anthropological investigation were used to develop contact counting sheets which were then administered to 32 individuals daily for a week, in two rural Gambian villages during the wet, early- and mid-dry season. GPS devices were deployed to the 32 individuals as well as 60 livestock (20 sheep; 20 goats and 20 cattle) to collect fine-scale space-use data. Contact types were grouped into indirect (close proximity without direct contact), contact with body surfaces, contact with body fluids and contact with body tissues. The contact counting and GPS data are being used to generate contact networks and understand the types, locations, durations and timings of human-livestock contact.

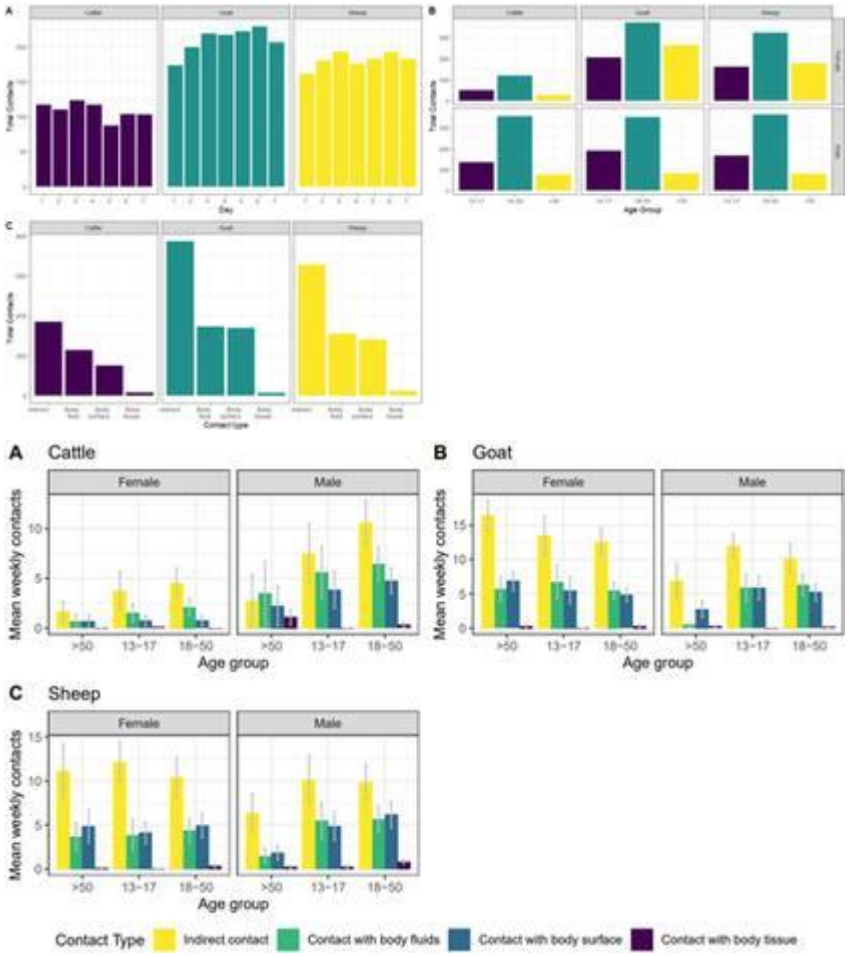
Results

The wet and early-dry season contact counting and GPS data have been collected, with the mid-dry season data collection scheduled for April 2026. Preliminary description of wet-season contact patterns show important differences in contact frequency by age, sex and contact type. Indirect contact was the most common type with goats and sheep but with cattle contact with body fluids was as common. Contact with body tissue was highest with cattle in the elderly male group, but generally low among other age groups and among females. Village and seasonal level differences will be analysed after completion of the data collection. Telemetry data from GPS devices show substantial variation in durations and ranges of movement between cattle and small ruminants during the wet-season. For people, movement was generally structured and predictable during the wet-season.

Conclusions

Integrating these qualitative and quantitative approaches will provide new insights into how the structure, frequency and nature of interspecies contact shape opportunities for pathogen spillover, emphasizing the importance of a One Health perspective that examines both relational practices and networks properties. Further analysis of the contact networks constructed from the contact counting and telemetry data will allow the drivers of contact patterns to be elucidated.

Funding: VW-Foundation



1184 – Viral composition of the bat species Miniopterus schreibersii from a single colony in metropolitan France: assessment of zoonotic risk

Lucie CAPPUCCIO (1), Victoire PERRAUD (1), Angela BRISEBARRE (1), Anthony LE NOZAHIC (2), Maxime LEUCHTMANN (3,4), **Laurent DACHEUX** (1)

1: Institut Pasteur, Université Paris-Cité, Environment and Infectious Risks Unit (ERI), 28 rue du Docteur Roux, 75724 Paris Cedex 15, France; 2: Charente Nature, Angoulême, France; 3: Nature Environnement 17, Surgères, France; 4: France Nature Environnement Nouvelle-Aquitaine, Angoulême, France

Background:

Bats are known to harbor a vast community of viruses, some of which are potentially zoonotic. For example, the species *Miniopterus schreibersii* has been shown to host various coronaviruses, different lyssaviruses, and the single filovirus present in Europe, the Lloviu virus (LLOV). This species therefore represents an excellent prototype for studying both the mechanisms of circulation of these viruses within colonies and those that contribute to barriers between species, two aspects that are covered by the European OneBAT program and its network of partners. In addition, the viral composition present in this bat species, at the level of a single individual and depending on the tissues and biological samples considered, remains largely unknown.

The objective of this study was therefore to examine and compare the viral composition, obtained using specific methods or without prior assumptions, of different samples taken from individuals from the same colony in mainland France.

Methods

Biological samples (saliva, feces, and blood) were collected from 20 bats during two separate sampling periods, in April (n = 12) and September (n = 8) 2024 (Figure 1). Total RNA was extracted from all sample

types. To ensure comprehensive diagnostic coverage, samples were first screened using targeted RT-(q)PCR for coronaviruses (saliva and feces), lyssaviruses (saliva), and LLOV (blood). Subsequently, all samples underwent viral metagenomic analysis either after random amplification (for blood and feces) or unamplified (saliva), followed by unbiased next-generation sequencing on the Illumina platform. Bioinformatics pipelines were used for taxonomic classification and phylogenetic reconstruction.

Results

Targeted molecular screening for lyssaviruses and LLOV yielded negative results across all individuals. While RT-qPCR detected alphacoronaviruses in the feces of 11 individuals (55%), saliva remained negative for these targets. Notably, the metagenomic approach demonstrated significantly higher sensitivity than targeted PCR, identifying alphacoronaviruses in 15 fecal samples (75%). Seasonal prevalence fluctuated, with 100% of September samples testing positive compared to 58% in April.

Ten complete genomes were successfully reconstructed, all belonging to the subgenus *Minunacovirus*, showing homology to Miniopterus bat coronavirus HKU8. Additional mammalian-associated viruses identified in feces included members of the *Picornaviridae*, *Astroviridae*, and *Nodaviridae* families, alongside a high abundance of insect-infecting viruses (Figure 2). Analysis of blood and saliva matrices was less diverse, primarily recovering *Totiviridae* in blood and *Herpesviridae* and/or *Spumaretrovirinae* in saliva.

Conclusion

This study provides a refined characterization of the *M. schreibersii* virome through the integration of targeted and unbiased metagenomics. While no high-priority zoonotic pathogens were identified in this cohort, the high prevalence and seasonal dynamics of *Minunacoviruses* highlight the complexity of viral shedding in this bat colony. To obtain a more comprehensive analysis of virus circulation and assess zoonotic potential, future work will include seroprevalence studies and virus characterization following isolation in bat cell lines.

Figure 1. Workflow of a *Miniopterus schreibersii* sampling session. Field procedures during a trapping campaign, illustrating the systematic collection of morphological and epidemiological data. Following tagging and and non-invasive or minimally invasive sampling, all individuals are released at the site of capture.

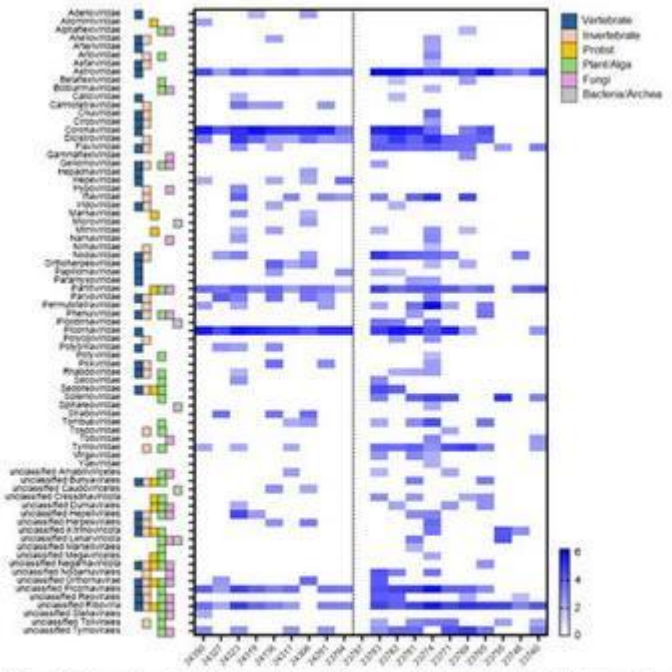


Figure 2. Metagenomic analysis of fecal samples from *Miniopterus schreibersii* bat species. The heat map displays results from an unbiased metagenomic analysis of feces collected from a single colony of the bat species *Miniopterus schreibersii* in mainland France. Sampling was conducted on two occasions in 2024 (summer and fall). Data are represented as the number of viral matches on a log10 scale for each viral family or category per sample. The primary hosts associated with these viral families are indicated by the color-coded legend.

1191 – Operationalising the One Health Joint Plan of Action in Europe: The Strategic Role of Veterinary Services; Lessons from the WOAH Regional Workshop

Budimir PLAVSIC, Mereke TAITUBAYEV, Lajos BOGNAR, Chadia WANNOUS, **Kurmanzhan DASTANBEK**
World Organization for Animal Health (WOAH), France

BackgroundThe One Health Joint Plan of Action (OH-JPA), developed by the Quadripartite partners, provides a global framework for coordinated action across human, animal, plant and environmental health sectors. Translating this vision into measurable multisectoral implementation requires empowered Veterinary Services (VS) with clear mandates, institutionalised coordination and the capacity to mobilise sustainable financing. In November 2025, the World Organisation for Animal Health (WOAH) Regional Representation for Europe convened a regional workshop in Athens to accelerate OH-JPA implementation, emphasising the role of VS in prevention, preparedness, governance and resource mobilisation. Delegates from WOAH Member Countries in the Europe region participated alongside experts, academia and partner organisations. This abstract summarises the actionable priorities identified through the regional dialogue.

MethodsThe workshop used a structured process combining plenary expert inputs, thematic group work, a simulation exercise, and moderated discussions. Participants assessed systemic barriers to One Health implementation, including governance fragmentation, surveillance gaps, limited cross-sector coordination and resource constraints. Conclusions were consolidated through a consensus-based process. Qualitative thematic analysis synthesised priority areas and cross-cutting enablers.

ResultsRecurring challenges included insufficient institutionalised cross-sector coordination; limited interoperability and routine sharing of surveillance data; unclear sectoral roles and responsibilities; inadequate sustainable financing for joint initiatives; and under-recognition of VS as a strategic entry point for risk reduction at the human–animal–environment interface.

Climate-sensitive zoonotic and vector-borne diseases were identified as key drivers for stronger cross-sector integration, including recent experiences with bluetongue, West Nile fever and epizootic

haemorrhagic disease. A simulation exercise revealed operational gaps in early reporting, intersectoral communication and coordinated response.

Participants endorsed six priority actions for enhanced regional support in 2026: (1) formalising inter-ministerial coordination platforms; (2) establishing joint risk-assessment and data-sharing protocols; (3) strengthening workforce capacity and One Health education; (4) reinforcing laboratory networks; (5) improving food safety governance and joint investigation protocols; and (6) developing sustainable financing mechanisms.

In several Member Countries, strengthened One Health coordination has already facilitated mobilisation of international financing for multisectoral pandemic prevention, preparedness and antimicrobial resistance mitigation. Investments are supporting integrated surveillance, laboratory capacity, workforce development and institutionalised governance, demonstrating the operational value of structured coordination.

ConclusionsThis WOAH-led workshop demonstrates that structured, member-driven processes can advance One Health from strategic commitment to operational delivery. By identifying systemic bottlenecks and defining concrete governance priorities, the initiative supported practical implementation of the OH-JPA across the Europe region.

Regional experience confirms the role of Veterinary Services as key operational connectors across sectors for early detection, surveillance, integrated risk management and coherent national One Health governance. These lessons are transferable to other settings and provide a feasible roadmap to strengthen governance, financing, surveillance integration, workforce capacity, laboratory systems and antimicrobial resistance stewardship while sustaining One Health impact.

1203 – One Planet for One Health

David GALLEGO TORRES (1), Linda AMARAL-ZETTLER (2), Joan BALLESTER (3), R.D. BARDGETT (4), Ana BASTOS (5), Eleni ZIKA (1)

1: European Research Council Executive Agency (ERCEA), Belgium; 2: Royal Netherlands Institute for Sea Research - NIOZ; 3: Instituto de Salud Global de Barcelona - ISGLOBAL; 4: University of Lancaster; 5: University of Leipzig

The concept of “One Health” explicitly recognises the key importance of ecological - environmental factors on human and animal health. This component of the definition of “One Health” consolidated around the mid 2000’s (Pitt and Gunn, 2024). Also around that time, in 2006, the European Research Council (ERC) was created with the goal of supporting fundamental research at the frontiers of knowledge in all academic disciplines. The comprehensive approach of “One Health” thus aligns with the holistic view of the ERC embracing the entire spectrum of research topics. This session will put the focus on the environmental aspects of One Health featuring 4 projects funded by the ERC across different academic disciplines. Our planet is a complex structure, with hydrosphere, atmosphere and geosphere hosting the biosphere, including, of course, humans. All components are intertwined in one system: One Planet for One Health.

Our speakers will present the impact of each component on the global system and their interaction with One Health. The project SoilResist (by Richard Bardgett) studies soils as hosts of a whole ecosystem that evolves under environmental and climate changing conditions. VIBRANT-SEA (by Linda Amaral-Zettler) addresses how life in the oceans reacts and adapts to the presence of plastics, still a new component of biogeochemical cycles. The project ForExD (by Ana Bastos) models the interaction of extreme events with forests and the biodiversity they host. The session will also consider the social aspects of climate and environmental changes and how human societies adapt to them, analysed by the project EARLY-ADAPT (by Joan Ballester).

Through these examples across disciplines we will demonstrate how bottom-up, curiosity-driven research funded by the ERC generates the knowledge required to confront global challenges and provides and essential contribution to address the broad topic of One Health.

References:

Sarah J Pitt, Alan Gunn, 2024. The One Health Concept. Br J Biomed Sci. 2024 Feb 15;81:12366. doi: 10.3389/bjbs.2024.12366

Poster zone 1

Sardines

140 – Cyanobacterial blooms at Canadian freshwater beaches: A multi-site prospective cohort study of exposure, health outcomes, and One Health implications

Binyam DESTA (1), **Jordan TUSTIN** (2)

1: University of Guelph, Canada; 2: University of Toronto, Canada

Background: Climate change is intensifying cyanobacterial (blue-green algae) bloom dynamics through warming waters, altered hydrology, and nutrient enrichment, increasing concern about human and animal recreational exposure risks worldwide. However, empirical One Health evidence linking environmental cyanobacterial indicators, recreational behaviour, and short-term health outcomes remains limited. This study aimed to characterize recreational exposure patterns, health outcomes, and environmental indicators across diverse freshwater beaches, using a One Health framework to assess climate-sensitive risks.

Methods: We conducted a two-year (2024–2025) prospective cohort study at seven freshwater recreational beaches across three Canadian provinces, spanning diverse climatic, ecological, and recreational contexts. Recreational water users were recruited on-site and completed baseline surveys capturing sociodemographic characteristics, recreational activities, and potential confounders, including concurrent Escherichia coli levels. Follow-up surveys administered 3–7 days later assessed acute gastrointestinal illness (AGI) and other symptoms. Companion dogs from participating households were concurrently enrolled. Environmental sampling measured cyanobacterial cell counts, total microcystins, and pigment-based indicators (phycocyanin and chlorophyll a). Analyses examined exposure patterns, illness incidence, and relationships among microbial indicators.

Results: A total of 2,324 individuals from 1,530 households were enrolled, with 66.6% completing follow-up. Recreational water contact varied markedly by site, reflecting differences in beach infrastructure, geography, and cultural use patterns. Children (0–14 years) exhibited the highest levels of intensive exposure, including swimming, head submersion, water ingestion, and sand contact. Pronounced heterogeneity was observed across educational and ethno-racial groups, indicating socially patterned exposure pathways. Overall, AGI incidence was low (2.1%), but higher among participants reporting water contact (3.0%) than among non-contact participants (1.3%), and substantially higher among those who swallowed water (6.9%). Among 256 dogs, 65.6% entered the water, and 56.3% ingested water; canine AGI incidence was 1.9%, with similar exposure-related gradients. Cyanobacterial concentrations were generally low but exhibited substantial spatial and temporal variability, including sporadic peaks. Cyanobacteria were not correlated with E. coli ($r = -0.02$), indicating distinct environmental drivers, while pigment ratios showed moderate associations consistent with bloom development.

Conclusions: This multi-site One Health study demonstrates that climate-sensitive cyanobacterial dynamics intersect with recreational behaviour to shape exposure risks for humans and companion animals, even in the absence of large visible blooms. Children and dogs represent high-contact groups with elevated exposure potential, underscoring the importance of targeted risk communication. The lack of correlation between cyanobacteria and fecal indicators highlights limitations of relying solely on traditional microbial monitoring. As climate change accelerates bloom variability globally, integrated One Health surveillance that links environmental indicators, human behaviour, and animal health will be critical for effective recreational water management and public health protection.

151 – Social network analysis of conservation and one health governance in Madagascar

Karine MAHEFARISOA (1), Hajaniaina RATSIMBAZAFY (2), Ellen DECAESTECKER (3), Leo DELPY (4), Jean HUGÉ (5), Nicolas ANTOINE-MOUSSIAUX (6), Raf AERTS (7)

1: KU Leuven, Leuven One Health Institute, MicrobiomeEcoEvo Unit, Interdisciplinary Research Facility Life Sciences, Engineering & Technology Group, Division Ecology, Evolution and Biodiversity Conservation, Biology Department, Belgium; 2: Systems Ecology and Resource Management Research Unit (SERM), Department of Organism Biology, Université Libre de Bruxelles - ULB, Av. F.D. Roosevelt 50, CPi 264/1, Brussels 1050, Belgium; 3: KU Leuven, Leuven One Health Institute,

MicrobiomeEcoEvo Unit, Interdisciplinary Research Facility Life Sciences, Engineering & Technology Group, Division Ecology, Evolution and Biodiversity Conservation, Biology Department, Belgium; 4: Lille Centre for Sociological and Economic Studies and Research (Clersé), UMR 8019, Université de Lille, Lille, France; 5: Department of Environmental Sciences, Open University of the Netherlands, Valkenburgerweg 177, Heerlen, 6419AT, the Netherlands; 6: Fundamental and Applied Research for Animals and Health Research Unit, Faculty of Veterinary Medicine, University of Liège, Liège, Belgium; 7: KU Leuven, Leuven One Health Institute, MicrobiomeEcoEvo Unit, Interdisciplinary Research Facility Life Sciences, Engineering & Technology Group, Division Ecology, Evolution and Biodiversity Conservation, Biology Department, Belgium

Madagascar, a globally recognised biodiversity hotspot, faces accelerating biodiversity loss and heightened risks of zoonotic diseases. Despite growing recognition of One Health, weak response systems and fragmented governance can undermine coordinated decision-making and information flow. We mapped the conservation–health governance network to identify influential actors, characterise structural cohesion, and assess the extent to which One Health is integrated in practice. Following the Laumann–Marsden–Prensky framework, a social network analysis (SNA) survey was conducted from 14 March to 24 June 2022 among 30 senior leaders (≥5 years' experience) working in biodiversity conservation and public health in Madagascar. Participants listed key collaborators involved in conservation and health projects and reported primary funding sources. Network influence was assessed using indegree, outdegree, and eigenvector centrality. Structural cohesion was evaluated using network density and centralisation. We also quantified the strength of One Health integration and interaction reported by participants. Respondents identified 287 actors, of which 54.4% were international entities. International organisations occupied central positions in both collaboration and funding networks, indicating strong influence over coordination and resource flows. In contrast, national and local government bodies were comparatively less connected and less central. Only a small number of stakeholders reported effectively integrating the One Health approach into routine conservation and health governance, suggesting that cross-sectoral collaboration remains limited and concentrated within a subset of actors. The governance network shows a strong reliance on international actors, driven primarily by access to funding and convening capacity, and limited local institutional anchoring. While international support provides crucial resources, sustainable One Health implementation requires strengthening national and local leadership and embedding coordination and financing mechanisms within accountable public institutions. SNA offers a practical diagnostic to identify fragmentation, reveal who holds coordination power, and guide reforms that improve integration across biodiversity and public health governance.

160 – Leveraging Artificial Intelligence to Strengthen Global AMR Responses: Evidence from the Global AMR R&D Hub

Frank {Thanh} Tu NGO

Global AMR R&D Hub, Germany

Antimicrobial resistance (AMR) has been described by the WHO as a "silent pandemic". Left unchecked, it presents escalating health and economic risks. While COVID-19 caused over seven million deaths globally, AMR is projected to result in up to ten million deaths annually by 2050. Its economic impact is similarly severe, with potential global GDP losses estimated at USD 3.4 trillion per year by 2030.

Mitigating AMR requires coordinated global action, including stronger regulations and financial incentives to support the development of new drugs. However, a major obstacle lies in the fragmentation of AMR funding, innovation pipelines, and evidence-based policies. What is urgently needed is a centralized platform that provides credible and timely funding data, and best practices to inform research, policy, and R&D activities.

This case study examines the Global AMR R&D Hub, a G20 initiative established to strengthen global AMR responses, focusing specifically on its efforts to apply artificial intelligence (AI) to improve funding data processing and generate policy insights. Based on participant observation and qualitative interviews with Hub staff and G20 government officials, the study finds that AI applications can triple data-processing speed and achieve accuracy rates of 80–90% in several funding categories. These gains help alleviate institutional constraints related to limited personnel and time. AI is also increasingly viewed by major funders, including governments and philanthropic organisations, as a key strategy to address AMR. Furthermore, the study also identifies persistent barriers to full-scale AI adoption, including technical limitations and gaps between programming expertise and AMR domain knowledge.

The findings point to broader implications for public policy. Similar machine-learning approaches could be applied to other grand challenges, such as pandemic preparedness, trade, or climate change, that require credible, timely data to inform policy decisions.

188 – Foodborne transmission of Cryptosporidium: Relevance of goat milk consumption in the epidemiological chain of cryptosporidiosis

Glenda Lídice Cortez Marinho SILVA (1), Victor Fernando Santana LIMA (1), Kalina Maria de Medeiros Gomes SIMPLÍCIO (1), Paula Regina Barros de LIMA (1), David Germano Gonçalves SCHWARZ (2), Maria Eduarda Storti de MELO (1), Guilherme Gomes da MACENA (1), Caio da Conceição VIDAL (1), José Eduardo Marques da SILVA (1), Eliomar Oliveria da SILVA (1), Roseane Nunes de Santana CAMPOS (1), Anita de Souza SILVA (3)

1: Universidade Federal de Sergipe, Brazil; 2: Universidade do Estado de Santa Catarina, Brazil; 3: Universidade Federal de Minas Gerais, Brazil

Context: Cryptosporidium is recognised as an important public health pathogen, mainly due to its zoonotic nature and the persistence of its oocysts in hosts and in the environment. Waterborne transmission is the route most commonly associated with outbreaks; however, emerging and re-emerging evidence, especially in low- and middle-income countries, has reported the presence of oocysts in food products, including raw milk, highlightingthe need for greater attention to the foodborne route in the epidemiological chain of cryptosporidiosis. In the Northeastern region of Brazil, goat dairy farming is predominantlybased on smallholder systems and plays a strategic role in food, nutritional and socioeconomic security for local populations. In this region, goat milk issold in small establishments and is not pasteurized, being commonly consumed raw.

Methods: The study was conducted in the semiarid region of the state of Sergipe, in northeastern Brazil, and involved 18 family-based farms producing goat milk for local sale. Eighty raw goat milk samples were collected during both summer and winter. The samples were obtained during milking and transported under refrigeration to the laboratory for analysis. Cryptosporidium was detected using the centrifugal sedimentation technique combined with modified Ziehl–Neelsen staining, a well-established method for identifying coccidian oocysts in Brazil.

Results: Cryptosporidium oocysts were detected in 63.8% (51/80) of the samples analysed. Among positive samples, at least one positive sample was detected in 94.4% (17/18) of the evaluated farms. These results corroborate previous studies conducted with raw cow's milk from family-based farming systems in the locality, in which Cryptosporidium oocysts were also identified, signalling the importance of considering foodborne routes as relevant pathways for the transmission of cryptosporidiosis. Conditions associated with this occurrence include recurrent biosecurity failures related to water quality, environmental management, milking hygiene, and milk storage, factors that compromise food safety and the resilience of the production system.

Conclusions: The high frequency of Cryptosporidium oocyst detection in raw goat milk highlights a significant challenge for food safety, nutrition, and sustainability in semi-arid regions. Although the presence of oocysts does not allow direct inference regarding viability or infectious risk, the results reinforce the need to consider the foodborne route as a relevant component in the epidemiological chain of cryptosporidiosis. WIthin the One Health framework, the findings underscore the need to strengthen biosecurity practices, agroecological management, access to high-quality water, producer training, and the promotion of pasteurization as strategies to support public policies aimed at health education and transmission risk mitigation.

217 – Measuring What Matters: Performance Evaluation Tools for Actionable One Health Governance

Xiao-Xi ZHANG

Shanghai Jiao Tong University School of Medicine, China, People's Republic of

Session Aim and Significance

Despite growing global consensus around One Health as a guiding framework for addressing complex health risks, countries continue to face a persistent gap between conceptual commitment and operational implementation. A central barrier lies in the absence of robust, comparable, and policy-relevant tools to assess One Health performance, prioritize investments, and evaluate cross-sectoral returns. While many countries have adopted multisectoral strategies, few possess systematic mechanisms to measure governance capacity, coordination quality, preparedness, and implementation effectiveness across human, animal, and environmental health systems.

This session addresses this gap by integrating three complementary strands of evidence generation: the Global One Health Index (GOHI), One Health performance evaluation frameworks, and multi-objective economic evaluation. The Global One Health Index provides a structured, indicator-based approach to quantify governance capacity, coordination mechanisms, preparedness, and delivery performance across sectors and administrative levels. Building on this foundation, the session moves beyond descriptive benchmarking to examine how performance metrics can be linked to decision-making, accountability, and financing mechanisms.

A core innovation of the session is the explicit integration of economic evaluation within One Health performance assessment. Speakers will present methodological advances in embedded cost-effectiveness analysis, multi-criteria decision analysis, and system-based economic modelling that capture cross-sectoral spillovers, long-term resilience benefits, and trade-offs that are often invisible in single-sector evaluations. These approaches are essential for informing joint financing arrangements, prioritization across ministries, and adaptive policy design in resource-constrained settings.

Empirical examples will be drawn from collaborative work in Southeast Asia (including Lao PDR and Cambodia), Africa, Japan's historical pollution-related public health crises, and contemporary environmental and zoonotic disease challenges in Latin America and the Middle East. These cases illustrate how performance metrics and economic evidence can jointly inform policy choices in low-, middle-, and high-income contexts.

The session brings together members and partners of the One Health Action Commission, academic institutions, public health agencies, and international organizations, including FAO, WHO, WHO Academy, and CGIAR/ILRI. Emphasis will be placed on governance relevance: how performance evaluation and economic evidence can support inter-ministerial coordination, joint financing, and policy learning across diverse institutional settings.

By linking metrics to mandates and evidence to action, this session aims to contribute to a more operational, accountable, and investment-oriented approach to One Health governance.

Educational Outcomes

Participants will gain:

Proposed Format

---

222 – Integrating phenotypes and genomes to map quantify extended-spectrum β-lactamase (ESBL) associated multidrug resistance in swine-associated Escherichia coli from Hungary

Ádám KEREK (1,2), Melinda NEMES-TERÉNYI (1,2), Ákos JERZSELE (1,2)

1: Department of Pharmacology and Toxicology, University of Veterinary Medicine Budapest, Budapest, Hungary; 2: National Laboratory of Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health and Food Chain Safety, University of Veterinary Medicine Budapest, Hungary

Background

Antimicrobial resistance (AMR) is a One Health challenge shaped by antimicrobial use across humans, animals, and the environment. Intensive swine production can amplify resistant Enterobacterales, and *Escherichia coli* is a sentinel species because it bridges commensal carriage, opportunistic disease, and horizontal gene transfer. We investigated multidrug-resistant (MDR) *E. coli* from Hungarian large-scale swine farms to quantify extended-spectrum β-lactamase (ESBL)/β-lactamase phenotypes and resolve their genomic basis with emphasis on mechanisms relevant to cross-sectoral risk.

Methods

In total, 203 *E. coli* isolates were obtained from four intensive swine farms and assessed by phenotypic susceptibility testing. ESBL and β-lactamase phenotypes were detected in 127/203 (62.6%) and 110/203 (54.2%) isolates, respectively. Whole-genome sequencing (WGS) was performed for 116 isolates, followed by resistome screening and phenotype–genotype reconciliation.

Results

WGS identified 82 resistance genes with 5,427 total gene hits across the dataset, indicating a dense resistome background in farm-associated MDR populations. ESBL-associated alleles were found in 50/116 (43.1%) genomes, dominated by *CTX-M* variants (*CTX-M-1/-32/-55/-8*) and *TEM* lineages (*TEM-1, TEM-150*). In isolates showing ESBL/β-lactamase phenotypes without canonical ESBL genes, near-universal presence of chromosomal *ampC/ampH* (115/116; 99.1%) supported β-lactamase overproduction as a plausible explanation for discordance. Additional determinants included aminoglycoside-modifying enzymes (20.7%), tetracycline genes *tetA–D* (25.9%), plasmid-mediated quinolone resistance (*qnrB5*, 1.7%), and ubiquitous efflux-associated genes (100%). Markers linked to colistin non-susceptibility were present in all genomes (chromosomal *pmrF/eptA/ugd*), while *mcr-1* occurred in 2.6%, underscoring the coexistence of intrinsic (adaptive) and mobile pathways.

Conclusions

MDR *E. coli* in Hungarian swine farms carry a layered resistome in which mobile ESBL elements coexist with chromosomally encoded adaptive β-lactamase and last-line drug resistance determinants. These findings support integrated One Health surveillance that combines phenotyping and WGS, alongside stewardship measures to reduce selection pressure and limit dissemination along animal–human–environment interfaces.

---

252 – One Health in Action: The role of Community Based Integrated Surveillance-Response Systems and use of rapid diagnostic kits in early confirmation and response to rabies outbreaks in Marsabit County, Kenya.

Boku BODHA (1), Ahatho EKALO (2), Ezekiel MOGAKA (3), Ludmila LOBKOWICZ (4), Jakob ZINSSTAG (5,6)

1: Department of Veterinary Services County Government of Marsabit, Kenya; 2: Department of Environment and Natural Resources County Government of Marsabit; 3: Department of Health Services County Government of Marsabit; 4: Malteser International One Health Project in Kenya and Ethiopia; 5: Swiss Tropical and Public Health Institute, Basel, Switzerland; 6: University of Basel, Peterplatz 1, CH-4003 Basel, Switzerland

Background: Rabies is a Neglected Tropical Disease (NTD) predominantly affecting poor and vulnerable populations residing in remote rural areas where 80% of human cases occur. Domestic dogs are responsible for human transmission of rabies. Globally, deaths due to rabies are poorly reported and documented. Annually there are 59,000 human deaths reported in over 150 countries, 95% of which occur in Africa and Asia. In Kenya, it is estimated that 2000 human deaths are attributed to rabies annually. In Marsabit County, the burden and associated risk factors for rabies are poorly understood due to weak surveillance systems, outbreak investigation, and research. In addition, previously in Marsabit, confirmation of a rabies case was cumbersome, as it involved cutting off the entire head of the affected animal and transportation of the same to the central veterinary laboratory in the capital city, a distance of over 500 km. This study explored the use of community resource persons in reporting of outbreaks and the use of rapid diagnostic kits in detection and confirmation of rabies at the field level.

Method: The study was conducted in 5 villages in the rural setup of Marsabit County, Kenya, which was one of the sites of the cross-border Community-Based integrated surveillance and response system (CB-iSRS) (Kenya/Ethiopia—Dirre Woreda/Marsabit County project. Community-based integrated surveillance was conducted using the Community Disease Reporters (CDRs), Community Health Promoters (CHPs), and Ward Climate Change Planning Committees (WCCPCs) from January to December 2025. The CHPs, CDRs, and WCCPCs reported suspected priority zoonotic diseases and other One Health issues using the CB-iSRS data collection tool (Kobo Toolkit) online. Once the report was received by the surveillance officers, veterinary laboratory officer and the CDR visited the affected village, collected samples (brain tissue), and used the rapid test kit for analysis (Lateral flow, ANIGENTM, South Korea). The result was relayed instantly to the affected community, and a follow-up action was decided.

Results: During the study a total of 37 suspected rabies cases were reported from 10 locations within Marsabit County. Of the reported cases, 25 involved animals (9 donkeys, 8 goats, 5 dogs, 3 cattle), and 12 were humans. Out of the 25 reported animal cases, 10 were picked by the CB-iSRS system within the study areas, and out of that, 50% (5/10) were confirmed using the rapid diagnostic kit. The remaining animal culprits could not be traced as of the time of reporting. The response was organized in response to the outbreak. A total of 1200 cattle and 50 dogs were vaccinated.

Conclusion: This study suggests that the use of CB-iSRS improves coordinated reporting of zoonotic diseases. Rapid antigen-based diagnostic kits reduce detection time, target the use of post-exposure prophylaxis, and therefore enhance response to outbreaks of rabies.

277 – Strengthening Climate Resilience of Communities and Primary Healthcare Services through a One Health Approach: Experience from the SENEYA Project in Senegal

Credo HOUNDODJADE, **Sophie OUVRARD**, **Serge BREYSSE**, Clemence DOUMENC-AÏDARA, Karel NANA, Patrick KARUME, Christian SAMBOU, Philippe CORREA
SOLTHIS

Background: Climate change poses a growing threat to human, animal, and environmental health in sub-Saharan Africa. In Senegal, the Sédhiou region faces multiple challenges including Extreme climatic variations, environmental degradation, inadequate waste management, and increased vulnerability of primary healthcare services. The SENEYA project was developed to improve the climate resilience of communities and primary health structures through a One Health approach integrating climate-smart strategies. The main objective was to test and adapt a Climate Vulnerability and Capacity Assessment (VCA) methodology - a systematic analysis tool to identify specific climate vulnerabilities of health facilities and develop targeted adaptation plans - to the primary care context, while strengthening community and professional capacities.

Methods: The project was implemented over two years (2025-2026) in the Sédhiou region, targeting the localities of Sédhiou and Djirédji. A participatory multi-stakeholder approach was adopted, mobilizing local communities, women's groups, health services, local authorities, and civil society organizations. Interventions were structured around four axes: (1) community awareness through radio broadcasts, home visits (VADI), and thematic events, (2) capacity building of professional and community actors, (3) adaptation of primary health structures through the VCA methodology including diagnosis, planning, and implementation of solutions, and (4) knowledge generation for advocacy. Data were collected using gender-sensitive tools and analyzed to document the process and results.

Results: The VCA methodology was successfully adapted to the primary healthcare context, enabling climate vulnerability assessments of health facilities and development of concrete adaptation plans. Implementation of VCA-identified solutions led to tangible improvements: enhanced health infrastructure, establishment of waste management and composting systems, revitalization of occupational health and safety committees (CHSCT), development of green spaces, planting of indigenous tree species, and mangrove restoration. A VCA methodological guide was developed to facilitate replication. Additionally, the project trained over 60 professional actors and 60 community actors in One Health approaches and sustainable healthcare practices. Awareness activities reached 1,000 households through VADI and thousands of listeners through 12 radio broadcasts. Ten endogenous adaptation actions were identified and four were supported with a gender focus. Events mobilized over 400 participants.

Conclusions: The SENEYA project demonstrates that the adapted VCA methodology constitutes a relevant and replicable tool for climate adaptation of primary health services within a One Health approach. Vulnerability assessments and adaptation plans enable targeted and effective interventions. Community engagement and identification of endogenous actions ensure sustainability. The results advocate for integrating the VCA methodology into health policies and scaling it up in other regions facing similar climate challenges.

280 – A framework for One Health research, policy and practice in forced migration: zoonotic disease dynamics as a model

Dorien BRAAM (1,2)
1: London School of Hygiene and Tropical Medicine; 2: University of Cambridge

Background: The One Health approach has become one of the leading frameworks to address the interlinkages between animal, environmental and human health, however, the concept is rarely considered in emergencies. Globally, countries and communities most vulnerable to disaster, conflict and related displacement are largely dependent on farmed animals for nutrition, health and livelihoods, however animals are rarely considered within humanitarian responses, often reducing the resilience of affected populations to further disasters and forced migration. Forced migration has doubled over the past decade, and continues to increase, with profound implications for both human and non-human animal health, particularly in relation to zoonoses, transmissible between animals and humans. Methods: Based on literature reviews and tested through a series of empirical case studies conducted between 2019-2022, we developed a novel framework for research, policy and practice to improve One Health outcomes in forced migration, using zoonotic diseases as a model. The aim of this framework is to enhance interdisciplinary understanding, informing policy development and practical implementation. Results: The mechanisms underlying any association between forced migration and zoonoses remain poorly understood, and responding appropriately represents a substantial societal challenge. Both human and animal migrants are often excluded from health systems, research, policies and responses, resulting in complex interlinked risks and vulnerabilities along the migration route. While zoonotic diseases are associated with forced migration, those most affected are already vulnerable prior to exposure, suggesting that heightened risk may be attributable less to inherent susceptibility but more to structural deficiencies. These observations highlight the need to reconsider how research, policy, and practice can more effectively address such contextual determinants. Conclusion: Zoonotic disease dynamics in forced migration contexts demand a theoretical and practical framework which preserves, rather than simplifies the complexity of One Health challenges in forced migration contexts.

286 – ANTIMICROBIAL ACTIVITY AND CYTOTOXICITY OF MEDICINAL PLANTS USED FOR CATTLE WOUND TREATMENT IN EPHRAIM MOGALE MUNICIPALITY, SOUTH AFRICA

Malebo Dorcas LEKGETHISHO (1), Prudence Ngalula KAYOKA-KABONGO (2), Olasunkanmi Stephen OLAWUWO (2)
1: Limpopo Department of Agriculture and Rural Development, South Africa; 2: University of South Africa

Introduction: Plant-based therapies are widely used in different parts of the world to treat animals and human ailments due to their accessibility, affordability, and effectiveness. Ethnoveterinary medicine is based on beliefs, knowledge, skills, and practices to safeguard the health and welfare of humans and animals. In the Ephraim Mogale municipality, animal wounds represent some of the major burdens to animal production, as they cause severe economic losses, impaired health, damaged hides, weight loss, loss of fertility, and death through wound infections and septicemia, which may lead to loss of commercial value. Due to lack of financial resources, farmers often resort to medicinal plants to treat animal wounds. However, there is no data on the efficacy, formulation, and guidelines on these medicinal plants in the municipality. Therefore, this study seeks to (1) investigate and analyze the efficacy of commonly used plants in treating animal wounds, (2) investigate the livestock practices in communal areas of the Ephraim Mogale Municipality and (3) isolate the compounds from selected plants

Material and Methods: Quantitative and qualitative research methods will both be used in this study. Qualitative data will be collected using semi-structured interviews to assess knowledge, attitudes, and perceptions of farmers in the municipality. Structured questionnaires will be developed to obtain data related to plants used for the treatment of cattle wounds. Samples of commonly used plants will be collected and transported to the laboratory for analysis. The Statistical analysis will be performed using Prism software (GraphPad), Thermatic software, & SPSS V28.0 (IBM Corp, 2021)

Discussion and conclusion: This study will be the first of its kind among Ephraim Mogale Municipality communal livestock farmers to investigate and analyze the medicinal plants having the potential to heal wounds and to document the practices used. The study will also validate the efficacy and safety precautions of the traditional medicines used in wound healing treatment potential in livestock.

291 – Knowledge, Attitudes and Practices of cattle farmers in Togo regarding antimicrobial resistance: a case study of the Maritime and Savannah regions

Yawovi Agbenoxevi KOHOE (1), Ali K. KADANGA (2), Essodina TALAKI (3), Oyétoundé DJIWA (1)
1: Food and Agriculture Organization of the United Nations, Togo; 2: University of Kara; 3: University of Lomé

Background: Antimicrobial resistance (AMR) is a global public health threat. In Togo, infectious diseases represent one of the major constraints on livestock farming in general and cattle in particular, leading to an increasing use of antibiotics. However, data on the knowledge, attitudes and practices (KAP) of cattle farmers regarding AMR are almost non-existent.

Objective: This study aimed to evaluate cattle farmers' KAP on antibiotic use and AMR in Maritime and Savannah Regions of Togo.

Methods: A cross-sectional study was conducted in Maritime and Savannah regions with 196 farmers selected according to the number of cattle in the prefectures. A structured questionnaire was administered face-to-face and descriptive and bivariate analyses were performed using Chi-square tests.

Results: The study revealed a widespread lack of awareness of AMR among cattle farmers. Indeed, 91.8 % of the 196 farmers could not define an "antimicrobial", 87.2 % were unaware of the purpose of using an "antibiotic" and 97.5 % had never heard of AMR. Practices were predominantly high-risk: 43.4 % of farmers were self-medicating, 45.4 % were getting their antibiotics from local markets, and 92.3 % were not adhering to the recommended duration of treatment (stopping as soon as symptoms improved). The concept of withdrawal period was unknown to 83.7% of farmers. Tetracyclines (66.1 %) were the most widely used antibiotics and the most associated with treatment failures perceived by farmers (24 %). Multivariate analysis identified higher educational attainment, cattle farming training and belonging to the Savannah region as factors significantly associated with better knowledge and practices.

Conclusion: This study reveals that cattle farmers in Togo have very limited knowledge about AMR and mostly inappropriate antibiotic use practices. Self-medication, non-compliance with treatment times and ignorance of the waiting period are worrying.

300 – Bacillus anthracis in South Africa, 1975–2013: are some lineages vanishing?

Kgaugelo LEKOTA (1), Ayesha HASSIM (2), Gilles VERGNAUD (3), Henriette VAN HEERDEN (2)
1: North West University, South Africa; 2: University of Pretoria; 3: Université Paris-Saclay, Gif-sur-Yvette

Background

The anthrax-causing bacterium *Bacillus anthracis* comprises the genetic clades A, B, and C. In the northernmost part (Pafuri) of Kruger National Park (KNP), South Africa, both the common A and rare B strains clades occur. The B clade strains were reported to be dominant in Pafuri before 1991, while A clade strains occurred towards the central parts of KNP. The prevalence of B clade strains is currently much lower as only A clade strains have been isolated from 1992 onwards in KNP.

Methods

In this study 319 *B. anthracis* strains were characterized with 31-loci multiple-locus variable-number tandem repeat analysis (MLVA-31). B clade strains from soil (n = 9), Norther Cape Province strains (n = 22), and a animal derived isolates from KNP (n = 33) were further characterised by whole genome sequencing and compared to publicly available genomes. T

Results

he KNP strains clustered in the B clade before 1991 into two dominant genotypes. South African strains cluster into a dominant genotype A.Br.005/006 consisting of KNP as well as the other anthrax endemic region, Northern Cape Province (NCP), South Africa. A few A.Br.001/002 strains from both endemic areas were also identified. Subclade A.Br.101 belonging to the A.Br.Aust94 lineage was reported in the NCP. The tryptophan synthase subunit alpha gene (trpA), which results in a pseudogene in B-clade genomes separates the A- and B-clade genomes. These differences in biosynthetic cell wall genes suggest variation

in adaptability or cell growth of the B-clade strains in the environment, further influenced by the truncation of the trpA gene involved in spore germination.

Conclusions

The B-clade strains seems to be vanishing, while outbreaks in South Africa are caused mainly by the A.Br.005/006 genotypes as well as a few minor clades such as A.Br.001/002 and A.Br.101 present in NCP. This work confirmed the existence of the rare and vanishing B-clade strains that group in B.Br.001 branch with KrugerB and A0991 KNP strains.This study highlights the phylogenetic structure of NCP B. anthracis strains with distinctive SNP branches important for forensic tracing and novel SNP discovery purposes

---

370 – Polycentric governance and collective action as institutional conditions for implementing One Health prevention against zoonoses in Cameroon

Michael Brice TALLA SADEU (1,2), Ludovic TEMPLE (2,1)

1: Université de Montpellier; 2: Centre de coopération internationale en recherche agronomique pour le développement (CIRAD)

Context

The One Health (OH) framework promotes multisectoral integration for the prevention of zoonoses at the interface between humans, animals and the environment (Zinsstag et al., 2023). However, in many contexts in sub-Saharan Africa, OH remains a normative framework whose implementation at the territorial level remains limited (Olive et al., 2022). In Cameroon, the prevention of mosquito-borne zoonoses mobilises a plurality of public, private and community actors operating at different levels of governance. It structures an incomplete polycentric system, characterised by centralised authority, overlapping uncoordinated mandates and weak horizontal coordination. Drawing on the work of (Hess and E. Ostrom, 2007; E. Ostrom, 1990; V. Ostrom et al., 1961) on polycentric governance and collective action, this study examines the institutional and organisational conditions under which such a pluralistic governance structure can evolve into a functional polycentric system capable of effectively implementing OH prevention. Prevention is not conceptualised as a conventional public good, but as a process of collective “pooling” based on shared knowledge, practices, and coordination and rule-making mechanisms.

Methods

Following a survey to identify actors in zoonosis prevention, three participatory workshops were organised in Kribi with representatives from local authorities, civil society, the private sector and decentralised public administrations (Kribi 1st municipality). These workshops updated actor mapping, identified constraints, and analysed intersectoral interactions. A cross-cutting multi-stakeholder forum then facilitated a collective characterisation of the system and discussed institutional conditions for collective action. This approach documents the dynamics of intersectoral integration at the heart of OH territorialisation. Data were examined using a thematic grid focused on polycentric overlap, coordination, trust, and knowledge circulation, drawing on the Institutional Analysis and Development (IAD) and socio-ecological systems frameworks (Ostrom, 1990, 2009).

Results

Our findings emphasize differing governance approaches and confirm significant overlap in preventive mandates. While this overlap offers potential synergies, the lack of formal coordination perpetuates role ambiguity and limits integration. The multi-stakeholder forum provided a deliberative arena promoting collective learning, clarified responsibilities, and recognition of local knowledge. Participants identified several institutional conditions necessary for enhanced OH implementation: cross-sector dialogue platforms, explicit articulation of responsibilities, shared monitoring mechanisms, and greater inclusion of the animal and environmental sectors. These findings show that the polycentric model helps diagnose coordination deficits and the absence of cross-cutting rules that prevent transforming overlap into effective complementarity (Kassis and Bertrand, 2025).

Conclusion

This experience demonstrates that One Health effectiveness depends on institutional processes enabling the collective articulation of rules, trust, and cross-sector coordination. Strengthening One Health requires recognising prevention as a collective process of institutional structuring where actors co-produce rules, knowledge, and coordination mechanisms. Consequently, consolidating polycentric mechanisms is essential to support the co-construction of prevention at the territorial level, linking different sectors and governance scales.

---

376 – Operationalizing One Health Through Digital Integration: The Cameroon One Health Information System (COHIS) Experience

Elisabeth BETSI DIBONGUE (1), Sonna FOUOGUE (1), Gaspard AYISSI (1), Lorraine FOKOU (1), Khadidjah PARE (1), Audrey NGOSSO (1), Emmanuel BATOUM (2), Chirstian MOUANGUE (2), Boris OKIWAH (3), Serge NDONGO (3), Julius MURKE (4), Habiba MULLER (4), Conrad NKUO (1)

1: One Health Platform, Cameroon; 2: Ministry of Public health, Cameroon; 3: Ministry of Livestock, Fisheries and Animal Industries, Cameroon; 4: 4- GIZ-One Health Data Alliance Africa project, Cameroon

Background

Effective epidemic and pandemic preparedness and response depend on timely, integrated, and trusted data. The increasing frequency of zoonotic diseases, foodborne outbreaks, and antimicrobial resistance underscores the urgency of overcoming fragmented information systems. In many low- and middle-income countries, data remain siloed across human, animal, and environmental sectors, limiting coordinated surveillance and evidence-based decision-making.

In Cameroon, these structural fragmentation challenges have constrained multisectoral collaboration and delayed response capacities. To address this gap, the Cameroon One Health Information System (COHIS) was developed under the national One Health platform. COHIS aims to strengthen integrated surveillance, enhance data sovereignty, and enable adequate decision making through a coordinated preparedness and response mechanism across sectors.

Methods

COHIS was built on the Regional Pandemic Analytics Tool and developed through a participatory, multisectoral design process involving mainly the Ministries of Public Health, Livestock, Environment, and Agriculture. Rather than replacing existing systems, the platform builds interoperability bridges with established sectoral infrastructures, including DHIS2 for human health and CAHIS for veterinary services.

The development process included national stakeholder consultations, the establishment of a technical working group, multisectoral training sessions for analysts, and the drafting of data governance and information security frameworks to guide secure and regulated data sharing.

Technical implementation followed a phased approach: (1) deployment of nationally hosted sovereign servers; (2) capacity building for multisectoral analysts; (3) development of operational dashboards addressing priority use cases such as zoonoses, rabies, hazardous waste management, cross-border passenger surveillance, climate-linked influenza trends, pesticide residues; and (4) initial AI-readiness efforts, including predictive modeling and harmonization of sectoral datasets in preparation for future machine learning applications.

Results

COHIS dashboards are now actively used by ministries for surveillance and analytical purposes. The unified data mesh architecture integrates multiple data management, visualization, and security tools into a single platform, enabling analysts to combine datasets, configure dashboards, and build data pipelines without advanced coding skills or reliance on external consultants.

Key lessons from implementation highlight the central role of strong governance mechanisms and trust-building among institutions. Leveraging existing digital systems facilitated institutional acceptance and reduced duplication. Continuous capacity development proved essential to ensure local ownership and sustainability. Furthermore, institutional anchoring within the national One Health platform and the establishment of robust data-sharing and security framework were critical to operationalizing cross-sector collaboration.

Conclusion

COHIS demonstrates that integrated and digitized One Health information systems are achievable in resource-constrained settings when grounded in participatory governance and national ownership. By strengthening data integration, enhancing early detection capacities, and supporting coordinated response, COHIS contributes to improved epidemic preparedness.

Beyond technical integration, the initiative advances data sovereignty, institutional trust, and multisectoral collaboration, while laying the foundation for AI-enabled analytics. As such, COHIS offers a scalable and policy-relevant model for operationalizing One Health through digital innovation.

---

393 – Environmental and One Health Dimensions of Toxoplasmosis Awareness Among Pregnant Women in Sogakope, Ghana: A Cross-Sectional Study

Christopher Yaw DUMEVI (1,2), Naa-Adjeley Naomi IKEMEFUNA (1), Kwabla Cynthia SANGMORKIE (1), Nana Aba Setorwu EYESON (2,3), Christopher Mfum OWUSU-ASENSO (2,3), Dorcas Akuorkor TEIKO (1), Isaac Ekow ENNIN (1), James-Paul KRETCHY (1), Saviour Kweku ADJENTI (1), Patrick F. AYEH-KUMI (2)

1: School of Medical Sciences, Central University, Accra, Ghana, Ghana; 2: Department of Medical Microbiology, University of Ghana Medical School, Korle-Bu, Accra, Ghana; 3: DataInk Research Consult, Accra, Ghana

Background: Toxoplasmosis, caused by *Toxoplasma gondii*, is a preventable zoonotic infection with severe consequences for maternal and foetal health. Within a One Health framework recognizing the interconnectedness of human, animal, and environmental health, this study assessed knowledge and risk perception among pregnant women in Sogakope, Ghana—a high-transmission ecological setting where subsistence farming, cat ownership, and environmental exposure pathways converge.

Methods: A hospital-based analytical cross-sectional study was conducted from June to September 2025 among 399 systematically sampled pregnant women attending antenatal care at Sogakope District Hospital. An interviewer-administered structured questionnaire, developed *de novo* and pretested (Cronbach's α: knowledge=0.84, perception=0.78), assessed socio-demographic characteristics, obstetric history, toxoplasmosis knowledge, and risk perception. Knowledge and perception scores were categorized as poor (70%), moderate, or good (≥70%). Associations were analyzed using chi-square tests and multivariable logistic regression (p0.05 significant).

Results: Participants' mean age was 31.4±7.8 years; 44.9% owned cats. Awareness was critically low: only 6.8% had heard of toxoplasmosis, and 20.1% correctly identified its parasitic aetiology. Overall, 53.9% demonstrated poor knowledge, while 97.2% exhibited poor risk perception (Table 1). Parity showed significant association with knowledge level (p=0.04), with women of parity two demonstrating highest knowledge (31.0% good). A history of miscarriage was the sole factor significantly associated with positive risk perception (OR=4.84, 95% CI: 1.30–22.70, p=0.046). No other socio-demographic variables (education, residence, cat ownership) were significantly associated with knowledge or perception in multivariable analysis (Table 1).

Conclusions: This study reveals profound, population-wide gaps in toxoplasmosis awareness among pregnant women in a high-exposure Ghanaian setting, with prior adverse pregnancy outcome serving as the sole catalyst for risk perception—consistent with Health Belief Model constructs. The findings underscore an urgent need for integrated, One Health-informed interventions addressing the human-animal-environment interface: (1) structured toxoplasmosis education within routine antenatal care, (2) community-based environmental hygiene initiatives targeting soil and water contamination, and (3) veterinary public health messaging on responsible cat ownership. Such multisectoral collaboration is essential to mitigate congenital toxoplasmosis risk and advance maternal-child health targets within the Sustainable Development Goals.

Table 1: Toxoplasmosis Knowledge, Perception, and Associated Factors Among Pregnant Women (N=399)

Indicator	n	%
Knowledge Domains		
Ever heard of toxoplasmosis	27	6.8
Correctly identified parasitic cause	80	20.1
Aware of mother-to-child transmission	132	33.1
Aware of association with miscarriage/stillbirth	159	39.9
Overall Knowledge Level		
Poor (<70%)	215	53.9
Moderate/Good (≥70%)	184	46.1
Overall Perception Level		
Poor (<70%)	388	97.2
Positive (≥70%)	11	2.8
Factor Associated with Positive Perception	OR	95% CI
History of miscarriage	4.84	1.30–22.70

398 – Unveiling Brucellosis Risks in Breeding Herds and Humans: Case Study on Diagnostic Failures and Control Gaps in South Africa

Koketso Desiree MAZWI (1), Henriette VAN HEERDEN (2)

1: University of Pretoria, University of the Witwatersrand; 2: University of Pretoria

Brucellosis remains a major zoonotic pathogen of livestock, wildlife, and humans, with significant implications for reproductive losses and public health. The introduction of breeding animals with unknown *Brucella* status into previously *Brucella*-negative herds poses a substantial risk for disease introduction and sustained transmission. This case study describes two independent brucellosis outbreaks in South Africa involving abortion events, serial serological testing, bacteriological culture, and molecular confirmatory assays.

Across both herds, multiple rounds of screening were performed, including RBT, CFT, iELISA, qPCR, and culture from diverse samples. On the cattle farm, animals previously certified as brucellosis-negative demonstrated rising seropositivity from 2024 onward, with *B. abortus* detected in blood clots of the animals tested, including a suspect bull that tested seronegative afterwards. A *Brucella* positive human case occurred following direct exposure to the infected cattle farm. On the sable antelope farm, *B. abortus* was detected in two seropositive females through culture on lymph nodes and amniotic fluid, while *B. abortus* was also isolated from the semen of a seronegative breeding bull, suggesting that the bull was a carrier and posing a transmission risk to the herd.

The collective findings demonstrate that infected males in both cases testing seronegative with *B. abortus* detected in semen can serve as persistent reservoirs and facilitate transmission within breeding herds. The study emphasizes the diagnostic limitations of relying solely on standard serology, especially in chronically infected or wildlife species, and highlights the need for integrating iELISA and PCR into brucellosis-infected farms to facilitate complete eradication on these farms. Strengthened biosecurity, mandatory vaccination programs for livestock, and systematic testing of breeding bulls and wildlife are critical to preventing ongoing spillover between livestock, wildlife, and humans in SA.

405 – Operationalizing One Health in Fragile and Conflict-Affected Settings: Lessons from the West Bank, Palestine

Said ABUKHATTAB

Birzeit University, Palestinian Territories

Background

Fragile and protracted conflict settings, such as the West Bank, operate under constraints shaped by protracted political conflict, restricted sovereignty, territorial fragmentation, and limitations on movement and resource control. These conditions weaken surveillance systems, fragment regulatory authority, disrupt laboratory supply chains, and undermine antimicrobial stewardship and food system stability. Preparedness and response to emerging infectious threats and antimicrobial resistance (AMR) therefore remain constrained at the human–animal–environment interface.

Health risks are influenced not only by biological factors but also by political, infrastructural, and socio-ecological determinants shaping exposure pathways and response capacity. This programme examined whether a One Health approach could be institutionalized within these constraints and whether integrated cross-sectoral surveillance could strengthen preparedness, antimicrobial stewardship, and health system resilience.

Methods

Between 2020 and 2026, a phased One Health system-strengthening programme was implemented using mixed approaches. Governance structures and zoonotic risk priorities were assessed through stakeholder engagement, institutional mapping, and quantitative prioritization across human, animal, and environmental sectors. Workforce capacity and surveillance performance were evaluated to identify gaps in detection, reporting, and response.

Laboratory strengthening standardized protocols from sampling to genomic analysis. Metagenomic and sequencing approaches characterized AMR patterns and pathogen distribution across human, animal, food-chain, and environmental interfaces. An integrated One Health surveillance platform was piloted, linking laboratory harmonization, shared reporting systems, and wastewater monitoring to detect AMR hotspots and transmission pathways within a constrained environment.

Results

System assessment revealed gaps in surveillance coherence, laboratory interoperability, regulatory enforcement, and cross-sector coordination. Zoonotic prioritization identified nationally relevant threats amid fragmented reporting and limited screening. Workforce evaluation demonstrated capacity discrepancies affecting early detection and response.

Laboratory strengthening enabled standardized workflows and molecular diagnostics, facilitating the detection of multidrug-resistant pathogens and transmission pathways across sectors. The surveillance platform established cross-sector data exchange mechanisms and reporting channels linking health, agriculture, and environmental authorities. Wastewater monitoring identified AMR hotspots associated with urban density and intensive food production, demonstrating the feasibility of environmental surveillance despite constraints.

Conclusions

Fragile systems operating under protracted political conflict and restricted sovereignty should not be viewed as barriers to One Health implementation but as priority contexts requiring integration. Cross-sectoral surveillance can serve as an entry point for humanitarian and governmental actors in politically constrained environments. The phased integration of governance mapping, laboratory strengthening, workforce assessment, and environmental surveillance offers a replicable model adaptable to other fragile and conflict-affected settings. In protracted crises, One Health functions as a framework to mitigate AMR, zoonotic and emerging infections, and food system vulnerabilities while strengthening coordination and health system resilience. Framing One Health within humanitarian action highlights its potential to move beyond emergency response toward long-term resilience, equity, and sustainable institutional capacity.

---

411 – Zoonotic risks in the use of wildlife biodiversity in Togo: analysis of the wild meat supply chain using “One Health” approach

Oyetounde DJIWA (1), Moussa SMARAOU (2), Napo ALI (2), Yawovi KOHOE (1)

1: Food and Agriculture Organizations of United Nations, FAO-Togo; 2: Directorate of Forest Resources, Togo

Background: Togo has a diverse range of ecosystems and is home to more than 4,019 animal species divided into 827 families and 2,379 genera (SPANB Togo, 2021). However, the degradation of these ecosystems due to various threats and pressures such as hunting (Montblanc M., 2022), deforestation, bush fires, etc. That leads to enormous biodiversity loss. One concern is the epidemiological risk (Vicente J. & Höfle U.; 2025) due to the lack of a wildlife disease surveillance system. The wild meat's trade in Togo, although vital to communities, is a potential vector for emerging diseases. The current study, conducted with FAO support and funding from Global Pandemic Fund, aims to assess the health risks along the bush meat value chain.

Methods: A cross-sectional survey was conducted among 77 actors (hunters, traders, restaurant owners) in the wild meat value chain (Sapra R. L., 2022) in twelve Departments where hunting or capture of wild animals is intense in Togo. The information or parameters sought from respondents include: the species of wild animals hunted or captured, the method of transporting wild meat, the handling of carcasses, the use or non-use of protective equipment, the conservation of the meat, etc. A qualitative risk index (1-3) was assigned to each practice or parameter (Georgia K. M. et al ; 2023) in order to assess the level of exposure to health risks at each stage of the supply chain.

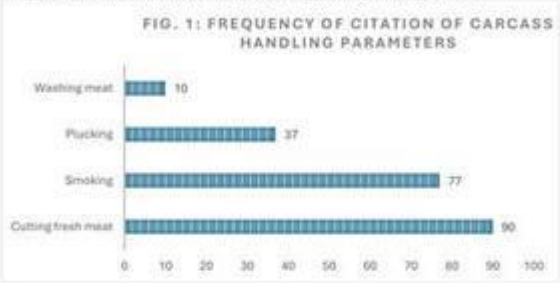
Results: Thirty-seven (37) of the most hunted species were identified, with a predominance of rodents posing a high zoonotic risk. The study reveals an almost total absence of biosecurity measures throughout the bush meat value chain: unsafe transport (direct contact), intensive handling of carcasses (dissection, cutting) without personal protective equipment (PPE), and no mechanisms for withdrawing risky products. The highest risk indices concern intermediate traders (2.44/3) and hunters (2.43/3).

Conclusion: This study constitutes the first systematic assessment of health risks along the wild meat value chain in Togo. Hunters and traders are daily exposed to a high risk of contamination by zoonotic due to bad practices and lack of protective measures. The lack of biosecurity at all levels of the value chain creates a favorable context to the emergence and spread of diseases. The results of our study call for urgent implementation of a national biosecurity program based on the "One Health" approach.

Titre : *Risques zoonotiques dans l'utilisation de biodiversité faunique au Togo : analyse de la chaîne d'approvisionnement en viande sauvage selon l'approche "Une Seule Santé"*
DJIWA O, SAMAROU M, ALI N, KOHOE Y,

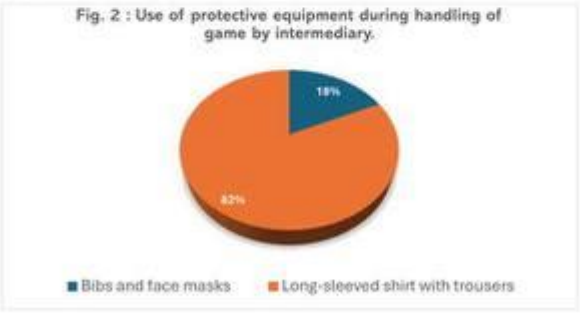
Wild meat handling by hunters

Fresh meat cutting (90%), meat smoking (77%), and plucking (37%) are the types of game handling most frequently cited by the hunters surveyed. Hunters also perform meat cutting/ after smoking and some of them (10%) proceed by washing meat (Figure 1).



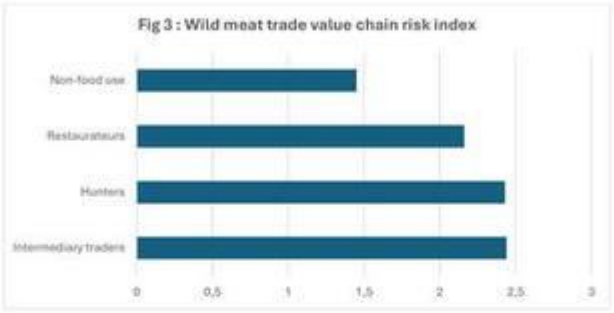
Handling of game by intermediary traders without protective equipment.

In the restaurant, workers handle whole carcasses or parts of game without protective equipment. Only 18% confirm that they wear protective equipment such as bibs and face masks or just a long-sleeved shirt with trousers (Figure 2).



Evaluation des risques

The results show high exposure to zoonotic diseases among all actors in the wild meat value chain, with varying levels depending on the group of actors. Hunters and restaurateurs are the most exposed to risk (Figure 3).



418 – Structured wildlife health networks as scalable mechanisms for integrating wildlife health into One Health implementation

Lesa THOMPSON (1), Valeria CAROLINA COLOMBO (2), Géraldine CORONADO PERTRIAUX (3), Kinzang DUKPA (1), Fayçal MEZIANI (4), Chadia WANNOUS (5)

1: Regional Representation for Asia and the Pacific, World Organisation for Animal Health, Japan; 2: Sub-Regional Representation in Brussels, World Organisation for Animal Health, Belgium; 3: Sub-Regional Representation for Southern Africa, World Organisation for Animal Health, Botswana; 4: Regional Representation for the Middle East, World Organisation for Animal Health, Lebanon; 5: Headquarters, World Organisation for Animal Health, France

Background

One Health implementation depends on practical mechanisms that enable sustained collaboration across animal, human and environment sectors. Wildlife health is increasingly recognised not as a standalone domain, but as an early risk signal for zoonotic spillover and emerging threats. WOAH supports this shift through network-based engagement, providing durable structures that link wildlife stakeholders into broader One Health surveillance, preparedness and governance processes and enable consistent integration of wildlife health into decision-making.

Methods

This abstract draws on inter-regional experience with WOAH-supported wildlife health mechanisms, including Focal Points for Wildlife and regional wildlife health networks. Each WOAH Member designates a Focal Point for Wildlife to support wildlife health activities and facilitate stakeholder networks. These Focal Points are connected through regional networks that enable regular communication and information exchange, complemented by periodic in-person WOAH training.

WOAH Representations have further supported the development of regional wildlife health networks addressing shared priorities among neighbouring Members.

In Asia and the Pacific, sub-regional wildlife health networks established since 2021 operate across East Asia, South Asia, Southeast Asia and the Pacific. Through regular virtual exchanges, in-person workshops and multisectoral activities focused on wildlife disease surveillance and spillover risk, these networks have facilitated deliberate inclusion of wildlife stakeholders in Quadripartite One Health workshops and national processes, strengthening cross-sector trust and shared understanding of emerging risks.

In Europe, webinars and workshops integrate external multisectoral stakeholders, strengthening collaboration in wildlife health surveillance and reporting. Public and animal health agencies have developed influenza early warning tools based on wild bird cases reported to WOAH through the World Animal Health Information System (WAHIS) and shared these with WOAH Focal Points, reinforcing the importance of wildlife disease reporting for zoonotic risk prevention.

In Africa, ZOOSURSY strengthens zoonoses surveillance through field studies addressing transmission between wildlife, domestic animals and humans. The project mobilises multisectoral networks and engages communities, illustrating how structured mechanisms can operationalise One Health at field level.

In the Middle East, Member leadership supported by WOAH increases visibility of wildlife health within conservation and trade discussions and facilitates its inclusion in priority disease roadmaps, strengthening entry points for integrating wildlife considerations into broader One Health coordination.

Results

Across regions, structured mechanisms have facilitated clear institutional entry points, strengthened trust-based networks and sustained multisectoral engagement. Formal WOAH mechanisms and informal communities of practice are complementary, supporting wildlife disease surveillance, spillover prevention and preparedness.

Conclusions

Looking ahead, planned wildlife health stakeholder mapping will further strengthen interoperability across sectors. These experiences demonstrate how wildlife health networks function as durable infrastructure for biodiversity–health integration within operational One Health systems.

424 – New One Health Gender Equality and Social Inclusion (OH GESI) Analysis Framework

Dominique CHARRON (1), **Natalia CEDIEL-BECERRA** (2), Maxine WHITTAKER (3), Salome BUKACHI (4)

1: One Health Institute, Ontario Veterinary College, University of Guelph, Guelph, Canada; 2: Facultad de Ciencias Agropecuarias, Universidad de la Salle, Bogotá, Colombia; 3: James Cook University, Townsville, Australia; 4: Institute of Anthropology, Gender and African Studies, University of Nairobi, Kenya AND Department of Anthropology, Durham University, UK

Background:

The gap is widening between high-level One Health (OH) policy commitments to equality and inclusion and real-world practice, in part due to gaps in widely used OH assessment, planning and implementation tools. This threatens success of OH implementation because the unique perspectives, knowledge and needs of large groups of people have not been considered. When they are ignored, the full picture of the health hazards may be incomplete or mistaken, and OH responses may fall short of their full potential to improve health. We drew on feminist scholarship and existing gender analysis and OH frameworks to develop a new OH Gender Equality and Social Inclusion assessment framework (OH-GESI) with the aim of strengthening gender equality, empowerment, and social inclusion in OH implementation

Methods:

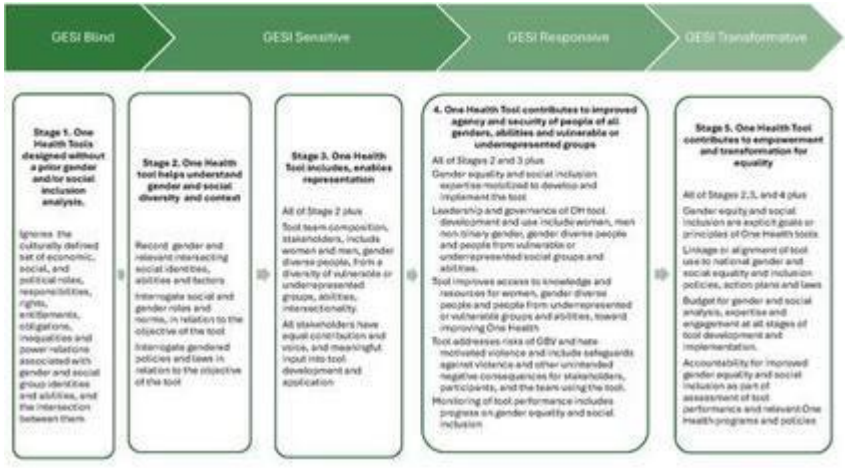
Using fourteen elements drawn from OH tools previously compiled by the OH High Level Expert Panel, the framework operates along a continuum from absence of gender equality and social inclusion considerations, through approaches that recognized some differences but do not address causes (sensitive) and approaches that begin to address them (responsive), ending with approaches that are transformative in that they seek to redress gender and social inequalities. The OH-GESI framework was used to analyse nine OH tools previously found to address gender equality and social inclusion considerations to some, or to a significant, degree.

Results:

Our analysis revealed major shortcomings among the tools with respect to gender and inclusion, while also pinpointing areas that could be addressed to strengthen existing tools. Two tools addressed eleven or more elements of the framework including those that reached the transformative level. Three tools addressed only one element each in the sensitive level of the framework. The remaining tools addressed between four and seven elements across the framework continuum.

Conclusion:

Beyond its practical application to developing more equitable and inclusive OH assessment, planning, implementation and evaluation tools, OH-GESI provides a rigorous gender and social inclusion analysis lens for OH implementation. The framework will be strengthened by further application and refinements. By aligning with the equity principles in the OH Joint Plan of Action and OHHLEP's core definition, OH-GESI aims to help organizations, governments and stakeholders translate equity and inclusion commitments into meaningful improvements to equity and inclusion on the ground.



444 – Organic Waste Flow as an ASF Vulnerability: A Multi-Sector Participatory Systems Workshop in Eastern Dominican Republic

Yussaira CASTILLO (1), Wendy GONZALEZ (1,2), Luis Pablo HERVE CLAUDE (3), **JP VILLANUEVA CABEZAS** (4,5)

1: Universidad Autónoma de Santo Domingo (UASD), República Dominicana; 2: Dirección General de Ganadería (DIGEGA), República Dominicana; 3: Lewyt College of Veterinary Medicine, Long Island University, United States; 4: Facultad de Medicina Veterinaria, Universidad San Sebastián, Chile; 5: The Nossal Institute for Global Health, The University of Melbourne, Australia

Background

African Swine Fever (ASF) has remained endemic in Hispaniola since 2021, representing the only active ASF outbreak in the Americas. The eastern Dominican Republic relies on organic food waste from one of the Caribbean's largest tourism regions to feed backyard pig production systems. This inter-sectoral chain, linking hotel waste generators, formal and informal collectors, and pig producers, forms a critical yet insufficiently characterised ASFV risk network. A participatory systems approach was required to characterise this chain, identify cross-sector vulnerabilities, and collaboratively develop feasible mitigation strategies.

Methods

A two-day multi-stakeholder workshop was conducted in Santo Domingo, Dominican Republic (February 24–25, 2026), as part of the PROCINORTE project, organised by the Facultad de Ciencias Agronómicas y Veterinarias, Universidad Autónoma de Santo Domingo. Pre-workshop activities included field visits to swill-using pig farms and meetings with Animal Health authorities (DIGEGA). Six stakeholder groups participated: hotel representatives, councils (ayuntamientos), Ministry of Environment, DIGEGA, pig producers, and academics. ASF was framed as a vulnerability of the entire organic waste system. Day 1 featured technical presentations on ASFV epidemiology, swill-associated transmission evidence, Caribbean knowledge, attitudes and practices, and the Puerto Rico regulatory experience, followed by participatory system mapping, pain-point identification, and sector-specific focus groups. Day 2 applied a Scenarios exploration, STEEP Analysis and Impact/Effort Matrix sequence to convert the system diagnosis into prioritised recommendations.

Results

System mapping revealed formal and informal waste chains characterised by inconsistent traceability, absent thermal treatment, and shared collection vehicles as key transmission risk nodes. STEEP analysis identified various barriers. Socially, cultural reliance on untreated organic waste as low-cost feed and a permissive enforcement culture persist across the system. Technologically, knowledge and equipment for thermal treatment exist and are accessible, but adoption is constrained by operational volume and entrenched practices. Economically, costs fall disproportionately on producers and collectors while enforcement benefits accrue to the state; ASF-related restrictions on agricultural financing further limit producers' investment capacity. Ecologically, improved waste management could reduce landfill load by 50–80% and decrease greenhouse gas emissions. Politically, Decrees require revision before key changes can be mandated. The Impact/Effort Matrix identified enforcement of existing landfill animal access regulations as the highest-impact, lowest-effort priority, while collector formalisation and thermal treatment standardisation were assessed as long-term. Infrastructure improvements for small-scale producers were identified as the most resource-intensive intervention, requiring substantial investment, legal reform, and institutional support.

Conclusions

ASF biosecurity in tourism-adjacent, waste-dependent pig production systems cannot be addressed by animal health authorities alone. The organic waste chain linking tourism, municipal waste management, and pig production demands coordinated One Health governance. Enforcing existing landfill regulations is an immediately actionable entry point. This workshop's methodology and outputs offer a transferable model for participatory ASF risk governance across the Caribbean region.

449 – Scaling One Health intelligence through Earth Observation and in-situ data fusion for climate–environment–ecosystem resilience

Sylvie TEYSSEYRE
Aerospace Valley, France

Rationale

Climate change is reshaping the interactions between ecosystems, animals and humans, increasing heat-related mortality, vector-borne diseases, waterborne outbreaks, air pollution impacts, food insecurity and mental health stressors.

Earth Observation (EO) provides continuous, harmonised and cross-border monitoring of environmental determinants of health (temperature, soil moisture, vegetation indices, air composition, flood extent, coastal dynamics). However, satellites do not observe health directly, they observe environmental drivers influencing health outcomes.

The transformative potential lies in **large-scale fusion of EO data with in-situ datasets** (health surveillance, entomology, demographic structure, infrastructure, socio-economic indicators). This integration enables actionable One Health intelligence: identifying where risk emerges, who is vulnerable, and when response capacity must be strengthened.

Despite technological maturity (Copernicus services, open data ecosystems), operational uptake in public health remains fragmented. This session addresses how to translate EO capabilities into scalable, ethically governed, decision-ready tools for health actors.

Objectives

Session Structure

Format: 3 short keynote interventions (10 min each), 2 operational case studies (15 min each), Moderated panel discussion (20 min), Audience Q&A (20 min)

Content Overview

1. From Environmental Signals to Health Intelligence

2. Operational One Health Applications

3. Scalability of One Health intelligence

Expected Outcomes

Added Value to the session

This session bridges environmental monitoring and operational public health, illustrating how EO can function as a **scalable public health sensor** within a One Health framework. It moves beyond theory toward implementation, focusing on decision-support, preparedness and ecosystem-informed prevention.

---

457 – Reframing AMR Risks: A Qualitative Analysis of Livestock-Targeted AMR Measures in Thailand

Sittichoke CHAWRAINGERN (1), Jane WILLIAMS (2), Chris DEGELING (1)
1: University of Wollongong; 2: The University of Sydney

Background

We are now in the tenth year of the WHO's Global Action Plan on antimicrobial resistance (AMR). A key feature of national responses to the Plan, antimicrobial stewardship programs and legal regulations are being enforced to reduce antimicrobial consumption in livestock industries. However, the projection analyses show that the global veterinary antimicrobial consumption continues to increase. Against this backdrop, this study examines the operationalization of livestock-targeted AMR measures in Thailand. In

addition to tracing operational processes, this analysis aims to investigatelocal and contextual factors that shape and complicate AMR policy operationalization.

Methods

This study employed a qualitative research approach, comprising in-depth interviews and document analysis. Ten interviewees were recruited through purposive sampling owing to their responsibilities in implementing livestock-targeted AMR measures in the Thai pig production systems. Policy documents relating to these measures, in both Thai and English, were reviewed.

Results

Our analysis reveals that when livestock-targeted AMR measures are introduced, the conceptualisation of AMR shifts from a health risk framework to a production problem one as evidenced by the emphasis placed on production standard controls. Interestingly, the production problem framework institutionalizes two parallel systems. The former focuses on establishing AMR surveillance in food animals to satisfy reporting requirements of global health treaties; and the latter enforces antibiotic regulations at the farm level through incentive programs that reward low antimicrobial consumption.Crucially the data that underpin these systems are never linked. The gaps between AMR surveillance systems and measures of farm level antibiotic use create incomplete feedback loops which fail toprovide actionable data to support local officials, and, more broadly, national interests.

Conclusions

Thailand's response to AMR in agriculture can be viewed as an incomplete response to heightened global health concerns about the threats posed by AMR in low-and-middle income countries (LMICs).The lack of connection and co-ordination between AMR surveillance systems and measures of farm level antibiotic use can be construed as a product of tensions between the goals of protecting human health and sustaining agricultural productivity. Based on findings, this analysis advocates for more research and policies that prioritize creating a virtuous feedback cycle that can enhance how antibioticsare used, rather than the current information systems that are strongly oriented towards meeting global health reporting requirements.

---

459 – Accelerators for Collaborative One Health Concepts to Actions: Countries Case Studies

Yin Myo AYE, Sarah VANDYK
FAO, Regional Office for Asia and the Pacific

Background

In the past decades, the high disease burden from zoonoses and One Health threats have highlighted the critical attention needed to address the threats posed to human health, animal health and production, as well as ecosystems. By fostering trans-sectoral coordination through, stakeholders can better manage risks through a One Health lens, and implement effective prevention and response strategies.

Methods

While there are numerous publications and guidelines available on One Health implementation, this article provides accelerators drawn from tangible examples of countries with One Health implementation experience and regional One Health initiatives in Southeast Asia to bolster the One Health strategies and implementation.

Results

One Health collaboration is inclusive of human health, animal health, plants, ecosystems, food security, production, and livelihood. Key insights from experiences in Southeast Asia can be harnessed to enhance the operationalization of One Health while also strengthening each sector in promoting responses to zoonotic and One Health threats, effectively transitioning from concept to action. Harmonizing the roles of various sectors, disciplines and stakeholders in One Health coordination is essential, as the collaborative approach encourages shared responsibility and ownership over sustainability efforts. Formalization with policy or legislation can bolster the functions and operations of the coordination mechanism, with inclusive representation within the governance structure. Academia and educators act

as valuable allies in embedding the One Health concept within educational frameworks that can promote awareness, an open mindset, preventive behaviour, and community engagement. Essentially, the integration of One Health activities with routine implementation supported by an effective monitoring and evaluation system is crucial. Advocacy at the policy level and among stakeholders is important for ensuring sustainability. One Health tools can support to address various One Health elements, enabling more efficient initial engagement across multiple sectors in each country.

Conclusion

Countries in the Southeast Asian region have operationalized One Health in unique approaches. By sharing countries' experiences, key insights into the accelerators that have contributed to successful One Health implementation will help other countries to operationalize One Health to suit their specific needs and context. This can also support strengthening each sector in promoting competencies included under the Joint External Evaluation and responses to zoonotic and One Health threats effectively, transitioning from concepts to actions.

---

473 – Reducing tick density along recreational trails in Ottawa, Canada: results from an integrated ecotone modification study using deltamethrin-treated and untreated woodchip barriers

Katarina OST (1), Roman MCKAY (1), Alexander STONE (2), Alison KRENTEL (3), Kate ZINSZER (4), Cindy FENG (5), Manisha KULKARNI (1)

1: University of Ottawa, School of Epidemiology and Public Health, Ottawa, ON, Canada; 2: The National Capital Commission, Ottawa, ON, Canada; 3: Bruyere Research Institute, Ottawa, ON, Canada; 4: Centre de recherche en santé publique (CReSP), Université de Montréal et Centre intégré de santé et de services sociaux du Québec du Centre-Sud-de-l'Île-de-Montréal, Montréal, QC, Canada; 5: Dalhousie University, Halifax, NS, Canada

Background: There is an increasing need for novel tick control strategies in many parts of Canada, including in Ottawa, Ontario, due to expanding tick populations and rising Lyme disease incidence. *Ixodes scapularis* ticks are the primary vector species responsible for the transmission of the Lyme disease bacteria (*Borrelia burgdorferi* sensu stricto (s.s.)) in this area. The rapid emergence of Lyme and other tick-borne diseases reflects complex interactions between environmental factors, wildlife host dynamics, and human use of peri-urban landscapes. Addressing this public health challenge therefore requires a multi-faceted, One Health approach to reduce public health risks, including mitigation strategies to reduce human exposure in recreational settings. **Methods**: We performed a 2-year experimental field trial at two sites in the Ottawa greenbelt to assess the effectiveness of ecotone modification to reduce questing tick density in a recreational setting. In each site, we allocated ten 50-metre trail segments to two intervention groups (one-meter-wide woodchip substrate borders, or deltamethrin treated woodchip borders placed alongside trails) or an untreated control group using stratified block randomization. Pre-treatment tick drags were completed at the beginning of each season, and environmental data were collected on canopy coverage, canopy type, soil moisture, and leaf litter depth. Post-intervention tick drags were completed at weekly intervals for 6 weeks in June-July 2022 and 2023, corresponding to peak nymphal tick season for both study years. We assessed the effect of treated and untreated woodchips compared to the control group on tick density using a mixed effects negative binomial regression. We controlled for the effects of weekly repeated sampling and randomization block as random effects as well as the possible effects of year, trail site, pre-treatment tick density, and environmental factors determined to be significant in a bivariate analysis at p0.05 significance level as fixed effects. **Results**: Of the 440 collected ticks (all species and stages) throughout the study period, 322 were adult or nymphal *I. scapularis* ticks. Out of 293 successfully tested ticks, 101 (34.5%) were positive for *B. burgdorferi*. The regression model revealed that treated woodchips significantly reduced *I. scapularis* adult and nymphal tick density by 99% (IRR=0.01, 95% CI: 0.001-0.08) when compared to control trail segments, whereas untreated woodchips reduced the density of *I. scapularis* adults and nymphs by 48% (IRR=0.52, 95% CI: 0.34-0.78). **Conclusions**: Ecotonal borders of both deltamethrin-treated, and untreated woodchip barriers significantly reduce tick densities in a recreational setting. These findings add to a growing list of One Health aligned treatment options that can be used to combat the rising issue of human tick encounters, as well as Lyme disease incidence.

478 – Linking National Biodiversity Strategies and One Health Action Plans: A Structured Method to Operationalize Biodiversity–Health Synergies

Jonathan SLEEMAN (1), Shruti GOGIA (2), Scott NEWMAN (2)

1: University of Minnesota, United States of America; 2: Food and Agriculture Organization of the United Nations, Regional Office for Asia and the Pacific, Thailand

Background

National Biodiversity Strategies and Action Plans (NBSAPs) and national One Health (OH) frameworks, including OH Strategic Action Plans, are central instruments for achieving the Kunming–Montreal Global Biodiversity Framework (GBF) targets and the One Health Joint Plan of Action (OH-JPA) action tracks, respectively. Despite substantial thematic overlap, these planning instruments are often developed and implemented in sectoral silos, limiting opportunities for coordinated action, co-financing, and measurable co-benefits. This project aimed to develop and apply a structured methodology to identify, map, and operationalize linkages between biodiversity and OH priorities at the national level.

Methods

We systematically reviewed publicly available NBSAPs and national OH Action Plans or equivalent documents across Asia and the Pacific. Five countries, Afghanistan, Bhutan, Sri Lanka, Thailand, and Viet Nam, had published both instruments and were included. A structured comparative policy analysis was then conducted to assess alignment, convergence, and operational synergies. Strategic objectives, priority actions, and investment opportunities were systematically extracted and mapped to identify points of convergence and divergence. Identified linkages were categorized using a defined synergy typology distinguishing direct overlaps, complementary actions, and shared co-benefit opportunities. Priority interventions were further assessed using an implementation-readiness and investment lens, considering alignment with GBF and OH-JPA targets, feasibility within existing institutional mandates, and potential for multi-sector delivery.

Results

Across countries, seven recurring priority areas emerged: (1) wildlife disease surveillance integrated with biodiversity monitoring systems; (2) human–wildlife conflict management linked to zoonotic risk reduction, including the creation of buffer zones; (3) livestock–wildlife biosecurity; (4) antimicrobial resistance (AMR) surveillance across environmental pathways; (5) climate-resilient ecosystem restoration for health security; (6) food safety and environmental contaminant monitoring; and (7) interoperable environmental–health data platforms. Digital surveillance infrastructure, biodiversity information-sharing mechanisms, and early warning systems consistently emerged as cross-cutting integration enablers. These findings indicate that biodiversity-health integration is not only conceptually aligned but institutionally feasible through coordinated governance, interoperable data systems, and jointly financed prevention-oriented investments.

Conclusions

Systematically linking NBSAPs and OH plans can transform parallel sectoral strategies into integrated, investment-ready action packages. The results enable countries to develop joint operational workplans outlining shared outcomes, responsible institutions, and integrated monitoring and evaluation frameworks. The crosswalk methodology and synergy typology provide a replicable framework for operationalizing biodiversity–health integration, strengthening institutional coordination, and accelerating progress toward both GBF and OH objectives. The findings also informed the development of an environmentally focused OH investment case in Bhutan.

487 – Bridging the Gap: A One Health Joint Risk Assessment of Rabies Persistence in Ubon Ratchathani, Thailand (2020–2025)

Pawinee DOUNGNGERN (1), Wansane TOANAN (2), Pumipat YODCHOMPOO (1), Serge MORAND (3,4,5), Soawapak HINJOY (6)

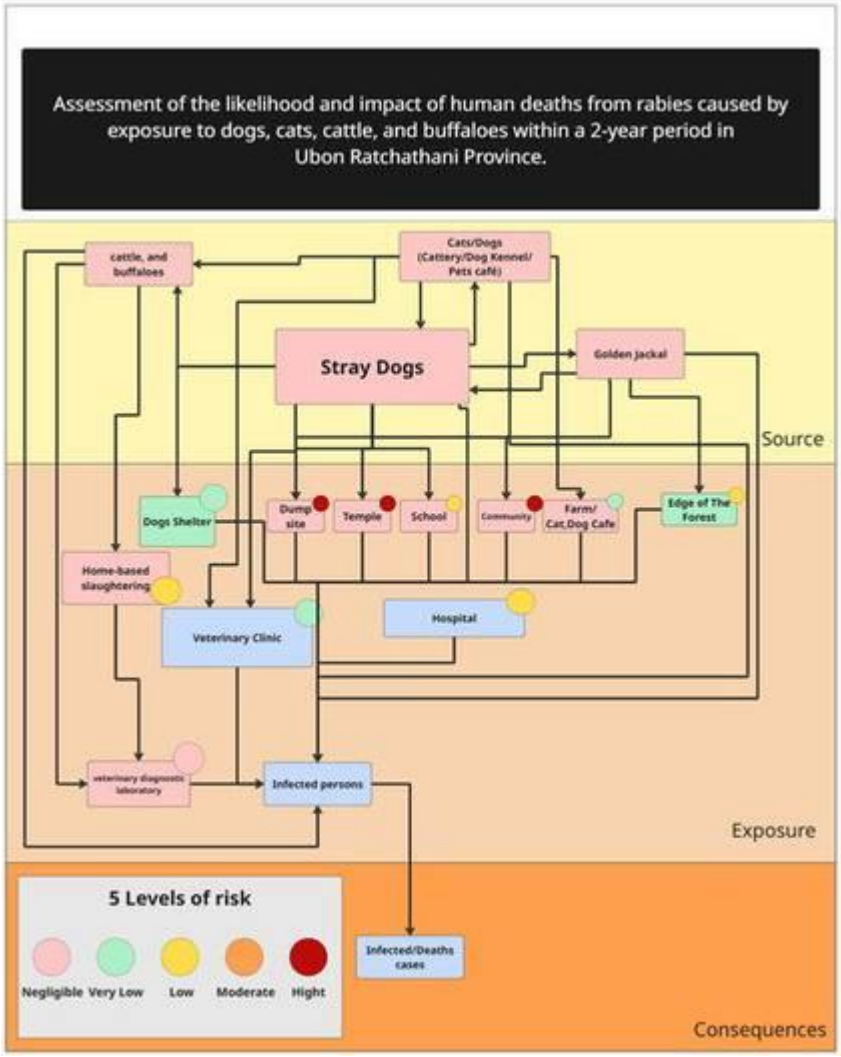
1: Division of Epidemiology, Department of Disease Control, Ministry of Public Health, Thailand; 2: Wildlife Conservation Office, Department of National Parks, Wildlife and Plant Conservation, Thailand; 3: IRL HealthDEEP CNRS; 4: Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand; 5: Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand; 6: Department of Disease Control, Ministry of Public Health, Thailand

Background: Thailand aims to eliminate dog-mediated human rabies by 2030. While human deaths have declined, animal rabies remains enzootic in provinces like Ubon Ratchathani. This persistent transmission at the human-animal-environment interface threatens public health security and creates a significant economic burden. This study applied a One Health Joint Risk Assessment (JRA) to move beyond traditional surveillance analysis by jointly identifying risk pathways, evaluating likelihood, identifying underlying drivers, and determining priority intervention points across sectors to inform risk-based interventions.

Methods: We conducted a descriptive analysis of national human and animal rabies surveillance data (2020–2025). In addition, a qualitative Joint Risk Assessment (JRA) was performed in December 2025 using the FAO–WOAH–WHO Operational Tool. This participatory process engaged stakeholders from public health, livestock, local government and community sectors in Ubon Ratchathani to jointly map transmission pathways. Risk pathways were identified across three high-interaction nodes: residential communities, temples, and waste dump sites. Likelihood, impact, and uncertainty were quantified using a standardized risk matrix to prioritize actionable interventions.

Results: While zero human rabies cases were reported during 2020–2025, animal transmission remained high, with a median of 22.5 confirmed cases annually (range: 5–62); 83% occurred in dogs. The JRA identified community settings as "Very High Risk" due to high stray dog density and sub-optimal vaccination coverage. Temples and dump sites were classified as "High Risk" nodes, as unmanaged reservoirs sustaining transmission. Despite the lack of human mortality, the economic impact is severe, with post-exposure prophylaxis (PEP) costs totaling approximately 166 million THB. The participatory JRA process revealed key root drivers, including ineffective stray population management, gaps in animal-vaccination ring-fence. These findings enabled stakeholders to jointly define targeted actions focusing directly on source control and high-risk environmental nodes.

Conclusion: This study demonstrates that One Health Joint Risk Assessment is an effective tool for identifying root causes of rabies persistence and translating complex epidemiological risks into tangible, cross-sectoral interventions. By focusing on high-risk environmental nodes and animal reservoirs, JRA supports evidence-based prioritization of actions, including strengthened dog population management, targeted vaccination strategies, and coordinated governance mechanisms Integrated data sharing between livestock and health sectors is critical to sustaining elimination.



489 – Operationalising One Health coordination for zoonotic hepeviruses: the ONWARD implementation model across European countries

Antonio RIVERO-JUAREZ (1,2), Branko VELEBIT (3), Reimar JOHNE (4), Florence ABRAVANEL (5), Gabor REUTER (6), Susanne DUDMAN (7,8), Nassim KAMAR (9), Lorena JEMERSIC (10), Ilaria DI BARTOLO (11), Imran HASSANOGLU (12), Adriana ANIȚĂ (13), Nigel COOK (14), Simona RUTA (15,16), Joao MESQUITA (17,18)

1: Clinical Virology and Zoonoses Research Group, Unit of Infectious Diseases, Hospital Universitario Reina Sofía, Instituto Maimónides de Investigación Biomédica de Córdoba (IMIBIC), Universidad de Córdoba (UCO), Córdoba, Spain; 2: Centro de Investigación Biomédica en Red de Enfermedades Infecciosas (CIBERINFEC), Instituto de Salud Carlos III, Madrid, Spain.; 3: Institute of Meat Hygiene and Technology, 11040 Belgrade, Serbia.; 4: Department of Biological Safety, German Federal Institute for Risk Assessment, Berlin, Germany; 5: Laboratoire de Virologie, Centre Hospitalier Universitaire de Toulouse, 31300 Toulouse, France; Institut Toulousain des Maladies Infectieuses et Inflammatoires (Infinity), CNRS U5051, INSERM U1291, Université de Toulouse, Toulouse, France.; 6: Department of Medical Microbiology, Medical School, University of Pécs, Szigeti út 12, Pécs, H-7624, Hungary; 7: Institute of Clinical Medicine, University of Oslo, Oslo, Norway.; 8: Department of Microbiology, Oslo University Hospital, Oslo, Norway; 9: Toulouse Rangueil University Hospital, INFINITY-Inserm U1291-CNRS U5051, Université de Toulouse, Toulouse, France; 10: Department of Virology, Croatian Veterinary Institute, 10000 Zagreb, Croatia; 11: Department of Food Safety, Nutrition and Veterinary Public Health, Istituto Superiore di Sanità, Rome, Italy; 12: Ankara Yildirim Beyazit University Faculty of Medicine, Ankara, Türkiye; Ankara Bilkent City Hospital, Infectious Diseases and Clinical Microbiology Department, Ankara, Türkiye; 13: "Ion Ionescu de la Brad" Iasi University of Life Sciences, Regional Center of Advanced Research for Emerging Diseases, Zoonoses and Food Safety, Romania.; 14: Jorvik Food Safety Services, York YO32 2GN, UK.; 15: "Carol Davila" University of Medicine and Pharmacy, Bucharest, Romania.; 16: "Stefan S. Nicolau" Institute of Virology, Bucharest, Romania.; 17: Clínicas Veterinárias, Instituto de Ciências Biomédicas Abel Salazar (ICBAS). Centro de Estudos de Ciência Animal (CECA), Instituto de Ciências, Tecnologias e Agroambiente (ICETA) Universidade do Porto. Porto, Portugal.; 18: Associate Laboratory for Animal and Veterinary Science (AL4AnimalS). Portugal.

Background: Zoonotic hepevirus infections are a growing yet under-addressed One Health challenge in Europe. HEV is a leading cause of acute viral hepatitis in many countries and ratHEV is increasingly recognised in humans, but the main limitation is an implementation gap. Surveillance still relies largely on retrospective, case-based signals and runs through parallel sectoral streams (human, animal, food-chain and environment) using different standards, denominators, spatial units and time scales. This fragmentation limits early interpretation of upstream change and coordinated prevention and contributes to heterogeneous diagnostic capacity and inconsistent clinical pathways in high-risk populations. Here, we present ONWARD, a pan-European implementation network designed to operationalise One Health coordination for zoonotic hepeviruses by harmonising standards and accelerating uptake across sectors.

Material and Methods: ONWARD (COST Action CA24140) is an EU-funded implementation network that operationalises One Health coordination for zoonotic hepeviruses across 32 European countries. It is structured into five Working Groups spanning diagnostics, clinical management, integrated surveillance, communication/training and policy alignment. Implementation is delivered through: (i) systematic mapping of current practice and capacity using harmonised tools (diagnostic algorithms, clinical pathways and surveillance protocols); (ii) co-development of interoperable standards and minimum datasets (SOPs for serology/molecular testing, sequencing workflows, case definitions, outcome measures and denominators); and (iii) deployment and uptake via COST instruments, including Training Schools, Short-Term Scientific Missions and targeted workshops.

Results: In the first six months, ONWARD has moved from framework to implementation. The governance and stakeholder-engagement structure of the Action have been internally mapped against the SAPEA One Health Operational Checklist to assess alignment with recommended European principles for effective coordination. The Action website and communication channels are now active, the first calls for Short-Term Scientific Missions and Conference Grants have been opened, and capacity-building activities have begun to support the uptake of harmonised methods across countries and sectors. A first training school on HEV and ratHEV sequencing has been organised to align sequencing workflows across clinical, veterinary, food and environmental sectors, enabling comparable genomic outputs. In addition, an initial situational report on HEV diagnostic practices in Europe, developed in dialogue with European public-health stakeholders, has helped identify priority gaps across countries and sectors and guide where harmonisation efforts should focus next. An External Scientific Advisory Committee including six HEV experts from Asia, Africa and the Americas has been established to strengthen global perspective. All planned and ongoing tasks are summarised in Table 1.

Conclusions: ONWARD is establishing a practical implementation pathway to reduce fragmentation and translate One Health evidence into coordinated diagnostics, surveillance and clinical management for zoonotic hepeviruses across Europe. By combining harmonised standards, structured capacity-building and stakeholder engagement, the Action provides a scalable model for operationalising One Health collaboration and strengthening preparedness for other zoonotic viruses.

Area of interest	What will be implemented
Diagnosis & Comprehensive Surveillance	• Harmonised laboratory standards across sectors: molecular protocols, serology evaluation protocols, sequencing/typing/WGS workflows. • Expanded detection in non-canonical matrices (food, surfaces, wastewater): consensus protocol for sampling and diagnosis. • Technology readiness for rollout: evaluation of cutting-edge diagnostics and AI-based surveillance systems. • Operational surveillance package: guidelines for active surveillance.
Clinical Management & Therapeutics	• Clinical harmonisation package: standards for clinical trials and outcome measurement criteria. • Decision-support enablers: validated biomarkers for infection outcomes. • Orphan-drug implementation pathway: consolidated report on potential antiviral compounds to guide prioritisation and next steps.
Prevention & Control	• Prevention guidance at key control points: farm-level risk management guidelines, hunting/environment risk reduction protocols, food safety and culinary practice protocols with public-facing brochures/infographics. • Evidence packages for risk management: animal product risk assessment and vaccine safety/efficacy review report. • Standardised infectivity assessment: cell culture protocol for infectivity analysis.

493 – Connecting Agricultural Practices and Zoonotic Risk in Rural The Gambia: Ethnographic Insights for One Health

Hellena DEBELTS
Robert Koch Institut, Germany

Background

Agricultural landscapes create contact interfaces where humans, livestock, wildlife, and vectors interact in ways that shape zoonotic disease transmission. Recently, The Gambia reported an avian influenza outbreak, while CCHF and RVF cases have been detected in all surrounding regions of Senegal. In rural The Gambia, human–animal interactions unfold within mosaic environments of village compounds, cultivated fields, wetlands, bushlands, and seasonal grazing areas. These landscapes are actively produced through farming, herding, and hunting. Understanding how everyday agricultural practices structure multispecies contact is therefore crucial for identifying ecological interfaces where zoonotic risks may emerge.

Methods

This study draws on twelve months of ethnographic fieldwork conducted within the transdisciplinary SENZOR project (A socio-ecological network approach to understanding zoonotic outbreak risk) in two rural villages in The Gambia's Central River Region. The villages represent contrasting agricultural ecologies: one located near forests and the river, the other in a more open savannah setting. Methods included participant observation, semi-structured interviews, and participatory mapping documenting farming practices, livestock management, wildlife encounters, and seasonal movements of people and animals across compounds, fields, wetlands, and surrounding bushlands.

Results

The analysis identifies three dynamics shaping multispecies interaction: crop choice, labour routines, and seasonal farming cycles. Rice cultivation involves intensive ploughing, planting, and harvesting that often bring women into close proximity with mosquitoes and rodents inhabiting field burrows. Maize, pumpkin, and watermelon attract non-human primates, prompting children and men to guard fields and occasionally kill these animals. Groundnut and millet cultivation structure livestock movements, including restrictions on small ruminant roaming and the timing of cross-border cattle migration into Casamance. After harvest, livestock return to graze crop residues in post-harvest fields alongside other animals. Groundnuts also attract bush pigs, while harvesting, processing, and storage practices draw rodents from fields into granaries and domestic spaces. Villagers further associate dense vegetation and cultivated areas with ticks, mosquitoes, humidity, and heat. Across both sites, seasonal farming cycles—including field clearing, ploughing with draft animals, weeding, harvesting, processing, storage, post-harvest grazing, and manure fertilization—create recurring but distinctly variating moments when agricultural labour, livestock grazing, wildlife foraging, and vector activity converge across space and time. These interactions are further shaped by deforestation, agricultural expansion, soil salinization, and changing rainfall patterns. The comparative design shows how different agricultural landscapes generate distinct multispecies contact patterns.

Conclusions

While One Health research identifies agricultural change as a driver of zoonotic emergence, less attention has been given to the social and seasonal practices organizing multispecies contact in rural landscapes. This study provides one of few ethnographic accounts of how everyday agricultural practices generate zoonotic interfaces in West Africa. Identifying these practice-based contact moments can strengthen landscape-sensitive One Health surveillance and support more targeted responses to zoonotic risk in rapidly changing rural environments.

501 – From Global Expectations to Federal Action: An Alignment Analysis of Antimicrobial Stewardship Governance in Canada with the Proposed Updated Global Action Plan on Antimicrobial Resistance

Shauna THOMAS
University of Ottawa, Canada

BackgroundIn response to the major global threat of Antimicrobial Resistance (AMR), the 2015 Global Action Plan on Antimicrobial Resistance (GAP) established a coordinated global framework and called on states to develop aligned national action plans. Canada's current national strategy, the Pan-Canadian Action Plan on AMR (PCAP), was updated in 2023 and remains in effect until 2027. The official draft of an updated GAP (GAP 2.0) was released in January 2026, with adoption anticipated later in 2026. Both instruments function as soft law, shaping state behaviour through normative guidance rather than binding obligations.

This research examines how Canada's antimicrobial stewardship (AMS) approach matches with emerging global expectations under GAP 2.0 and identifies strengths and gaps within Canada's governance framework. The study targets AMS because of its central role in mitigating AMR and because it allows for a deeper examination of stewardship-related policy tools. In addition to providing insight into Canada's current AMS governance landscape and future policy directions, the study offers a replicable analytical approach that other researchers can use to assess alignment between national or an organization's action plans and the updated global framework.

MethodsThe study used an alignment analysis framework comparing AMS-related guidance provisions in the draft GAP 2.0 with those contained in the PCAP. Guidance provisions were identified through a two-stage review and assessed using a coding framework adapted from previous alignment studies (Willemsen et al., 2022). Each GAP 2.0 provision was categorized as strongly aligned, partially aligned, or not aligned with PCAP provisions.

Results were presented using a colour-coded comparison table (Table 1) where GAP 2.0 provisions were placed on the vertical-axis as the reference standard representing emerging global expectations, while PCAP provisions were placed on the horizontal-axis to assess how Canada's national stewardship actions align with those international guidance provisions. Green cells reflect strong alignment, yellow partial alignment, and red no alignment.

ResultsThe alignment analysis identified 17 AMS-related guidance provisions in GAP 2.0 and 8 AMS-relevant provisions in the PCAP. The overall alignment score was 23/34 (67%), indicating moderate alignment between Canada's national action plan and emerging global stewardship guidance. Eight provisions demonstrated strong alignment, seven showed partial alignment, and two showed no alignment. Areas of strongest alignment included awareness and education, and multisectoral governance. The weakest alignment was observed in environmental stewardship provisions.

ConclusionsCanada's AMS framework shows moderate alignment with developing global expectations, suggesting general readiness to adapt to the upcoming GAP 2.0. However, the analysis highlights environmental stewardship, including antimicrobial disposal and environmental contamination pathways, as an underdeveloped component of Canada's AMS governance framework. Strengthening environmental stewardship within national action planning represents an important opportunity to improve policy coherence and advance a more balanced One Health response to AMR.

504 – First Genomic Detection of Veterinary Viruses of Concern at Human–Animal Interfaces in Rural Ghana Using a One Health Metagenomics Framework

Julia PAOLI (1,2,3,4), Nídia S. TROVÃO (5,6,7,8), Theo ODOOM (9), Quaneeta MOHKTAR (10), William TASIAME (11), Benita ANDERSON (12), Daniel TAWIAH-YINGA (9), Kuttichantran SUBRAMANIAM (1,13), Michael VON FRICKEN (1,2,4), Ivy Gloria MENSAH (10), Sherry Ama Mawuko JOHNSON (14), **Carla MAVIAN** (1,3,15,16)

1: Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; 2: Department of Environmental and Global Health, University of Florida, Gainesville, FL, USA; 3: Department of Pathology, Immunology and Laboratory Medicine,

University of Florida, Gainesville, FL, USA; 4: One Health Center of Excellence, College of Public Health and Health Professions, University of Florida, Gainesville, Florida, USA; 5: Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, Bethesda, Maryland, USA; 6: Department of Pathobiology, College of Veterinary Medicine, University of Illinois Urbana-Champaign, Urbana, IL, USA; 7: Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign, Urbana, IL, USA; 8: National Center for Supercomputing Applications, University of Illinois Urbana-Champaign, Urbana, IL, USA; 9: Accra Veterinary Laboratory, Veterinary Services Directorate, Accra, Ghana; 10: Noguchi Memorial Institute for Medical Research, University of Ghana, Accra, Ghana; 11: School of Veterinary Medicine, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana; 12: Veterinary Services Directorate, Ministry of Food and Agriculture, Accra, Ghana; 13: Department of Infectious Diseases & Immunology, College of Veterinary Medicine, University of Florida, Gainesville, Florida, 32610, USA; 14: School of Veterinary Medicine, CBAS, University of Ghana, Accra, Ghana; 15: Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa; 16: Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Stellenbosch, South Africa

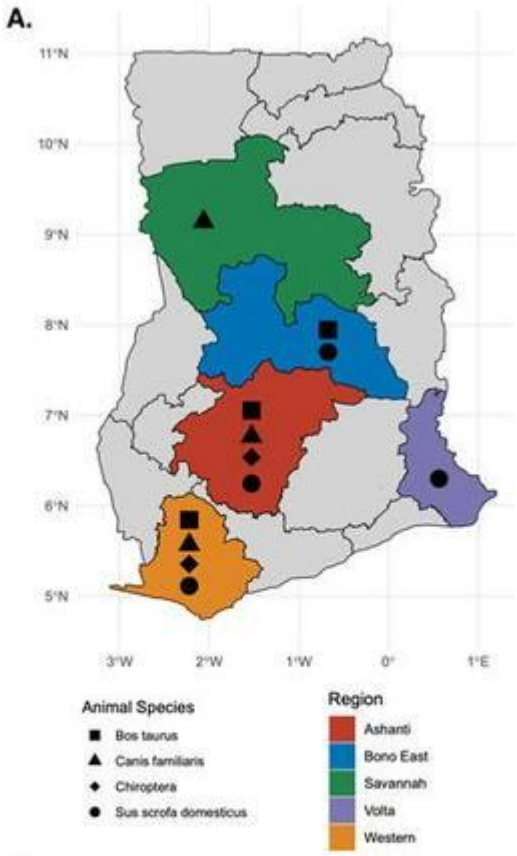
BackgroundViruses of veterinary importance threaten animal health, livestock productivity, and local economies, particularly in regions with dense livestock populations and frequent human–animal interactions. Genomic surveillance remains limited in many parts of West Africa, leaving important gaps in understanding pathogen circulation and potential cross-species transmission. This study aimed to identify pathogenic viruses of veterinary relevance across livestock (cattle, pigs), domestic animals (dogs), and wildlife (bats) in Ghana.

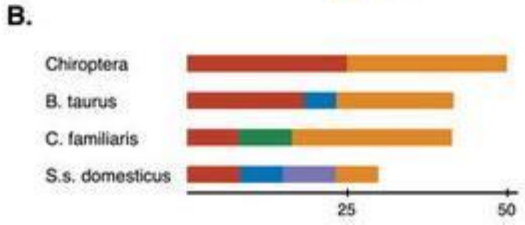
Materials and Methods Animals were sampled in 2023 from communities in five of Ghana's 16 administrative regions (Figure 1). Viral RNA was extracted from serum and tissue samples, converted to cDNA, and sequenced using the Illumina NextSeq. Viral genomes were identified through de novo assembly using MEGAHIT. Phylogenetic relationships were reconstructed using IQ-TREE and BEAST.

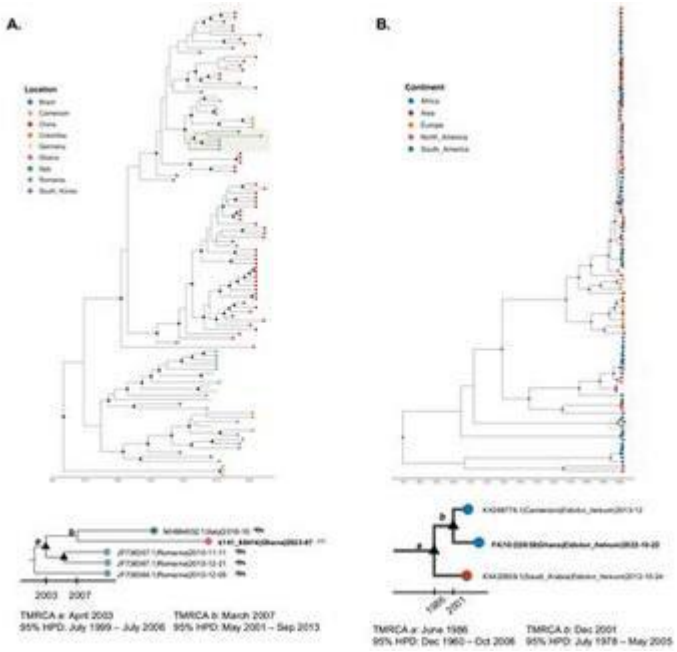
Results

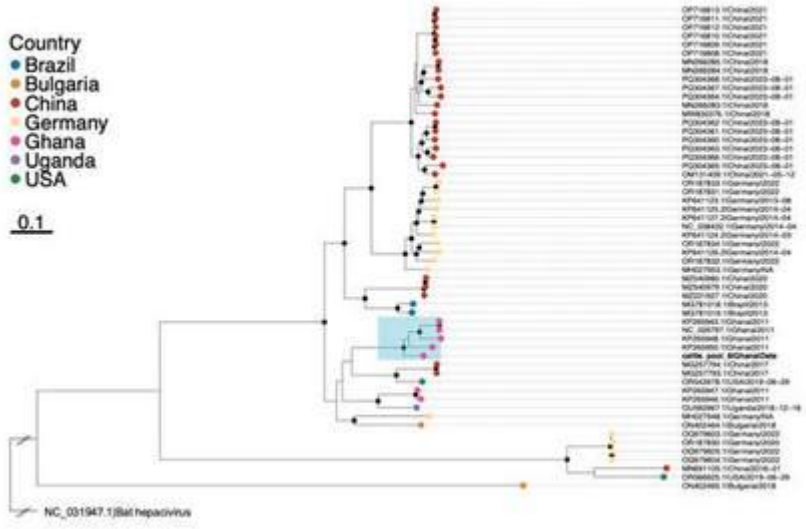
We sampled 165 animals comprising cattle (n = 43), pigs (n = 30), dogs (n = 42), and six species of wild bats: *Eidolon helvum* (n = 8), *Epomops buettikoferi* (n = 22), *Epomops franqueti* (n = 7), *Hypsignathus monstrosus* (n = 1), *Lissonycteris angolensis* (n = 1), and *Nanonycteris veldkampii* (n = 11). We generated full-genome sequences of Porcine Parvovirus 3 (PPV3) in pigs, Bovine hepacivirus (BovHepV) in cattle, and Canine Parvovirus (CPV) in dogs, along with a complete Rotavirus A (RVA) segment 1 genome from a straw-colored fruit bat (*Eidolon helvum*). The Ghanaian PPV3 strain clustered with European wild boar sequences, suggesting possible intercontinental links and underscoring the need for improved surveillance in pig populations [Figure 2]. Phylodynamic reconstruction estimated the TMRCA of our Ghanaian PPV3 strain to be March 2007 [Figure 2]. The bat-derived RVA grouped with *E. helvum* strains from Cameroon and Saudi Arabia in the 16R VP1 genotype lineage [Figure 2]. The estimated TMRCA of the Ghanaian RVA sequence was December 2001 [Figure 2]. BovHepV clustered with Ghanaian cattle sequences from 2011, indicating sustained circulation and representing the first publicly available genome from Ghana in over a decade [Figure 3]. The CPV genome grouped within genotype 2c and showed highest similarity to Chinese strains, constituting the first publicly available CPV-2c sequence from Ghana. Together, these findings reveal the circulation of diverse viral pathogens across domestic animals and wildlife in Ghana and highlight the value of metagenomic approaches for detecting viruses at the animal–human interface.

ConclusionsThese findings demonstrate the value of genomic surveillance at wildlife–livestock interfaces for detecting viruses circulating across multiple host species. By generating new viral genomes for Ghana, including the first publicly available sequences in over a decade for some pathogens, this study provides baseline data for monitoring viral evolution and transmission pathways. Expanding genomic surveillance in Ghana and across West Africa will support early detection of emerging pathogens and improve prevention and control strategies for viruses of veterinary and zoonotic importance.


A.
11°N
10°N
9°N
8°N
7°N
6°N
5°N
3°W
2°W
1°W
0°
1°E
Animal Species
Bos taurus
Canis familiaris
Chiroptera
Sus scrofa domesticus
Region
Ashanti
Bono East
Savannah
Volta
Western


B.
Chiroptera
B. taurus
C. familiaris
S.s. domesticus
25
50


A.
B.
2003
2007
TMRCA a: April 2003
95% HPD: July 1999 – July 2006
TMRCA b: March 2007
95% HPD: May 2001 – Sep 2013
TMRCA a: June 1986
95% HPD: Dec 1960 – Oct 2008
TMRCA b: Dec 2001
95% HPD: July 1978 – May 2005



514 – Practitioner's perspectives on Access to Rabies Post-Exposure Prophylaxis in Tanzania: A mixed-methods and theoretically-informed study to inform policy and practice

Kennedy LUSHASI (1), Eleanor REES (2), Camille BARKER (2), Nai Rui CHNG (2), Ally HALFAN (1), Christian Tetteh DUARMOR (1), Elaine FERGUSON (2), Felix LANKESTER (3,4), Husna HOFFU (2), Joel CHANGALUCHA (1), Lwitiko SIKANA (1), Mikolaj KUNDEGORSKI (2,5), Katie HAMPSON (2)

1: Ifakara Health Institute, Tanzania; 2: School of Biodiversity, One Health & Veterinary Medicine, College of Medical, Veterinary & Life Sciences, University of Glasgow, Glasgow, UK; 3: Paul G. Allen School for Global Animal Health, Washington State University, Pullman, Washington, United States of America; 4: Global Animal Health Tanzania, Arusha, Tanzania; 5: Fjelltopp Ltd, UK,

IntroductionRabies remains a preventable yet fatal disease that continues to claim lives in low- and middle-income countries due to barriers in accessing post-exposure prophylaxis (PEP). With Gavi, the Vaccine Alliance, now supporting PEP provision in rabies-endemic countries, understanding access barriers is critical.

MethodsWe used mixed-methods to synthesise quantitative data on bite patients (>10,000) captured through an Integrated Bite Case Management platform across four regions of Tanzania, with qualitative data from hotline calls and peer-support chat established among health and veterinary workers from 2018 to 2024. We applied an expanded healthcare access framework comprising six dimensions: availability, accessibility, affordability, accommodation, acceptability, and appropriateness to guide our analyses and assess barriers and facilitators to PEP delivery and uptake in these regions.

ResultsWe identified interconnected barriers to PEP access including recurrent vaccine stockouts (up to 9.2% regionally); long travel distances that were greater for rural patients (on average: 34 vs 13 km for urban patients) who represented the majority at risk; and unaffordable direct and indirect costs leading bite victims to either not start or abandon PEP, incur risky delays or default to traditional remedies. Incorrect bite patient management, including misuse of biologicals sold at unregulated private pharmacies led to preventable deaths, while insufficient vaccination supplies and inadequate service hours, increased risks and costs to patients. Despite these gaps, peer-support mechanisms improved patient management and real-time problem-solving.

Conclusions

PEP delivery in Tanzania is undermined by systemic barriers across all access dimensions. Addressing these requires decentralizing vaccine delivery to prioritized accessible facilities, ensuring reliable stock and supplies for intradermal administration, reducing patient costs, strengthening health worker capacity through training and support, and regulating private providers. Lessons from Tanzania highlight the need

for context-sensitive, equity-focused strategies to maximize the impact of Gavi's investment and accelerate progress toward Zero by 30.

525 – Strengthening One Health Preparedness for Leptospirosis in Puerto Rico: Integrated Surveillance, Clinical Decision Support, and Post Disaster Risk (2019–2021)

Ralph RIVERA-GUTIERREZ (1), Claudia MUNOZ-ZANZ (2), Luis J. SANTIAGO-RAMOS (3)

1: University of Puerto Rico Graduate School of Public Health, Puerto Rico (U.S.); 2: University of Minnesota School of Public Health, Minnesota (U.S.); 3: University of Puerto Rico School of Health Professions, Puerto Rico (U.S.)

Leptospirosis imposes recurrent clinical and public-health challenges in Puerto Rico, with case surges observed after extreme rainfall and hurricanes. To inform preparedness, we conducted active hospital-based surveillance for acute undifferentiated febrile illness (UAFI) across four emergency departments (2019–2021) and paired it with community animal sampling to identify reservoirs, serovars, and environmental triggers of spillover. Diagnostic confirmation relied on PCR and serology; data encompassed clinical syndromes, labs, and demographics.

We identified 28 cases (16 from active enrollment; 12 via referrals). Patients were predominantly male (71%; mean age 43 years) and commonly presented with lower back pain, headache, fatigue, vomiting, myalgia, and calf pain, alongside elevated AST, hyperglycemia, thrombocytopenia, proteinuria, and hematuria; severe disease included hemorrhagic signs and acute kidney injury with jaundice. Circulating strains included *L. interrogans* Icterohaemorrhagiae/Copenhageni, *L. borgpetersenii* Ballum/Guangdong, and *L. kirschneri* (no serovar match). Animal sampling revealed high positivity in rodents and dogs, consistent with urban reservoirs that amplify risk after environmental disruption.

Preparedness implications include: (1) deploying integrated One Health surveillance that fuses hospital case signals, veterinary and wildlife data, and hydrometeorological indicators into early-warning thresholds; (2) strengthening clinical decision support (triage pathways and diagnostics for UAFI in post-storm periods); (3) enhancing laboratory capacity and data-sharing across sectors; and (4) prioritizing targeted interventions (reservoir control and community risk communication). While economic evaluation was beyond our study scope, these measures are expected to reduce avoidable admissions and improve resource allocation by intervening at high-risk times and places. The work aligns with WOHC 2026's emphasis on preparedness, resilience, and evaluation of integrated interventions.

533 – Watershed condition shapes environmental AMR in Fiji, supporting nature-based solutions for upstream prevention

Alice LATINNE (1), Samuel J BLOOMFIELD (2), Alison E MATHER (2), Gemma LANGRIDGE (2), Lisa CROSSMAN (2), John WAIN (2), Serge MORAND (3), Christopher UZZELL (4), Ponipate BALEINAMAU (5), Akanisi CAGINITOBA (1), Maria LALAMACUATA (5), Waisea NAISILISILI (1), Kelera NAIVALU (5), Timoci NAIVALULEVU (5), Vilisi NAIVALULEVU (5), Ingrid QAUQAU (1), Mereia RAVOKA (1), Andrew TUKANA (1), Stacy JUPITER (1), Jacqueline THOMAS (4), Aaron JENKINS (4)

1: Wildlife Conservation Society, Suva, Fiji Islands; 2: Quadram Institute Bioscience, Norwich, UK; 3: Kasetsart University, Bangkok, Thailand; 4: University of Sydney, Sydney, Australia; 5: Fiji National University, Suva, Fiji

Antimicrobial resistance (AMR) is an emerging public health concern in Pacific Island countries, where wastewater pollution, climate change and agricultural intensification may accelerate environmental dissemination, yet surveillance outside clinical settings remains limited. Environmental AMR data are particularly scarce despite many communities relying on untreated surface waters for domestic use. Understanding how watershed condition influences environmental resistomes is therefore critical for identifying upstream prevention opportunities that complement existing AMR control strategies.

We collected water, sediment and sanitation swab samples from diverse environmental sources across 29 communities in five Fijian watersheds spanning gradients of anthropogenic activity and waterborne disease burden. Water samples were vacuum-filtered and DNA was extracted from filters as well as directly from sediment and swab samples. A total of 296 samples were sequenced using the Illumina MiSeq platform. Sequencing reads were processed using Kraken2 for taxonomic classification and

FastDeMe for identification of antimicrobial resistance genes (ARGs) across major antibiotic classes. Environmental drivers of ARG richness and composition were analysed using negative binomial generalized linear models and distance-based redundancy analysis (dbRDA) linking ARG patterns with land use, livestock density, human population and water quality indicators.

ARG richness varied strongly among sample types and watersheds. Sanitation swabs harboured the highest richness, followed by water and sediments. Across watersheds, total ARG richness varied 2.4-fold, indicating substantial spatial heterogeneity in environmental resistomes. Across all watersheds, β-lactam resistance genes were the most diverse class, while aminoglycoside, tetracycline, sulfonamide, phenicol, macrolide and diaminopyrimidine resistance genes were widespread.

Landscape-scale analyses revealed that watershed land use strongly shapes environmental AMR patterns. In aquatic environments, ARG richness increased with both forest cover and livestock density, and ARG composition followed a dominant gradient from forested to livestock-influenced catchments. Livestock-dominated waters were enriched in resistance genes associated with human and animal antibiotic use, whereas forested catchments were characterised by resistance genes typical of environmental bacteria, indicating a weaker anthropogenic AMR signal. In sediments, ARG patterns reflected land-use disturbance: ARG richness increased with timber plantation cover, while ARG composition was associated with both plantation cover and recent deforestation, revealing a disturbance gradient linked to agricultural intensification. Together, these findings demonstrate that watershed condition shapes environmental AMR pathways in Pacific Island settings.

These results provide empirical evidence that nature-based solutions, particularly forest protection, watershed restoration and sustainable land management, can help limit the environmental dissemination of antimicrobial resistance associated with human and livestock antibiotic use while strengthening climate-resilient One Health strategies. They position watershed conservation as a practical upstream intervention linking ecosystem management, public health and climate resilience in Pacific Island contexts.

537 – How causes of fever in southern Angola vary with age and season and associate with clinical outcomes: a hospital-based study.

Helga MAMEDE GONÇALVES (1), Maria ANTUNES (2,3), Jorge SEIXAS (1), Marcelo FERREIRA (1,4)

1: GHTM/IHMT/UNL, Portugal; 2: Faculty of Medicine, University Agostinho Neto; 3: Central Hospital Dr. António Agostinho Neto; 4: Department of Parasitology, Institute of Biomedical Sciences, University of São Paulo

Background: Acute febrile illnesses in sub-Saharan Africa are often attributed to malaria, yet many patients test negative for malaria parasites, complicating diagnosis and treatment. In southern Angola, data on the causes of fever beyond malaria remain scarce, hindering effective clinical management.

Methods: We conducted a hospital-based observational study, with 849 febrile patients across all ages (range, 2 months to 94 years) enrolled in September-October 2023 and May-June 2024 in two tertiary hospitals of Lubango city that serve 7 million people in southern Angola. We used clinical assessments and locally available laboratory diagnostics to assign likely causes of fever and applied logistic regression analysis to identify factors associated with an increased risk of hospital admission and death.

Results: We found that 67.6% of patients tested negative for malaria by microscopy, with upper (13.1%) and lower (19.4%) respiratory infections and gastrointestinal infections (16.7%) being leading causes of nonmalarial fever. The frequencies of specific clinical entities, such as gastrointestinal, upper respiratory, and genitourinary infections, varied markedly with age, and malaria predominated at the beginning of the dry season. Malaria and lower respiratory infections were associated with a significantly increased risk of hospitalization, while malaria and central nervous system infections were linked to higher mortality. Empirical antibiotic use was widespread, even among nonbacterial cases.

Conclusions: These findings underscore the need for improved diagnostic and risk stratification strategies to guide targeted treatment of febrile illnesses and reduce unnecessary antibiotic use in Angola's healthcare settings.

Table 1. Demographic characteristics, clinical presentation, and outcomes of study participants, Lubango city, Southern Angola, 2023-24.

Characteristic	Number (%)
Age (years)	
0.0-4.9	259 (30.5%)
5.0-14.9	165 (19.4%)
15.0-29.9	201 (23.7%)
30.0-44.9	123 (14.5%)
≥ 45.0	101 (11.9%)
Sex	
Female	385 (45.3%)
Male	464 (54.6%)
Hospital	
Children's Hospital Pioneiro Zeca	411 (48.4%)
Central Hospital Dr. Agostinho Neto	438 (51.6%)
Month of enrollment	
September 2023	260 (30.6%)
October 2023	241 (28.4%)
May 2024	285 (33.6%)
June 2024	63 (7.4%)
Pre-hospitalar care since symptom onset	
Previous visit to primary health care facility	286 (33.7%)
Use of antipyretics	537 (63.2%)
Use of antimalarials	140 (16.5%)
Use of antibiotics	177 (20.8%)
Fever	
Duration of reported fever (median [range], days)	4 (<1 to 60) days
Fever (axillary temperature ≥ 37.5°C) at presentation	790 (93.0%)
HIV infection status	
Self-reported HIV-positive status	17 (2.0%)
Positive rapid diagnostic test (RDT) for HIV at admission	32 (3.8%)
Self-reported or positive RDT at admission	37 (4.4%)
Nutritional anthropometry	
Children 0-4.9 years (weight data for n=254 and height data for n=247)	
Wasting (weight-for-age *z* score <-2.0)	105 (41.3%)
Stunting (height-for-age *z* -score <-2.0)	131 (53.0%)
Children and adolescents 5-19.9 years (weight and height data for n=229)	
Underweight (BMI-for-age *z* score <-2)	52 (22.7%)
Adequate weight (BMI-for-age *z* score from -2.0 to 0.9)	171 (74.7%)
Overweight (BMI-for-age *z* score from 1.0 to 1.9)	4 (1.8%)

Obesity (BMI-for-age *z* score ≥2.0)	2 (0.9%)
Adults ≥20 years (weight and height data for n=338)	
Underweight (BMI<18.5)	82 (24.3%)
Adequate weight (BMI from 18.5 to 24.9)	199 (58.9%)
Overweight (BMI from 25.0 to 29.9)	46 (13.6%)
Obesity (BMI≥30.0)	11 (3.2%)
Cause of fever identified at enrollment[a]	
Upper respiratory tract infection	111 (13.1%)
Lower respiratory tract infection	165 (19.4%)
Gastrointestinal or hepatic infection	142 (16.7%)
Genitourinary infection	43 (5.1%)
Central nervous system infection	22 (2.5%)
Skin/joint/mucosal infection	38 (4.5%)
Fever with another focus or no focus identified	103 (12.1%)
Positive microscopy for malaria	275 (32.4%)
28-day follow-up	
Complete recovery	558 (68.2%)
Partial recovery	157 (18.5%)
Death during hospital stay	103 (12.3%)
Transferred to another hospital	31 (3.6%)
Final outcome	
Discharge without admission	397 (46.8%)
Admission to the study hospital or another hospital	452 (53.2%)
Death at the study hospital or another hospital	108 (12.7%)

[a]One patient may be classified into two or more clinical syndromes.

Table 2. Cause of fever according to patient's age, Lubango city, Southern Angola, 2023-24.

	Frequency (%) by age group (years)						
Cause of fever identified at enrollment	**0.0-4.9**	**5.0-14.9**	**15.0-29.9**	**30.0-44.9**	**≥45.0**	**Total**	***P*** **(χ^2 test)**
Upper respiratory tract infection	46 (17.8%)	23 (13.9%)	22 (10.9%)	14 (11.4%)	5 (4.9%)	110 (12.7%)	0.016
Lower respiratory tract infection	45 (17.4%)	39 (23.6%)	34 (16.9%)	24 (19.5%)	24 (23.8%)	166 (23.8%)	0.336
Gastrointestinal or hepatic infection	66 (25.5%)	24 (14.6%)	24 (11.9%)	15 (12.2%)	13 (12.9%)	142 (16.7%)	<0.0001
Genitourinary infection	5 (1.9%)	5 (3.0%)	10 (5.0%)	11 (8.9%)	12 (11.9%)	43 (5.1%)	<0.0001
Central nervous system infection	6 (2.3%)	5 (3.0%)	6 (3.0%)	2 (1.6%)	3 (3.0%)	22 (2.6%)	0.933
Skin/joint/mucosal infection	17 (6.6%)	8 (4.8%)	5 (2.5%)	5 (4.1%)	3 (3.0%)	38 (4.5%)	0.274
Fever with another focus or no focus identified	24 (9.3%)	21 (12.7%)	28 (13.9%)	18 (14.6%)	12 (11.9%)	103 (11.9%)	0.495
Positive microscopy for malaria	68 (26.2%)	48 (29.1%)	79 (39.3%)	43 (35.0%)	37 (36.6%)	275 (32.4%)	0.028
Total	259	165	201	123	101	849	

Frequencies of the 3 most common diagnoses in each age group are underlined.

540 – Environmental and stigma-related factors associated with water and food insecurity among female sex workers and men who have sex with men living with HIV in Kampala, Uganda

Carmen LOGIE (1), Ying WANG (1), Moses OKUMU (2), Frannie MACKENZIE (1), Gerald PANDE (3), Aidah NAKITENDE (4), Brenda KATISI (4), Peter KYAMBADDE (3), Lawrence MBUAGBAW (5), Julien BRISSON (1)

1: Factor-Inwentash Faculty of Social Work, University of Toronto, Toronto, Canada; 2: Faculty of Social Work, University of Illinois at Urbana-Champaign, Urbana, USA; 3: Mulago Hospital, Kampala, Uganda; 4: Utafiti Kamili Centre, Kampala Uganda; 5: Department of Health Research Methods, Evidence and Impact, McMaster University, Hamilton, Canada

Background: Across sub-Saharan Africa, the frequency and intensity of extreme weather events (EWE) exacerbate food and water scarcity and intensify structural vulnerabilities (e.g., poverty and displacement) that limit access to HIV care and compromise treatment adherence. Food and water insecurity compromise the wellbeing of socially marginalized populations, including people living with HIV, yet important knowledge gaps remain regarding their co-occurrence and the broader environmental and social drivers shaping these intersecting resource insecurities. The study objective was to examine associations between environmental and stigma-related factors with food and water insecurity among young female sex workers and men who have sex with men (MSM) living with HIV in Kampala, Uganda.

Method: We conducted a cross-sectional survey with a HIV clinic-based sample of people living with HIV (aged 18-35) in Kampala. We conducted logistic regression models stratified by population (female sex worker, MSM) using blockwise (hierarchical) modelling to estimate environmental (e.g., traumatic

exposure severity to EWE [e.g. requiring assistance, displacement]) and stigma-related factors (HIV-related stigma, Everyday Discrimination, and structural stigma [including the harmful impacts of criminalization]) associated with food insecurity, water insecurity, and concurrent food and water insecurity.

Results: Participants (n=465) included n=240 female sex workers (mean age: 25.7, standard deviation [SD]: 2.90) and n=225 MSM (mean age: 27.6, SD: 3.54). More than three-quarters of participants reported food insecurity, over 45% water insecurity, and 45% concurrent food and water insecurity. Traumatic exposure severity to EWE was associated with: food insecurity (among female sex workers: adjusted odds ratios [aOR]=1.31, 95% confidence interval [CI]: 1.04–1.64; among MSM: aOR=1.62, 95%CI: 1.30–2.03), water insecurity (among female sex workers: aOR=1.18, 95%CI: 1.02-1.35; among MSM: aOR=1.29, 95%CI: 1.08-1.53), and concurrent food and water insecurity (among female sex workers: aOR=1.18, 95%CI: 1.02-1.35; among MSM: aOR=1.44, 95%CI: 1.20-1.73). Everyday Discrimination was associated with water insecurity (among female sex workers: aOR=1.03, 95%CI: 1.01-1.06; among MSM: aOR=1.08; 95%CI: 1.03-1.08) and concurrent food and water insecurity (among female sex workers: aOR=1.04, 95%CI: 1.01-1.07; among MSM: aOR=1.08, 95%CI: 1.03-1.13). Among female sex workers, HIV-related stigma was associated with concurrent water and food insecurity (aOR: 1.03, 95% CI: 1.01-1.08) and structural stigma was associated with water insecurity (aOR=1.21;95% CI: 1.01-1.45).

Conclusion: Increased exposure to traumatic environmental stressors and stigma, particularly Everyday Discrimination (day-to-day experiences of mistreatment), were associated with increased odds of water and food insecurity, even when adjusting for socio-demographic factors. Our findings build on research on how socially marginalized populations, such as female sex workers and MSM, may be disproportionately affected by EWE due to stigma, criminalization, and reduced access to social networks and familial support. HIV care interventions can address these socio-environmental determinants, and disaster risk reduction and climate adaptation programs can consider the needs of socially marginalized people living with HIV.

544 – Application Development for Climate Change and Air Pollution Impact on Human Health in Northern Thailand: Public Health Surveillance for Climate Change (PHS2C)

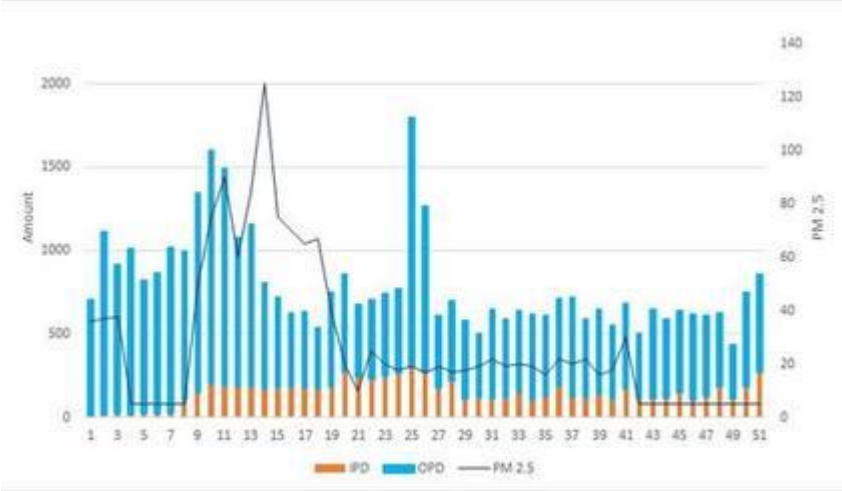
Suwat CHARIYALERTSAK (1), **Kannikar INTAWONG** (1), Napaphat POPROM (1), Waraporn BOONCHIENG (1), Woravut KOWATCHARAKUL (2), Kittiphan CHALOM (2), Vorabodin VINSIRIVORAKUL (2), Nakhon MONKOLCHOTYADA (2)
1: Chiang Mai University, Thailand; 2: Chiang Mai Health Office, Ministry of Public Health, Thailand

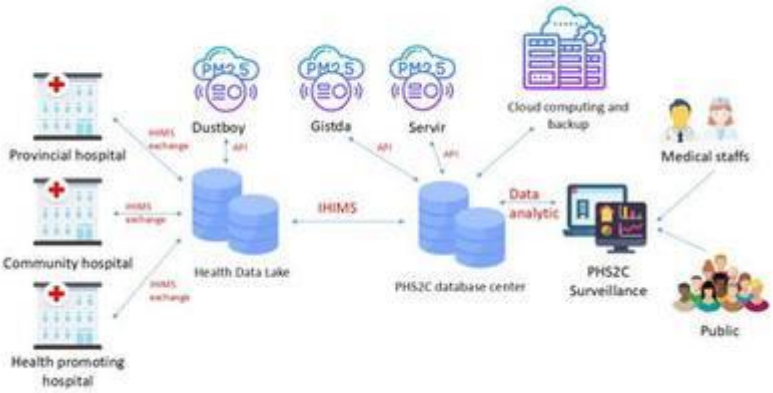
Background: Climate change, as a result of human activities, impacts 3.3 to 3.6 billion people world. In northern Thailand, PM2.5 concentrations are very high from wildfire and burning for agricultural activity. These high levels have adverse health consequences among human. Health information related to PM2.5 exposureshould ideally be easily accessible to healthcare providers, and updated in close to real-time, to mitigate risk and allocate healthcare resources. Therefore, we aimed to develop an application to integrate air-quality data and monitooring the impact on a number of related diseases from PM 2.5 and climate changes that need hospital services and hospitalization in Chiang Mai, Northern Thailand.

Methods: The Public Health Services for Climate Change website was developed to integrate of data ingestion, analytic, and outcome monitoring. The data retrieval from all public hospitals under Chiang Mai Provincial Public health office through their Health Integral Management System using application programing interfaces. This data is delivered into an analytic ecosystem that uses innovative applications including Vertica for big data storage, Superset, and JupyterHub for data visualization and analysis.

Results: We developed a closely real-time data platform by week that collects and monitors diseases burden in both hospital outpatient and inpatient cases including non-communicable diseases and other health conditions related to PM 2.5 and climate information. This platform serves as a vital tool for evidence-based decision-making, by enabling timely epidemic control measures, optimal resource management, and effective implementation of focused public health services to reduce disease impact in Chiang Mai.

Conclusions: The platform provides an enhanced data resource for surveillance of the burden of the diseases associated with the air pollution and climate changes. Future work will expand the geographic scope to increase coverage in northern Thailand.





560 – Metagenomic Discovery and Pathological Characterization of Canine Viral Infections for Improved Diagnostics

Ilja WEINSTEIN, Tarja SIRONEN, **Ravi KANT**
Helsinki University, Finland

Background: Dogs are the most common companion animals in Finland and share close environments with humans, creating opportunities for the circulation of infectious agents. Canine respiratory disease complex (CIRD) and meningoencephalitis of unknown origin (MUO) are significant health concerns in veterinary medicine and are often suspected to involve viral triggers. However, the canine virome remains poorly characterized, and current diagnostic methods such as PCR and immunoassays detect only known pathogens. Consequently, the true diversity and clinical relevance of viral infections in dogs remain largely unknown. This project aims to investigate the diversity, prevalence, and potential clinical relevance of viral pathogens in dogs using pathogen-agnostic metagenomic sequencing combined with pathological verification. We hypothesize that previously unrecognized or genetically divergent viruses contribute to respiratory and neurological diseases in dogs and that integrating metagenomics with pathology will improve detection and understanding of canine viral diseases.

Methods: The study will be conducted at the University of Helsinki, including the Veterinary Teaching Hospital, the Department of Veterinary Biosciences, and the Department of Virology. A case–control design will be implemented, enrolling approximately 200 dogs presenting with clinical signs of respiratory infection and 200 clinically healthy controls. In addition, post-mortem tissue samples from at least 40 dogs diagnosed with MUO or other suspected viral diseases and 40 control dogs will be collected. Clinical samples will include conjunctival, oral, nasal, and rectal swabs and serum, while post-mortem samples will include tissues from lungs, brain, lymph nodes, and intestines. Viral nucleic acids will be extracted and subjected to metagenomic next-generation sequencing using Illumina and Oxford

Nanopore platforms. Bioinformatic pipelines developed by the research team will assemble and classify viral sequences, identify known and novel viral genomes, and quantify viral abundance. Statistical analyses will evaluate associations between viral agents and clinical or histopathological findings. For selected viruses, in situ hybridization will be applied to tissue sections to verify the localization of viral nucleic acids within lesions.

Results: The project is expected to generate a comprehensive characterization of the canine virome associated with respiratory and neurological diseases. We anticipate identifying both established and previously unknown viruses, characterizing their genomic diversity, and determining their associations with clinical symptoms and pathological lesions. The integration of sequencing data with histopathology will provide evidence for the presence and tissue distribution of viral agents in disease-affected organs.

Conclusions: This study will advance knowledge of viral diversity and disease associations in domestic dogs and improve diagnostic approaches for canine viral infections. By combining metagenomics with pathological validation, the project will contribute to earlier detection of emerging viral pathogens and support a One Health perspective on animal and human health.

564 – One Health Investigation of Canine Leptospirosis Outbreak in Urban Singapore: Integrating Veterinary, Environmental and Public Health Responses

Zhan Pei HENG (1), Kelvin HO (1), Denise TAN (2), Wilson TAN (2), Jason TAN (2), Lee Ching NG (2), Tony TEO (2), Charlene Judith FERNANDEZ (1), Tze Hoong CHUA (1)

1: National Parks Board, Singapore; 2: National Environment Agency

Background: Leptospirosis is a zoonotic disease of global concern, particularly in tropical climates with high rainfall. In January 2024, a cluster of canine leptospirosis cases occurred within close proximity in an urban residential neighbourhood in Singapore within a short period of time, prompting a joint investigation by One Health agencies to determine the source of infection, implement control measures, and evaluate the effectiveness of inter-agency collaboration in outbreak response to control and reduce the spread of disease.

Methods: A joint One Health investigation was conducted by the Animal and Veterinary Service (AVS), a cluster of the National Parks Board, National Environment Agency (NEA), and Ministry of Health (MOH). Epidemiological investigation included movement and medical history analysis of affected dogs and household health assessments. Environmental investigation involved field inspections, rat trapping, and burrow identification across the affected neighbourhood. Laboratory testing included PCR and microagglutination testing (MAT) of canine samples, and PCR testing of trapped rats for Leptospira species identification.

Results: The four dogs started showing clinical signs between 1-10 January 2024. All four dogs were confirmed positive for leptospirosis through PCR testing of blood and/or urine samples. Two dogs died despite treatment. One dog that died and one dog that survived had prior vaccinations against leptospirosis. Movement history revealed that the dogs were exposed to leptospirosis infection during routine walks in the neighbourhood, with no common boarding facilities or significant travel history. Environmental investigation identified the presence of rat infestation with 11 burrows detected across 13 apartment blocks. Of 14 rats trapped, three tested positive for *Leptospirainterrogans*. MAT result of one dog revealed high titres for non-vaccinal serovar *L*. Bratislava (1:12,800), suggesting vaccine-breakthrough infection. The outbreak coincided with a period of heavy rainfall between December 2023-January 2024, consistent with known leptospirosis epidemiology. Public health measures included advisories to veterinarians and dog owners, media statements to raise public awareness, and prophylactic treatment recommendations for exposed individuals. The outbreak was assessed as resolved in February 2024 as there was no new cases and more than 2 incubation periods had passed.

Conclusions: This investigation demonstrates successful One Health collaboration in outbreak response, identifying local environmental contamination as the infection source. The detection of non-vaccinal serovars in canine cases highlights gaps in current vaccination strategies. Heavy rainfall likely increased environmental contamination risk by displacing infected rats and facilitating bacterial survival. This case underscores the importance of integrated surveillance, environmental management, and public education in preventing zoonotic disease transmission in urban settings.

570 – Emergent pan-azole-resistant Aspergillus fumigatus in poultry farms: Implications for One Health

Bianca GOMES (1,2), Miguel J.N.RAMOS (1,3), Mónica NUNES1 (1,3), Carla VIEGAS (2,4), Ricardo DIAS (1,3)

1: CE3C- Center for Ecology, Evolution and Environmental Changes FCUL, Universidade de Lisboa, Portugal; 2: H&TRC – Health & Technology Research Center, ESSL– Escola Superior de Saúde de Lisboa, Instituto Politécnico de Lisboa; 3: iXLab - Innovation for National Biological Resilience, Faculdade de Ciências, Universidade de Lisboa, Lisboa 1749-016, Portugal; 4: NOVA National School of Public Health, Public Health Research Centre, Comprehensive Health Research Center, CHRC, REAL, CCAL, NOVA University Lisbon, Lisbon, Portugal

Background: *Aspergillus fumigatus* is a thermotolerant environmental fungus and the main etiological agent of aspergillosis in humans and animals. Its pathogenicity is largely attributed to its small conidia, being easily inhaled and its ability to grow in diverse environmental conditions. Recently, fungal infections have become more challenging to treat due to rising azole resistance, often associated with mutations in the *cyp51A* gene. In this context, poultry farms have been identified as reservoirs of potential azole-resistant *Aspergillus*, with animal bedding serving as a source of pathogen dissemination within farms and the surrounding environment.

Aim: This study aimed to assess the occurrence of azole-resistance *Aspergillus fumigatus* in poultry farms. Environmental samples (n=405) from 5 poultry farms were collected across two seasons (summer and winter), including air, electrostatic dust cloths (EDC), bedding material, feed and surface swabs.

Methods: Samples were cultured on selective media (DG18-Dichloran-glycerol agar), at 37°C to target thermotolerant *Aspergillus* species with pathogenic potential. *A. fumigatus* sensu *stricto* isolates were selected based on thermotolerance criteria (50ºC). Azole susceptibility screening was performed using the main clinical triazoles (Itraconazole (ITR); Voriconazole (VOR); Posaconazole (POS), following EUCAST guidelines. Isolates showing reduced susceptibility to azoles were subjected to whole genome sequencing and a target analysis of the *cyp51A* gene to characterize molecular mechanisms of resistance.

Results: Section *Fumigati* was the most prevalent among *Aspergillus* species detected in air (80%), bed (79%) and swabs (50%) supporting its widespread presence in poultry farm environments. The highest number of *A. fumigatus* isolateswere recovered during winter mainly from air (n=40/120) and bed (n=39/120) samples, suggesting that reduced ventilation and increased humidity favours fungal growth. Azole susceptibility testing identified 7 isolates, (6 from bedding; 1 from air) pan-azole-resistant resistant (ITR, VOR, POS), of which four carried the TR34/L98H mutation in the *cyp51A* gene. Resistant isolates were recovered from bedding and one air sample, supporting bedding as potential reservoir of resistance and air as a route of dissemination.

Conclusion: Overall, our findings indicate that poultry farms, particularly bedding material, can act as reservoir of clinically relevant azole-resistant *A. fumigatus* strains, with potential implications for occupational health, food safety, and environmental contamination. The detection of the TR34/L98H mutation, widely linked to frequent use of azoles in the environment (agriculture, industry), underscores the interconnected risks of agricultural practices, environmental health, and clinical outcomes. These results reinforce the urgent need to integrated surveillance systems and cross-sectoral collaboration under the One Health framework to monitor antifungal resistance and mitigate risks at the human–animal–environment interface.

574 – Designing One Health interventions through community lens including mental Health

Fatou NDOYE (1,5), Marjan LENAMAN (2), Jean Augustin TINE (1,3), Abdourahmane SOW (1,4), Kees BOERSMA (5), Elhadji SOW (6), Mouhamadou Bachir WILANE (7), Andree Prisca NDOUR (8), Helena Aminiel NGOWI (9), Gilbert FOKOU (10), Emikpe BENJAMIN (11), Kathrin Heitz TOKPA (12), Bassirou BONFOH (12)

1: Cheikh Anta Diop University of Dakar (UCAD), Institute of Health and Development (ISED), Senegal; 2: Diversity Focus-One Health Social Sciences (OHSS) and Food systems, Nijmegen, the Netherlands; 3: Ministry of Health and Social Action (MSAS), Senegal; 4: Public Health Unit, Institute Pasteur de Dakar (IPD), Senegal; 5: Vrije Universiteit Amsterdam, Social sciences and Humanities, Organization Sciences, the Netherlands; 6: Ministry of Livestock and Animal Production Service, Kédougou, Senegal; 7: Coordination of Global Health Security Program Senegal (SP-HCSS-OH), Senegal; 8: Ecole Inter-Etats des Sciences et Médecine Vétérinaires (EISMV), Senegal; 9: Sokoine University of Agriculture, Department of Veterinary Medicine and Public

Health, Morogoro, Tanzania; 10: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Research Support Unit (UAR); 11: Dean, School of Veterinary Medicine, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana; 12: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire

The One Health (OH) approach has emerged as a comprehensive approach that recognizes the interconnectedness between countries, institutions, sectors and disciplines to tackle complex health challenges. Despite progress in OH implementation, the approach often insufficiently integrates mental health and remains poorly adapted to local contexts. Previous global health emergencies (Ebola and Covid-19) have caused major social and psychological disruptions, generating fear and denial of disease and control measures. This study aims to investigate stakeholder OH perspectives, and design adapted interventions that go beyond infectious diseases to a more broader health sphere focusing on mental health. The research draws on experiences in Senegal from Permanent Secretariat of the National High Council for Global Health Security OH in 2022, epidemiological investigations during first case detection Crimean Congo Hemorrhagic Fever (CCHF) in 2023 with Institut Pasteur de Dakar in collaboration with Prevention Division (DP) and COUS at Ministry of health, and further field investigation in 2024. A mixed method approach was used to collect data through participatory observations, field reports from 8 OH platform meetings, and 9 interviews from IPD/DP epidemiological investigation. 35 Key informant interviews were conducted both with governmental and local actors involved in epidemic management. 434 livestock keepers were surveyed to assess their knowledge on zoonotic diseases and OH interventions in their localities during public health events. Case stories from 31 victims-caregivers affected by Covid-19 (10), rabies (10), CCHF (9), and unknown diseases (2) and from livestock keepers (4) who lost animals to other zoonotic diseases. The study identified indicators of psychological distress among victims. Case narratives highlighted that psychological distress was linked to multiple factors, including fear of infection and death, experienced stigmatization, the loss of family members and livestock, socio-economic consequences, and limited psychosocial support and mental health services during outbreaks. Analysis of the OH coordination platform showed that emergency responses are primarily organized around multisectoral collaboration between human health, animal health, and environmental sectors, with operational activities largely focused on surveillance, case detection, and contact tracing. However, this coordination rarely includes social scientists, psychologists, or dedicated psychosocial support services, resulting in limited integration of mental health considerations in zoonotic disease preparedness and response. Study further shown low knowledge of zoonotic diseases (18,4%) among livestock keepers due to low-risk perception, which showed a significant association with poor level of formal education ($p = 0.03$). Most farmers (87.1%) reported being unaware of the OH approach, finding the concept largely unfamiliar. The Study suggests that OH interventions should be designed to bridge central decision making, operational strategic planning, and community levels integrating local knowledge, strengthen cross-sector collaboration with additional key discipline as psychology, and foster meaningful community ownership.

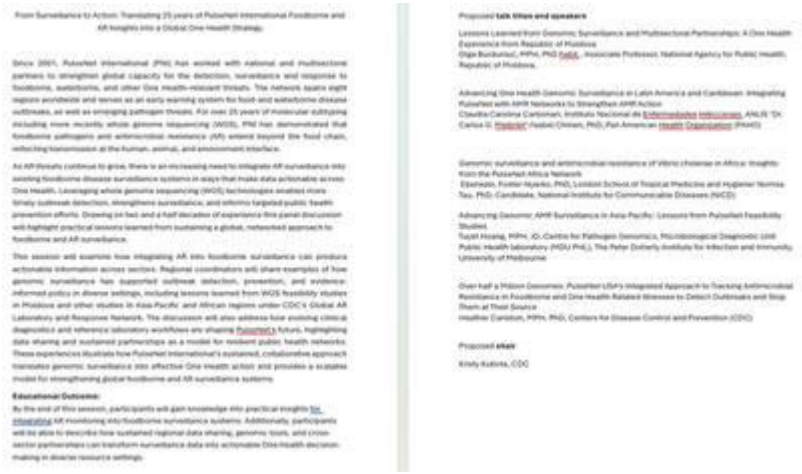
582 – From Surveillance to Action: Translating 25 years of PulseNet International Foodborne and AR Insights into a Global One Health Strategy

Kristy KUBOTA

U.S. Centers for Disease Control and Prevention, United States of America

Since 2001, PulseNet International (PNI) has worked with national and multisectoral partners to strengthen global capacity for the detection, surveillance and response to foodborne, waterborne, and other One Health–relevant threats. The network spans eight regions worldwide and serves as an early warning system for food-and waterborne disease outbreaks, as well as emerging pathogen threats. For over 25 years of molecular subtyping including more recently whole genome sequencing (WGS), PNI has demonstrated that foodborne pathogens and antimicrobial resistance (AR) extend beyond the food chain, reflecting transmission at the human, animal, and environment interface.

As AR threats continue to grow, there is an increasing need to integrate AR surveillance into existing foodborne disease surveillance systems in ways that make data actionable across One Health. Leveraging whole genome sequencing (WGS) technologies enables more timely outbreak detection, strengthens surveillance, and informs targeted public health prevention efforts. Drawing on two and a half decades of experience this panel discussion will highlight practical lessons learned from sustaining a global, networked approach to foodborne and AR surveillance.



585 – Defining tetracycline ECOFF and resistance determinants in Clostridioides difficile across One Health reservoirs

Frederico ALVES (1), Mariana GOMES (1), Miguel PINTO (2), Filipa DIONÍSIO (1), João Paulo GOMES (2), Mónica OLEASTRO (1)

1: National Reference Laboratory of Gastrointestinal Infections, Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge (INSA), Lisbon, Portugal; 2: Genomics and Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge (INSA), Lisbon, Portugal.

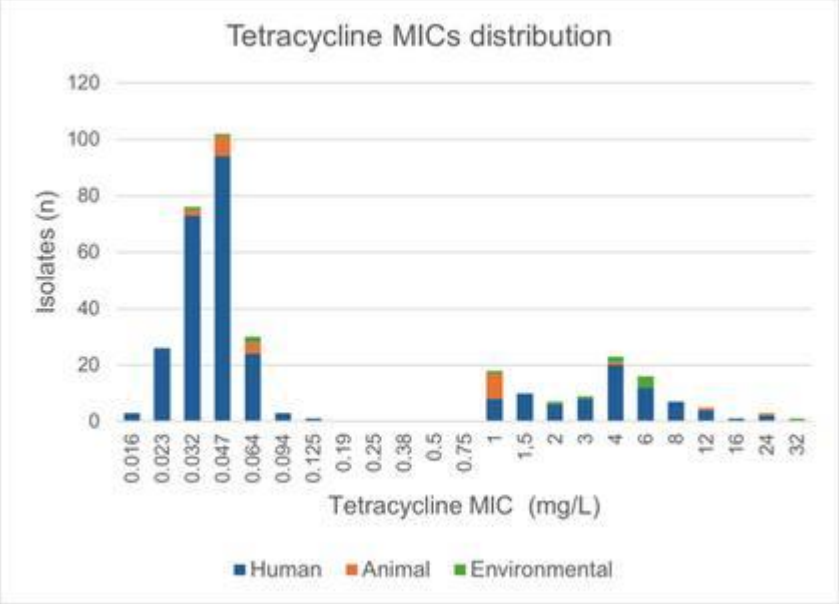
The increasing community-associated burden of *Clostridioides difficile* infection (CDI) underscores the role of non-human reservoirs in the transmission network. Antimicrobial resistance has substantially influenced *C. difficile* epidemiology worldwide, facilitated by the species' marked genomic plasticity and ability to acquire resistance determinants. Interpretation of tetracycline resistance remains challenging due to the absence of species-specific breakpoints, with most studies relying on generic criteria or detection of *tet(M)*. In this study, we aimed to characterize tetracycline resistance phenotypes and genotypes of *C. difficile* from human, animal, and environmental sources, and to propose an epidemiological cut-off value (ECOFF). WGS was used to characterize *tet*-associated genes and their mobile genetic elements.

A total of 813 isolates collected between 2020 and 2025 were included: human (n=643), animal (n=119), and environmental (n=51). Prior to January 2025, animal and environmental isolates and a subset of human isolates (n=385) were screened for *tet(M)* by PCR. Tetracycline minimum inhibitory concentrations (MICs) were determined using Etest® for all *tet(M)*-positive isolates, and 23 *tet(M)*-negative isolates served as controls. From January 2025 onwards, tetracycline MIC testing was incorporated into the national antimicrobial surveillance panel, adding 258 human isolates. During this phase, *tet(M)* PCR was performed only for isolates with MIC ≥1 mg/L, except selected MIC 1 mg/L isolates used as negative controls. A representative subset of 166 isolates underwent WGS.

Among *tet(M)*-positive isolates (n = 61), MICs ranged from 1–32 mg/L. The 23 *tet(M)*-negative controls showed MICs of 0.023-0.094 mg/L, except for two isolates with a MIC of 4 mg/L. MIC distribution was independent of isolate source. Based on these data, an ECOFF of 1 mg/L was proposed to discriminate non-wild-type (resistant) from wild-type (susceptible) isolates. Prospective application of this ECOFF to human isolates collected from January 2025 onwards (n=258) identified 37 (14.3%) as resistant (MIC 1-12mg/L), including 26 *tet(M)*-positive strains. Susceptible isolates (n=221) displayed MICs of 0.016-0.094 mg/L, with no isolates presenting intermediate values between 0.094 and 1 mg/L. WGS confirmed PCR detection of *tet(M)*. Among *tet(M)*-positive isolates, 19/59 harboured additional *tet* genes: *tet(40)* (n=11), *tet(44)* (n=5), and *tet(O)* (n=3). Of 13 resistant *tet(M)*-negative isolates, nine were sequenced and carried *tetA(P)* and *tetB(P)*, supporting their independent contribution to resistance. Multiple transposons harbouring *tet* genes were identified, highlighting the role of mobile genetic elements in dissemination.

The proposed 1 mg/L ECOFF demonstrated strong concordance with tetracycline resistance genotypes, supporting standardized susceptibility interpretation in *C. difficile*. Validation across human, animal, and

environmental reservoirs emphasizes their interconnectedness and reinforces the need for a One Health approach to antimicrobial surveillance and stewardship.



594 – Reactive bioindicators of ecosystem regeneration following deer population control in peri-urban parks

Camille DESBIENS (1,2), Martin LECLERC (2,3), Jean-Pierre TREMBLAY (1,2,4)

1: Département de Biologie, Faculté des Sciences et de Génie, Université Laval, Québec, Qc, Canada; 2: Centre d'étude de la forêt, Université Laval, Québec, Qc, Canada; 3: École supérieure d'aménagement du territoire et de développement régional, Université Laval, Québec, Qc, Canada; 4: Centre d'études nordiques, Université Laval, Québec, Qc, Canada

Background:

In peri-urban parks of Eastern North America, high densities of white-tailed deer (*Odocoileus virginianus*) suppress forest regeneration through intense browsing and increase risks of tick-borne diseases, threatening both ecosystem resilience and human health. This issue is central to *PARCS en santé*, a Canadian One Health initiative that integrates ecological, social and public-health perspectives to improve the ecological integrity of peri-urban parks, protect biodiversity and reduce tick-borne diseases risk. As part of this initiative, our project aims to develop reactive plant indicators capable of monitoring ecosystem recovery following deer population control and to integrate these bioindicators into a decision-support dashboard. We hypothesized that deer density drives browsing intensity on regenerating vegetation and that browsing, survival, and growth of planted seedlings could serve as reactive indicators of early forest recovery. These indicators will ultimately support adaptative management of peri-urban parks and deer populations.

Methods:

Considering previous alteration of standing vegetation from heavy deer browsing, we implemented annual experimental plantings of five seedling species in four peri-urban parks in Greater Montreal that are under a deer culling program. For each planted seedling, we monitored monthly browsing and survival, and seasonal growth. We then examined how deer density estimated before and after culling operations influenced browsing, mortality, and growth patterns, and assessed finer-scale temporal dynamics to refine both our sampling design and management recommendations.

Results:

Across the four parks and five species combined, each additional deer per km² increased browsing probability by 2.9% and mortality probability by 1.5%, while annual seedling growth decreased by 0.09 cm. These patterns align with existing literature, but our results also show that selected seedling species and associated metrics are sensitive to local variations in deer density, confirming their suitability as reactive

bioindicators. At finer temporal scales, browsing hazard increased by 1.6 % and mortality hazard by 5.7 % per additional deer per km², revealing short-term dynamics that annual assessments cannot capture and providing managers with more precise information to adjust deer management.

Conclusion:

Our study shows that experimental planting of seedlings provides a sensitive method for detecting early signals of forest recovery following deer population control. Integrated into the *PARCS en santé* dashboard, these indicators will enable managers to track ecosystem regeneration, anticipate ecological risks, and adapt interventions accordingly. By linking ecological restoration to human and ecosystem health, this project aligns directly to the One Health approach and supports healthier, more resilient communities.

---

598 – Health in a Changing Climate: Portugal's Responses to Climate Threats in the Global Context

Sindy SILVA, Isabel CRAVEIRO

Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, 1349-008, Portugal

Background:

Climate change represents one of the greatest global health challenges of the 21st century. Heatwaves, wildfires, water insecurity, and infectious diseases disproportionately affect vulnerable populations. In Europe, including Portugal, extreme events have become more frequent, requiring resilient health systems. Although international frameworks such as the Paris Agreement and the 2030 Agenda, which established the Sustainable Development Goals (SDGs), promote the integration of climate and health policies, their implementation varies across countries. Objective:To map the strategic responses and policies implemented by Portugal to address climate change with impacts on health, highlighting alignment with global initiatives.

Methods:

A rapid review was conducted following guidance from the World Health Organization and the Cochrane Rapid Reviews Group.

Research question: What responses has Portugal implemented to address climate change with impacts on health?

Data sources and inclusion criteria: PubMed search (2019–2026) using the descriptors: "Portugal"[Title/Abstract] AND ("climate change adaptation"[Title/Abstract] OR "climate policy"[Title/Abstract]). Full-text articles in English focusing on adaptation policies and health were included. Official policy documents retrieved from the website of the Portuguese Environment Agency (APA) were also analyzed.

Selection and extraction: Study selection and data extraction were conducted by a single reviewer using predefined criteria.

Results:

Portugal has developed a structured set of climate strategies and policy instruments aligned with global and European commitments. The analysis identified the implementation of six strategic instruments related to climate policy in Portugal: the National Strategy for Adaptation to Climate Change (ENAAC, 2015-2025), the Action Programme for Adaptation to Climate Change (P-3AC, 2019-2022), the National Energy and Climate Plan (PNEC 2030), the Roadmap for Carbon Neutrality 2050 (RNC 20219-2050), the Framework Law for Climate (2021-2030) and the National Adaptation Roadmap 2100 (RNA 2023-2100). These instruments set short-, medium- and long-term mitigation and adaptation targets, aligned with international initiatives such as the Paris Agreement, Agenda 2030, the EU Strategy on Adaptation to Climate Change and the European Green Deal (Figure 1). However, although these instruments recognise the potential impacts of climate change on health, including deteriorating air quality, heatwaves and extreme events, the explicit integration of health into climate strategies remains limited. Furthermore, few mechanisms for monitoring and evaluating health impacts are identified in these policies (Table 1).

Conclusion:

Portugal has made progress in developing climate strategies aligned with global agendas. However, assessments of their impacts remain limited, particularly regarding public health outcomes. Due to its rapid review design, this study presents limitations related to the depth of analysis and the scope of the literature included. Future research should assess the effectiveness of these strategies, develop climate–health indicators, and support evidence-based policymaking, particularly for vulnerable populations.

Figure 1. Portuguese Climate Strategies: Timeline and Alignment with the Global Context (2010–2100)

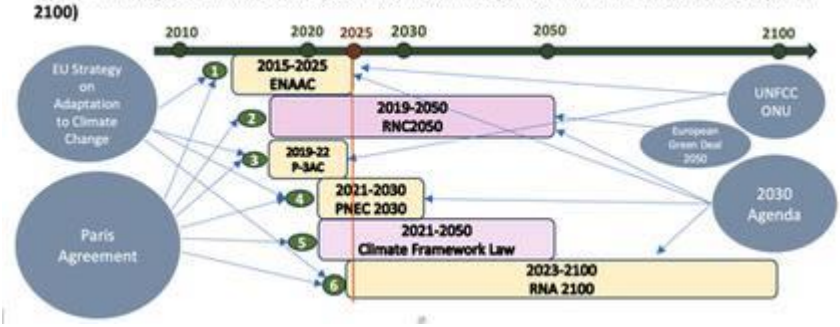


Table 1. Overview of Climate Policy Instruments in Portugal and Their Links to Health

Nº	Policy Instrument	Objectives	Health relevance	Nº Evaluation
1	ENAAC	Integrates climate adaptation into national public policies	Recommends adapting health services to climate risks	1
2	RNC2050	Targets and measures for carbon neutrality by 2050	Impacts air quality and respiratory health	Not reported
3	P-3AC	Adaptation measures aligned with ENAAC and EU funding	Reduces risks from heat, floods, vector diseases	Not reported
4	PNEC 2030	National mitigation and adaptation targets until 2030	Improves air quality and active mobility	Not reported
5	Climate Framework Law	Establishes climate stability and carbon neutrality rights	Recognizes climate impacts on public health	Not reported
6	RNA 2100	Assesses climate risks and long-term adaptation pathways	Evaluates future health impacts of climate change	Not reported

---

600 – Advancing One Health Governance and Advocacy for Sustainable Health Security in Tanzania

Gabriel SHIRIMA (1), Beatus LYIMO (1), Esther KIMARO (1), John-Mary VIANNEY (1), Knight-Jones THEODORE (2), Magreth KAREMBU (3), Salum MANYATTA (4)

1: Nm-aist, Tanzania; 2: ILRI, Kenya; 3: ISAAA AfriCenter, Kenya; 4: Prime Ministers Office-One Health Section, Tanzania

Background

Emerging and re-emerging infectious zoonotic disease outbreaks, including Marburg, Ebola, Rabies, Anthrax and COVID-19 have underscored the need for coordinated approaches to health threats arising at the interface between human, animal and the environment. In response, Tanzania institutionalised the One Health (OH) approach as both a governance framework and an advocacy platform to strengthen national health security, multisectoral coordination, and policy coherence.

ObjectiveTo examine how governance structures and strategic advocacy have shaped the institutionalisation and sustainability of the OH approach in Tanzania.

MethodsA descriptive review of national policy frameworks, coordination mechanisms, and advocacy initiatives was conducted. The analysis focused on high-level political engagement, multisectoral coordination under the Prime Minister's Office and stakeholder mobilisation across sectors.

Results

One Health governance in Tanzania is anchored under the Prime Minister's Office through the One Health Section, ensuring high-level political oversight and inter-ministerial accountability. Key collaborating institutions include the Ministries of Health, Livestock and Fisheries, Natural Resources and Tourism and the Vice President's Office Tanzania (Environment). with one focal person from each institution. These institutions coordinate through a National OH Steering Committee and Technical Working Groups, which facilitate joint planning, surveillance integration, risk assessment, laboratory networking, and outbreak

preparedness and response. At subnational levels, regional and district OH multisectoral coordinating committees operationalise coordination, particularly in high-risk ecosystems.

Despite having a OH Strategic Plan and OH implementation plan, advocacy is stll greatly needed for the advancement of One Health governance in Tanzania. Establishment of the Parliamentarian`s Alliance for OH/AMR in particular enhanced strategic engagement with policy makers and facilitated distribution of over 500 OH fact sheets to Members of the National Assembly in 2024.

Formalised multisectoral coordination structures, improved prioritisation of zoonotic diseases, enhanced joint outbreak investigations, and increased recognition of environmental determinants of health were the notable achievements reported. The One Health Conference held in Tanzania in November, 2024 as part of advocacy efforts, has also contributed to improved awareness among senior officials, sectoral leaders and technical officers. On the other hand sustainability was hugely challenged by donor dependency though currently funding has been embeded frrom national budgets.

Conclusion

Tanzania's experience demonstrates that effective One Health implementation requires not only formal governance structures but also high-level sustained advocacy to secure political ownership, mobilise domestic resources, and institutionalise cross-sectoral accountability. Integrating governance and advocacy provides a viable pathway for sustaining One Health as a cornerstone of national and regional health security.

Key words: *One Health, Governance, Advocacy,*

---

606 – Modelling male Ebola survivor population dynamics and their influence on future outbreaks

Enagnon Bruno LOKONON (1,2), Caroline FAKAS (3), Daniel T. HAYDON (3), Bassirou BONFOH (2)

1: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Côte d'Ivoire; 2: Laboratoire de Biomathématiques et d'Estimations Forestières, Université d'Abomey-Calavi, Benin; 3: School of Biodiversity, One Health & Veterinary Medicine, College of Medical Veterinary and Life Sciences, University of Glasgow, Glasgow, United Kingdom

Background: Emerging and reemerging infectious diseases threaten public health in Africa. WHO reveals an accelerating trend in zoonotic spillover, with a 63% increase in outbreaks over the last decade (2012–2022) relative to 2001–2011. Ebola is one of the major zoonotic viral diseases in Africa, with high human mortality rates of 60–90%. Since 1976, 40 outbreaks have occurred, driven by spillover and transmission from survivors. Previous studies suggest over 70% of recrudescent events in West Africa result from male-to-female sexual transmission, though the broader epidemiological role of male survivors remains unclear.

Methods: We developed a stochastic model to analyze the dynamics of the male convalescent population, and their potential role in determining the number of future Ebola outbreaks. The size of Ebola outbreaks was modelled assuming a negative binomial distribution. We assumed that new Ebola outbreaks arise as a result of a constant rate of spillover from a natural reservoir, and from recrudescent events arising from a male convalescent population at a fixed per capita rate. We employed Markov chain Monte Carlo (MCMC) techniques to estimate the model parameters. Convalescent recovery (clearance) rates were varied to explore different recovery scenarios from male survivors.

Results: We estimated the average size of Ebola outbreaks to be 1042.03 individuals (95% CI: [660.11, 1494.20]), with an annual survival probability of 0.56 (95% CI: [0.55, 0.57]). The natural rate of spillover is estimated to be 0.91 (95% CI: [0.75, 0.99]) per year, and the rate of recrudescence to be 0.00015 (95% CI: [0.000041, 0.00028]) per convalescent per year. We identify a threshold condition below which the model predicts a stable equilibrium number of convalescents, and above which the convalescent population will grow exponentially. The parameterized model sits within this stable domain. The results showed that the dynamics of the convalescent population and the number of outbreaks depend critically on how fast the male survivors recover from the disease (Figs.1,2). Average equilibrium male convalescent population sizes were estimated to be 15,774 (standard deviation of 10004) for recovery rate r= 0.1 and 378 (standard deviation of 658) for r= 0.9. The model predicted on average 3.4 outbreaks (standard deviation of 1.07) per year for r= 0.1 and one outbreak (standard deviation of 0.5) per year for the higher recovery rates. For r≤

0.147 per year, human-initiated outbreaks exceed natural spillovers by at least twofold, suggesting male survivors may drive future outbreaks.

Conclusions: Our estimations improved understanding of the Ebola male convalescent population dynamics, which depend on the viral clearance rate. Cohort studies of Ebola male survivors are needed to enable longitudinal analyses and long-term surveillance of viral persistence in seminal fluids. Safe sexual practices among male survivors are recommended to reduce transmission risk and help prevent future outbreaks.

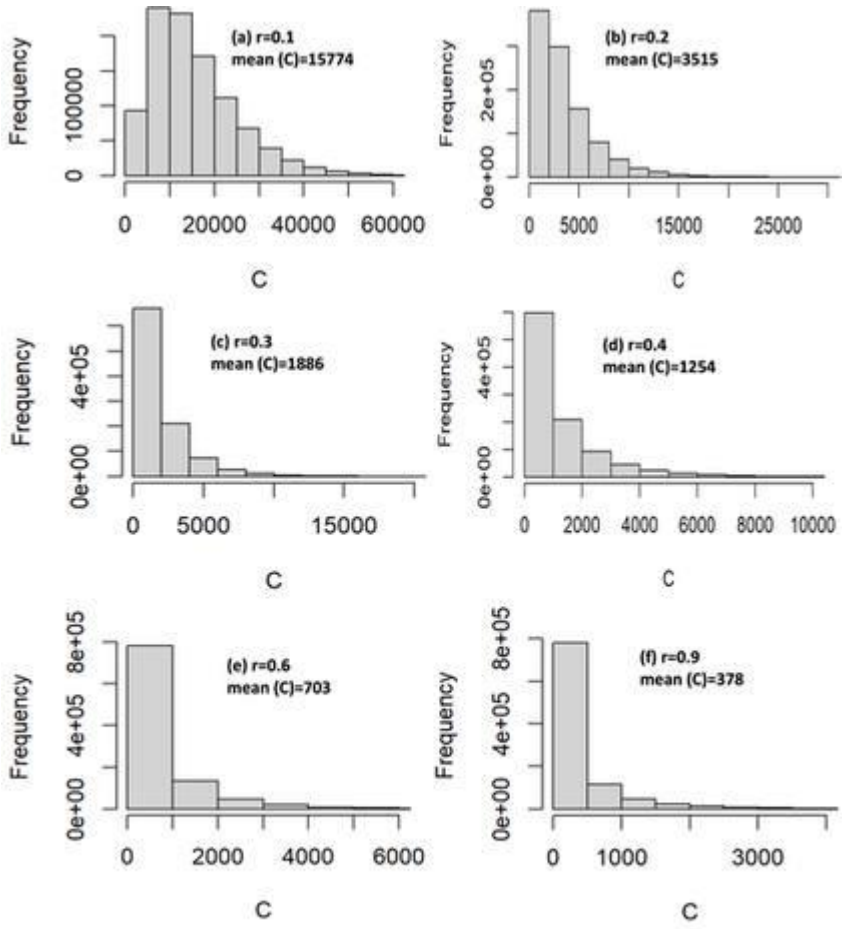


Figure 1: Distribution of convalescent population C around the stable equilibrium for: recovery (clearance) rate (a) $r = 0.1$, (b) $r = 0.2$, (c) $r = 0.3$, (d) $r = 0.4$, (e) $r = 0.6$, (f) $r = 0.9$, generated by simulation of the fully parameterized model.

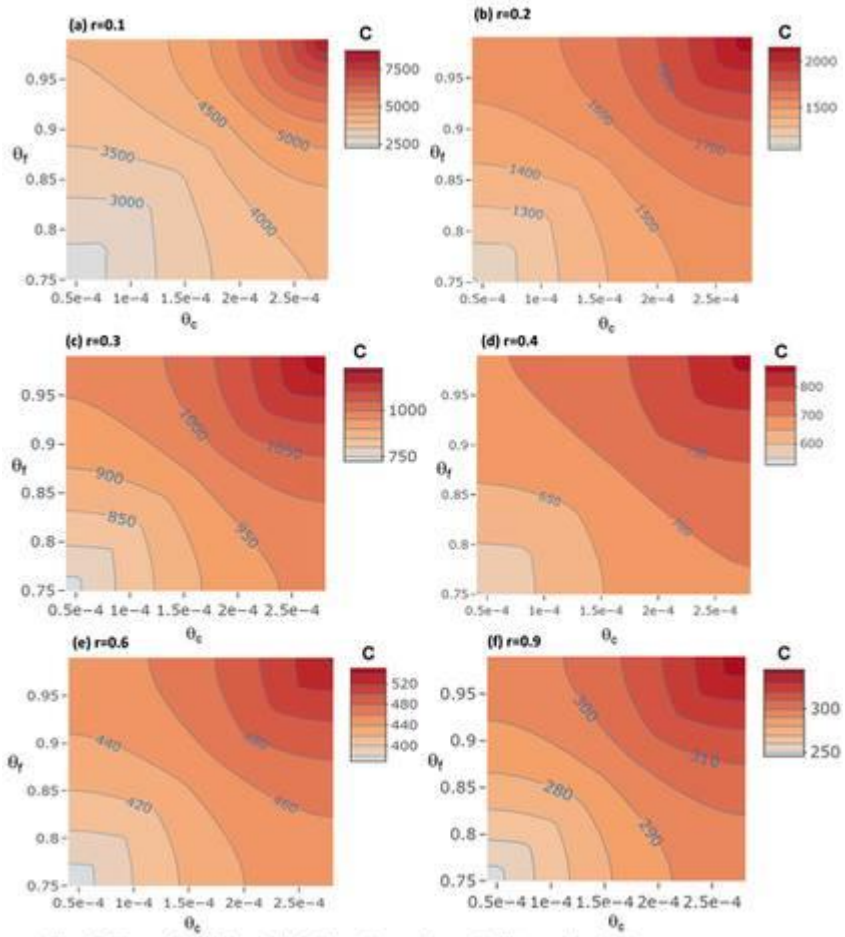


Figure 2: Contour plots of the combined effects of per capita rate of spillover originating from convalescents (θ_c) and rate of spillover from natural reservoirs (θ_f) on the number of convalescents (C) for: recovery (clearance) rate (a) $r = 0.1$, (b) $r = 0.2$, (c) $r = 0.3$, (d) $r = 0.4$, (e) $r = 0.6$, (f) $r = 0.9$.

614 – Characterizing Interspecies Contact at Human-Wildlife-Livestock Interfaces by Integrating Local Spatial Knowledge and Animal Movement Data in Kenyan Rangelands

Stephanie MITCHELL (1,2,3), Lucrecia AGUILAR (4), Shaleen ANGWENYI (2,11), Nelly BARGOIYET (2), Blair COSTELLOE (6), Giacomo D'AMMANDO (5), Andrew B. DAVIES (22), Meshack GAGA (6), Michael KAELO (7), David KIMITI (8), Adams KIPCHUMBA (9), Rashid LEBUNGE (10,11), Elizabeth NASIEKU LELENGUYA (11), Purity CHEROTICH MIGLO (5), Niels MOGENSON (7), Tom MORRISON (12), Tracy MONTGOMERY (16,17), Arthur MUNEZA (9), Toby OTIENO (13), Abigael SIMALOI PERTET (6), Rhoda SERETI (14), Jared STABACH (15), Eli STRAUSS (16,17), Sam TOME (7), Daniel WATURU (14), Abraham D. FLAXMAN (18,23), Peter RABINOWITZ (1,2,18,19), James HASSELL (3,20), Julianne MEISNER (1,2,18,21)

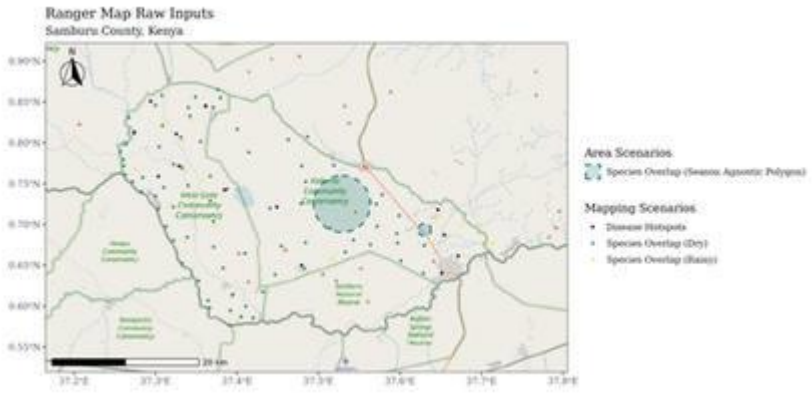
1: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA, United States; 2: Center for One Health Research, University of Washington, Seattle, WA, United States; 3: Smithsonian National Zoo Global Health Program, Washington DC, United States; 4: Harvard University, Cambridge MA, United States; 5: Save the Elephants, Nairobi, Kenya; 6: Mara Elephant Project, Nairobi, Kenya; 7: Kenya Wildlife Trust, Nairobi Kenya; 8: Grevy's Zebra Trust, Nairobi, Kenya; 9: Giraffe Conservation Foundation, Windhoek, Namibia; 10: Nature Embassy, Nanyuki, Kenya; 11: Mpala Research Center, Nanyuki, Kenya; 12: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow, UK; 13: Ewaso Lions, Nairobi Kenya; 14: Directorate of Veterinary Services, Nairobi, Kenya; 15: Smithsonian National Zoo & Conservation Biology Institute, Front Royal, VA, United States; 16: Department of Integrative Biology, Michigan State University, East Lansing, MI, United States; 17: Mara Hyena Project, Nairobi, Kenya; 18: Department of Global Health, University of Washington, Seattle, WA, United States; 19: Department of Medicine, University of Washington, Seattle, WA, United States; 20: Yale School of Public Health, New Haven, CT, United States; 21: Department of Epidemiology, University of Washington, Seattle, WA, United States; 22: Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, United States; 23: Institute for Health Metrics and Evaluation, Department of Health Metrics Sciences, University of Washington, Seattle, WA, United States

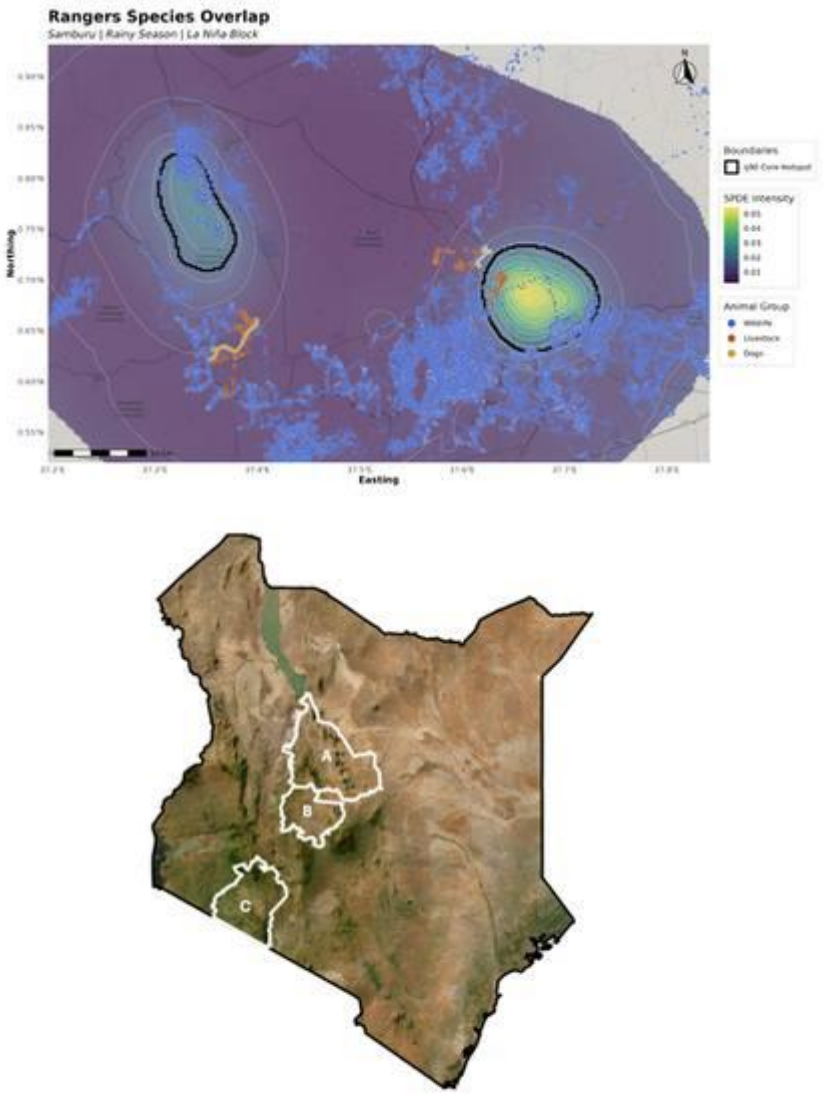
Background: In Kenyan rangelands, zoonotic pathogens threaten wildlife and domestic animal populations. Identifying where wildlife and domestic animals come into contact is essential for understanding zoonotic disease risk at human-wildlife-livestock interfaces (HWL) and for guiding One Health surveillance, land management, and conflict mitigation. Yet these contact zones remain difficult to characterize because local spatial knowledge (LSK) and animal movement data are rarely analyzed together. Using participatory mapping and multi-species GPS telemetry across three Kenyan rangeland systems, we tested whether LSK can independently characterize wildlife-domestic animal contact opportunity across seasons and El Niño–Southern Oscillation (ENSO)-informed climate strata to support spatial contact network construction relevant to zoonotic pathogen transmission.

Methods: Wildlife telemetry data were collected longitudinally (2017–2025), whereas domestic animal GPS data and LSK were collected during a single field season (2025). LSK recorded perceived areas of wildlife presence and wildlife-domestic animal contact opportunity through participatory mapping sessions with pastoralists and wildlife rangers. Digitized LSK locations were modeled as Poisson-distributed spatial counts using SPDE-INLA, producing continuous contact opportunity surfaces that represented where wildlife-domestic animal shared landscape use was modeled as lower or higher across the landscape. Primary q90 hotspots were defined as areas above the 90th percentile of modeled contact opportunity. Animal GPS telemetry was converted into spatial occupancy and stratified by season and ENSO-informed climate stratum. LSK-modeled hotspots were compared with independently processed telemetry using an area-adjusted concentration ratio, with ratios >1 indicating greater spatial concurrence than expected from hotspot area alone. Spatial divergence was additionally characterized using distance to the nearest hotspot boundary.

Results: Wildlife-domestic animal spatial co-occurrence differed substantially among landscapes. Among domestic-animal-occupied pixels, the proportion also occupied by wildlife was 27.0% for dogs and 36.1% for livestock in Samburu, 66.2% and 82.9% in Laikipia, and 94.9% and 97.2% in Narok, respectively. LSK-modeled interspecies contact hotspots showed spatial concurrence with telemetry, with 19 of 24 (79%) q90 LSK–telemetry comparisons having concentration ratios >1. Spatial concurrence varied by landscape and LSK source; neither pastoralist- nor ranger-modeled LSK consistently showed greater spatial concurrence with telemetry. Instead, pastoralist and ranger knowledge captured complementary, context-dependent patterns of wildlife-domestic animal contact opportunity relevant to zoonotic disease transmission.

Conclusions: Across study sites, LSK identified landscape-level wildlife-domestic animal contact opportunities that frequently showed spatial concurrence with independently processed animal telemetry. Participatory mapping can help prioritize zoonotic disease surveillance where telemetry is limited and provide complementary spatial evidence where movement data are available. Integrating LSK with GPS telemetry provides a scalable framework for identifying contact opportunity zones and supporting spatial contact network construction at the HWL interface. LSK-modeled contact zones should be interpreted as hypotheses for disease-relevant contact opportunity rather than confirmed disease-risk areas, observed contact, or pathogen transmission.





Study Locations in Kenya. Counties outlined in white: Samburu (A) Laikipia (B) Narok (C)

618 – A one-health approach to identify gene reassortment hotspots of highly pathogenic avian influenza A (H5) virus in Eurasia since 1997

Day-Yu CHAO, Bo-Jia CHEN, Chun-Chen LIANG, Hong-Dar Isaac WU
National Chung-Hsing University, Taiwan

Background

The global circulation of the Goose/Guangdong/1996-lineage (Gs/Gd)-descended H5 viruses is highly pathogenic and has led to diversification of the HA gene through gene reassortment (gRA) with low pathogenic avian influenza viruses (LPAIV), increasing their adaptability to different hosts. While mapping the hotspots of gene reassortment between HPAIV and LPAIV is crucial, two main challenges exist. First, most studies used only the H5 gene to infer its epidemiological transmission and evolution. However, no lineage information is available for other AIV gene segments. Second, wild birds are considered the natural reservoir of LPAIV; however, their geographical distribution and the quantitative risk in contributing to gRA are unknown. In this study, we developed a one-health approach by integrating viral genomic data, wild bird distribution, and environmental factors to identify the ecological niche of gene exchange since 1997.

Methods

Multiple data sources up to 2023, including complete genomes of global avian influenza viruses, the EurAsia eBird dataset, poultry density, and land-cover distribution, were curated. Due to the large number of sequences, a standardized pipeline and algorithm were established to ensure sequence quality and consistent genotyping. Different genotypes of H5 viruses indicate gRA. Genotype hotspot analysis and a three-stage case-control study design were deployed to examine the association between environmental factors, including wild bird species distribution, and gRA hotspots.

Results

From 1997 to 2023, HPAIV H5 subtype exhibited increasingly complex genetic exchanges, with a total of 136 genotypes identified in this study. Three distinct waves were observed from mono-genotype-dominant (2000–2013) to multi-genotypic co-circulation (2014–2021), followed by regional endemicity (2022–2023). The matched-pair study found that bird species in the orders Anseriformes, Charadriiformes, and Passeriformes are significantly positively associated with RA-hotspots, which were further developed into a poly-species risk score (PRS). The environmental drivers associated with RA-hotspots include PRS and different landcover types. Interestingly, the dynamic changes in H5 HPAIV genotypes are consistent with the transition of environmental drivers from waterfowl to landfowl,

Conclusions

The rapid evolution and reassortment of HPAIV H5N1 underscore the urgent need to monitor and assess the risk of emerging variants to mitigate future risks. Our study provides a comprehensive analysis of the spatiotemporal changes in HPAIV reassortment over the past 20 years in Eurasia, using a novel approach that integrates ecological modeling and viral sequence genotyping. The dynamic genotype changes during 2000–2021 corresponded to the transition in poultry farming indices toward chicken stocking density. The risk map of RA hotspots in Eurasia from this study could provide insights for targeted surveillance and mitigation strategies.

628 – Breastfeeding as a One Health Strategy: Advancing Maternal–Child Health, Environmental Sustainability, and Policy Governance in the Philippines

Efrelyn IELLAMO

University of the Philippines Manila, Philippines

Background:

Breastfeeding is widely recognized as a cornerstone of maternal and child health, providing optimal nutrition, strengthening infant immunity, and reducing maternal health risks. Beyond these well-documented benefits, breastfeeding also contributes to broader societal and environmental outcomes that align with the One Health framework, which emphasizes the interconnectedness of human, environmental, and socio-economic systems. In low- and middle-income countries, breastfeeding promotion policies may simultaneously improve population health, reduce environmental burdens associated with commercial milk production, and strengthen health system resilience. The Philippines has implemented several legislative and policy initiatives aimed at protecting and promoting breastfeeding. However, the extent to which these policies reflect an integrated One Health approach has not been systematically examined.

Objective:

This study examines breastfeeding governance in the Philippines as a One Health strategy by analyzing how national policies integrate human health protection, environmental sustainability, and multisectoral.

Methods:

A qualitative policy analysis was conducted using key Philippine legislative and regulatory frameworks that support breastfeeding promotion. Major policies analyzed included Executive Order No. 51 (Philippine Milk Code), Republic Act 7600 (Rooming-In and Breastfeeding Act), Republic Act 10028 (Expanded Breastfeeding Promotion Act), and Republic Act 11148 (First 1,000 Days Law). Policy documents and implementing guidelines were systematically reviewed using a One Health analytical lens focusing on three domains: (1) human health outcomes, particularly maternal and infant health protection; (2) environmental implications associated with infant feeding practices, including resource use and waste generation; and (3) governance mechanisms that facilitate multisectoral coordination among health,

labor, and local government institutions. The analysis explored how these policy instruments collectively support integrated approaches to health promotion and sustainable development.

Results:

Findings indicate that breastfeeding promotion in the Philippines contributes significantly to improved public health outcomes, including enhanced infant immunity, reduced risk of infectious diseases, and decreased maternal morbidity associated with breast and ovarian cancers. From an environmental perspective, breastfeeding reduces reliance on industrial milk production and formula supply chains, which are associated with high carbon emissions, water consumption, and plastic waste from packaging. By supporting natural infant feeding practices, breastfeeding policies contribute to more sustainable food systems and reduced environmental impact. Governance mechanisms embedded within Philippine breastfeeding policies demonstrate strong multisectoral collaboration among government agencies, healthcare institutions, workplaces, and local government units. These coordinated efforts illustrate a systems-based approach consistent with the principles of One Health.

Conclusion:

Breastfeeding promotion policies in the Philippines represent a scalable and cost-effective One Health strategy that simultaneously advances maternal and child health, environmental sustainability, and inclusive governance. Integrating breastfeeding promotion into global One Health agendas may strengthen preventive health systems while contributing to climate and sustainability goals. The Philippine experience provides important policy insights for countries seeking holistic and sustainable approaches to early-life health interventions.

Thematic Analysis of Breastfeeding Policies in the Philippines Using a One Health Framework

Policy Document	Human Health Theme	Human Health	Environmental Theme	Governance Theme	Key Insight from Policy Analysis
EO 51 – Philippine Milk Code	Protection of infant nutrition and breastfeeding practices	Reduced reliance on formula production and packaging	Reduced reliance on formula production and packaging	Regulation of breastmilk substitute marketing	Protects breastfeeding as the optimal infant feeding practice.
RA 7600 – Rooming-In and Breastfeeding Act	Early breastfeeding initiation and maternal-infant bonding	Encourages natural feeding practices	Encourages natural feeding practices	Institutional breastfeeding support in hospitals	Strengthens early-life health interventions.
RA 10028 – Expanded Breastfeeding Promotion Act	Supports breastfeeding among working mothers	Supports breastfeeding duration	Sustains breastfeeding duration	Workplace lactation stations and employer responsibilities	Integrates maternal health with labor policies.
RA 11148 – First 1,000 Days Law	Maternal and child nutrition and development	Maternal and child nutrition and development	Supports sustainable nutrition practices	Multisectoral nutrition governance	Strengthens national nutrition and early-life health programs.

633 – Programmable CRISPR-Cas9 host depletion improves microbial detection in metagenomic rodent surveillance

Joachim MARIEN (1), Emilie VAN VYVE (1), Mare GERAERTS (1), Baraka MWAMUNDELA (3), Tine COOREMAN (1), Apia MASSAWE (3), Sophie GRYSEELS (2), Lucinda KIRKPATRICK (4), Herwig LEIRS (2), Kevin ARIEN (1), Philippe SELHORST (1)

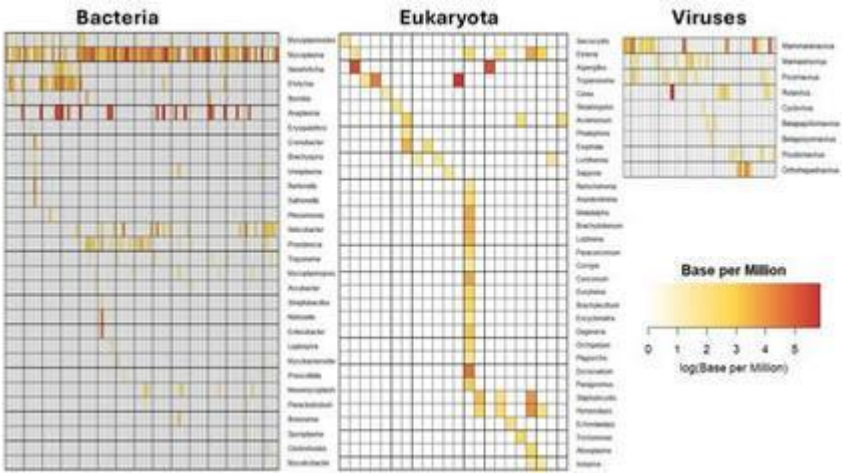
1: Department of Biomedical Science, Institute of Tropical Medicine Antwerp, Antwerp, Belgium; 2: Evolutionary Ecology group, Department Biology, University of Antwerp, Wilrijk, Belgium; 3: Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania; 4: Prifysgol Bangor University, Bangor, United Kingdom

Background: Unbiased pathogen surveillance in reservoir hosts is often constrained by the overwhelming abundance of host nucleic acids in metagenomic sequencing libraries. Here, we combine a flexible CRISPR-Cas9 host-depletion approach with metagenomic sequencing to improve detection of low-abundance microbes in small-mammals, and we report the pathogen diversity recovered from wild-caught rodents in Morogoro, Tanzania.

Methods: We first designed a rodent DASH (Depletion of Abundant Sequences by Hybridization) panel targeting cytoplasmic and mitochondrial rRNAs (18S, 5.8S, 28S, 12S, 16S) and an abundant mitochondrial transcript (ND2) in *Mus musculus* and *Mastomys natalensis.* In serum samples host depletion markedly reduced rRNA backgrounds and increased the proportion of viral reads, outperforming a commercial depletion reagent and enabling ND2 depletion not achieved by the kit. We then applied this workflow to 436 wild small mammals (pooled into 93 serum libraries) sampled in 2021 and 2023, dominated by *M. natalensis*. After stringent filtering against controls, we detected mammal-associated sequences from nine viral families, 15 bacterial genera, and 17 eukaryotic parasite genera.

Results: Viral reads were identified in 39 pools and yielded complete genomes from multiple taxa (Fig 1). Notably, we recovered six full mammarenavirus genomes clustering within the Morogoro/Mopeia arenavirus clade, all from pools containing only *M. natalensis*. We also retrieved two orthohepadnavirus genomes related to musk hepatitis shrew virus from pools containing *Crocidura* spp., highlighting shrews as potentially underappreciated viral reservoirs. A complete rotavirus A genome was recovered from *M. natalensis*, alongside cycloviruses, a mammastrovirus related to rat mammastrovirus, and multiple picobirnavirus segment 2 sequences. Among bacteria, Mycoplasma was most frequently detected, followed by Anaplasma and Ehrlichia, with additional detections including Borrelia, Bartonella, and Salmonella.

Conclusions: these results demonstrate that programmable host depletion can make metagenomic wildlife surveillance more sensitive and cost-effective, while revealing substantial viral and microbial diversity in a key African rodent reservoir system.



637 – Cropland expansion and intensification decouples host-climate interactions and erodes pathogen buffering in a major zoonotic reservoir.

Lucinda KIRKPATRICK (1), Joachim MARIEN (2,4), Apia MASSAWE (3), Herwig LEIRS (4)

1: Bangor University, Bangor, United Kingdom; 2: Institute of Tropical Medicine, Antwerpen, Belgium; 3: Sokoine University of Agriculture, Morogoro, Tanzania; 4: University of Antwerp, Antwerp, Belgium

Anticipating zoonotic spillover risk requires understanding how host demography, community diversity, and pathogen dynamics respond to accelerating global change. Yet long-term datasets that capture all three simultaneously remain exceptionally rare, particularly in sub-Saharan Africa where transformation of natural landscapes is most rapid. Here we present analyses of a 30-year monthly capture-mark-recapture dataset from Morogoro, Tanzania, combined with concurrent screening for Morogoro virus (MORV), a mammarenavirus hosted by *Mastomys natalensis*, one of Africa's most widespread rodent reservoir hosts. Using wavelet analysis, distributed lag nonlinear models, and regime shift detection, we show that *M. natalensis* populations have undergone a fundamental demographic regime shift since approximately 2012, decoupling from climatic drivers and declining markedly in abundance across multiple sites, consistent with a landscape-scale process. Regime shifts align temporally with agricultural intensification in the surrounding area rather than with climatic forcing, suggesting that cropland expansion has eliminated key source populations and eroded recolonisation potential. Critically, exposure to MORV was more strongly predicted by host community diversity than by abundance or climate, with a strong negative relationship consistent with a dilution effect. However, this protective effect was dynamic, lagged, and seasonal, demonstrating that biodiversity's buffering capacity against zoonotic spillover can be lost and regained within annual cycles. Together, these findings suggest that agricultural intensification has pushed this system toward an ecological tipping point, simultaneously driving demographic collapse and eroding the natural pathogen buffering that host diversity provides. These dynamics, detectable only through rare long-term datasets, highlight that spillover risk in degraded landscapes may be highly sensitive to small fluctuations in host community composition, with important implications for how ecosystem restoration could rebuild disease resilience.

643 – Wildlife Inclusion in AMR National Action Plans: A Global Policy Analysis

Nicholas BOR (1), Aidan KEANE (2), Geoff SIMM (1), Jessica MITCHELL (1)

1: Division of Global Agriculture and Food Systems, Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK;; 2: School of Geosciences, University of Edinburgh, UK.

Background: The aim of this policy analysis was to determine the extent to which wildlife has been incorporated into antimicrobial resistance (AMR) policy documents—publication forthcoming.

The One Health approach calls for equitable integration of human, animal, and environmental sectors in AMR governance and interventions. Although wildlife is increasingly recognised as part of the ecological interface through which resistance may emerge and spread, its representation within national policy frameworks remains unclear. Previous analyses of AMR policy documents have assessed aquaculture inclusion, human health interventions, or regional assessments of wildlife representation. To date, no global study has systematically examined the extent to which wildlife is incorporated into AMR National Action Plans (NAPs) or the context in which it is referenced.

Methods: This study analysed NAPs that had been uploaded onto the World Health Organization (WHO) library as of November 2025. The NAPs were searched for the key terms “wildlife” or “wild” which were used to identify wildlife references. The policy documents were analysed using Braun and Clarke’s reflexive thematic analysis approach. Relevant excerpts containing the search terms were **extracted verbatim, reviewed within the context of the original NAPs, and used to generate initial codes**. The codes were compared and grouped based on conceptual similarity to generate themes that reflect the patterns in which wildlife was framed within the policy documents. The generated themes were reviewed and refined to ensure coherence and clear distinction between them. The number of NAPs containing wildlife references was recorded.

Results: 177 AMR NAPs from 145 countries, representing all six WHO regions, were reviewed. Of these, 20 (11%) contained at least one explicit reference to wildlife. Across these 20 NAPs, a total of 58 wildlife mentions were identified, indicating limited global policy integration of wildlife.

Reflexive thematic analysis identified four contexts in which wildlife was discussed: One Health definitions (23/58, 40%), proposed actions (18/58, 31%), governance (10/58, 17%), and section headings (7/58, 12%). Most references appeared within broad One Health definitions, where wildlife was

acknowledged conceptually. Mentions related to proposed actions included calls for surveillance of resistance in wildlife and increased research in the sector. However, both One Health definitions and proposed actions lacked operational detail or implementation mechanisms. Governance-related references primarily involved the inclusion of wildlife-affiliated institutions in national AMR coordinating committees. Finally, some mentions appeared only within document section subheadings without substantive discussion. These findings highlight the limited inclusion of wildlife in AMR policy frameworks.

Conclusions: The limited and largely symbolic inclusion of wildlife in AMR NAPs suggests an uneven operationalisation of the One Health approach. Strengthening wildlife integration within national AMR governance frameworks could be key to achieving truly cross-sectoral AMR mitigation strategies.

649 – The Impact of Public versus Private Healthcare Spending on Healthy Life Expectancy: A Dynamic Panel Analysis of 87 Countries from 2000 to 2019

Heriberto MARIN-CENTENO, Elba DIAZ-TORO, Ralph RIVERA-GUTIERREZ
Recinto de Ciencias Medicas, Universidad de Puerto Rico, Puerto Rico (U.S.)

Background Healthy life expectancy (HALE) captures both longevity and quality of life, providing a comprehensive measure of population health. Yet, little is known about how public versus private healthcare expenditures affect HALE over time.

Methods We analyzed a balanced panel of 87 countries from 2000–2019, prior to COVID-19 disruptions. A dynamic panel model using two-step System GMM was applied, with the annual growth rate of HALE as the dependent variable. Public and private healthcare expenditures per capita (five-year lags) were the main explanatory variables, controlling for GDP per capita, aging, population density, gender composition, caloric intake, education, prior health status, and year effects.

Results Public health spending showed robust positive associations with HALE across multiple lags. The cumulative five-year elasticity was 0.0489 (p 0.0001), equivalent to approximately 111 additional days of healthy life expectancy for a sustained 10% increase in public spending. In contrast, private spending showed no significant effect (elasticity = 0.0014; p = 0.9118).

Conclusions Public healthcare investment consistently promotes healthier, longer lives, while private expenditure contributes little to population-level gains. Strengthening public financing, particularly for preventive care and infrastructure, offers a more equitable and sustainable pathway to health promotion. These findings reinforce the critical role of public systems in advancing health equity and inform ongoing debates on health financing reform.

655 – Operationalizing a gender sensitive One Health approach in rural communities of Burkina Faso and Sénégal: The ELUZO project

Marine HUBERT (1,2), **Maude GILBERT-VANASSE** (8), Abdoul Kader ILBOUDO (3), Alexis KAFANDO (4), Rosalie SECK (5,11), Michèle BOUCHARD (6,9), Heather M. MURPHY (7), Jane PARMLEY (7), Zékiba TARNAGDA (3), Adama FAYE (10), Hélène CARABIN (1,2,6,9)
1: Université de Montréal, Faculté de médecine vétérinaire, Saint-Hyacinthe, Québec, Canada; 2: Groupe de Recherche en Épidémiologie des Zoonoses et Santé Publique (GREZOSP), Université de Montréal, Saint-Hyacinthe, Québec, Canada; 3: Institut de Recherche en Sciences de la Santé (IRSS), Ouagadougou, Burkina Faso; 4: Société d'étude et de Recherche en Santé Publique (SERSAP), Ouagadougou, Burkina Faso; 5: Ministère de l'Agriculture, de la Souveraineté Alimentaire et de l'Élevage (MASAE), Dakar, Senegal; 6: École de Santé Publique, Université de Montréal, Montréal, Canada; 7: Ontario Veterinary College, University of Guelph, Ontario, Canada; 8: UdeM international, Université de Montréal, Québec, Canada; 9: Centre de recherche en santé publique (CReSP), Université de Montréal, Québec, Canada; 10: Université Cheikh Anta Diop de Dakar (UCAD), Institut de Santé et Développement, Dakar, Sénégal; 11: COMI (Cooperation for the World in Development), Roma, Italy

Introduction: Livestock systems are central to the livelihoods of rural communities in Senegal and Burkina Faso, where women and girls manage poultry, small ruminants, and pigs. Limited access to water, sanitation, health and veterinary services increases the risk of zoonotic disease transmission at the human-animal-environment interface.

The ELUZO project (“Elles Luttent contre les Zoonoses”) is a women-centered, intersectoral One Health initiative aiming to reduce zoonotic disease risks and strengthen gender equity while co-developing community-driven interventions. Coordinated across 11 institutions in Canada, Senegal, and Burkina Faso, ELUZO brings together experts in human, animal and environmental health, social sciences, gender, WASH, and epidemiology, in collaboration with national One Health platforms, local ministries and non-governmental organizations. A unique feature of ELUZO lies in its governance model, which bridges research and international development approaches through a multi-country, multisectoral and multi-disciplinary structures and places communities - especially women and girls – at the centre of identifying challenges and co-designing intervention. The project also integrates capacity-building through One Health and gender-equity trainings at institutional and community levels.

Methods: A mixed-methods baseline assessment (June-September 2024) was conducted across 5 villages in Senegal and 6 villages in Burkina Faso. Quantitative household surveys included approximately 1800 respondents in Burkina Faso and 1100 in Senegal. Qualitative activities included 27 focus groups, 34 interviews, and 12 participatory mapping exercises, complemented by direct field observations and literature reviews. Triangulation across all sources was done to identify convergent patterns in livestock practices, zoonotic risks, environmental conditions, and gender dynamics. Findings were presented to communities during feedback meetings to inform the participatory selection of interventions.

Results: Across both countries, five domains of concern emerged: 1) livestock management practices, including free-ranging systems and hygiene/biosecurity ; 2) limited human and animal health and environmental services and access ; 3) WASH and solid waste issues, such as the absence of latrines, restricted water access and poor waste management; 4) under-reporting or non-reporting of animal diseases, particularly at slaughter, due to lack of trained inspectors, fear of economic losses, and low integration of local surveillance systems; 5) gender inequities affecting women’s decision-making and access to resources.

Following the presentation to community meetings, villages prioritized feasible, affordable and relevant interventions; in Senegal, construction of community latrines and solid waste disposal sites; in Burkina Faso, rehabilitation of non-functional water points and training of meat inspectors with appropriate inspection areas.

Conclusion: ELUZO demonstrates how combining quantitative and qualitative methods with community participation can operationalize a gender-sensitive One Health approach in rural West Africa. This integrated methodology enabled the identification of local priorities, and the co-design of realistic interventions reflected the local needs. The community-selected interventions strengthen local resilience and ensure women’s empowerment within One Health actions.

660 – Beyond the conventional: Environmental phage as an adjuvant for treating multidrug resistant Pseudomonas aeruginosa infections

Clinton MOODLEY (1,2), Dean BRINK (1), Lynthia PAUL (1,2), Stefan OPPERMAN (1,2)

1: University of Cape Town, Department of Pathology, Division of Medical Microbiology, Cape Town, South Africa; 2: National Health Laboratory Service, Microbiology Laboratory, Groote Schuur Hospital, Cape Town, South Africa

Background: Antimicrobial resistance (AMR) is a naturally occurring phenomenon, exacerbated by antibiotic misuse and overuse, and contributes to significant morbidity and mortality. In 2019, AMR directly caused 1,27 million deaths and was associated with 4,95 million deaths, of which 72% were associated with six WHO high-risk pathogens belonging to the ESKAPE group. There is a critical need to explore alternative therapeutic options. Phage therapy involves the use of one or more virulent bacterial viruses to destroy a pathogen underlying infection. Phages have several advantages when compared to antibiotics including narrow host ranges, ubiquity in nature, and efficacy against AMR bacteria. This study investigated whether lytic phage could be isolated from treated effluent that may exhibit antibacterial activity against a panel of multidrug resistant *Pseudomonas aeruginosa* (MDR-PA) clinical isolates, as a potential adjuvant to conventional antibiotic therapy.

Methods: Effluent was provided by the City of Cape Town Municipality, Cape Town, South Africa. Samples were pre-processed by filtering to remove residual bacteria and debris, and stored at 4°C. A collection of 23 MDR-PA was obtained from a repository at the Division of Medical Microbiology, University of Cape Town, South Africa (UCT HREC R009/2020). To screen for phage activity, double agar overlay assays, direct

spot testing, and electron microscopy were employed. To investigate genomic resistance mechanisms to the phage, the collection underwent Oxford Nanopore long read sequencing and bioinformatic analyses.

Results: Only 10/23 MDR-PA exhibited lytic phage plaques using the double agar overlay assay, and 3/10 were confirmed to have consistent lytic activity with direct spot testing, using the purified phage plaques. Isolate 11 produced plaques with reproducible lytic activity and 5 plaques were subsequently selected for further characterization. Of these, 2/5 were classified using electron microscopy, suggestive of siphovirus with virion heads ≈66nm, and contractile tails ≈170nm.

ONT sequencing of 22/23 bacterial isolates, *in silico* Multi Locus Sequence Typing, and core genome phylogeny indicated a wide distribution among know MDR-PA lineages and STs, indicating a broad microbial host range representation. Several diverse antiviral defence systems were distributed across the bacterial cohort, with 61% of these indicating abortive infection mechanisms. Antiviral systems were varied between linages although all isolates contained at least one integrated prophage, and one isolate harboured 23 different antiviral defence types.

Conclusion: This study highlighted the presence of lytic environmental phage from wastewater in South Africa. Moderate activity was noted against a panel of clinical MDR-PA, with a diverse array of antiviral systems and integrated phage conferring resistance. This pilot study serves as a platform for further large-scale screening of environmental samples to develop a local phage repository as a resource for adjuvant antimicrobial therapy against multidrug resistant bacterial infections.

662 – Microbial emissions from manure processing: Towards a monitoring framework to protect public health

Sophia DOLLMANN (1), Jack SCHIJVEN (1,2), Marina STERK (1), Sharona DE RIJK (1), Ciska SCHETS (1), Ana Maria DE RODA HUSMAN (1,2)

1: National Institute for Public Health and the Environment (RIVM), The Netherlands; 2: Utrecht University, The Netherlands

Background: With an increase in manure processing in the Netherlands and uncertain risks of microbial emissions for residents, the question arises how to efficiently monitor microbial emissions from manure processing. The objective of this study is to provide initial steps to monitor microbial emissions from pig farms with manure processing in order to assess potential risks to public health.

Methods: Intestinal enterococci (IE) and spores of sulfite-reducing Clostridia (SSRC) were selected to indicate the possible presence of manure-borne pathogens in air surrounding (on-farm) manure processing. Besides sampling manure and air at varying distances upwind and downwind from the manure processing plant, the atmospheric dispersion of IE and SSRC was predicted up to 2000 m by applying a Gaussian plume model.

Results: IE and SSRC were detected in raw manure and in all processed manure samples, except for the fraction treated with a membrane bioreactor. Also in air, IE and SSRC were found in varying concentrations. The modelled indicator concentrations in the air decreased at greater distances from the manure processing plant.

Conclusions: Since IE and SSRC were detected in raw and processed manure as well as in air, it may be concluded that IE and SSRC are suitable indicators for monitoring microbial emissions from manure processing. The Gaussian plume model was used to estimate the emission strength and predict the dispersion of indicators over greater distances. Uncertainties in the estimated emission strength and the predicted concentrations were due to the limited number of measurements, differences in and restrictions of the study locations, and possible influence of farm emissions on the measured indicator concentrations. Model uncertainties can be improved by further research at centralized manure processing plants with a single emission source. These initial steps provide insights into the dispersion of microbial emissions of manure processing and can provide input for a monitoring framework.

666 – Effect of antioxidant-enriched feed on growth performance and gut microbiota composition in broiler chickens

Máté HETYÉSY (1,2), Hedvig FÉBEL (3), Ákos JERZSELE (1,2), Ádám KEREK (1,2)

1: Department of Pharmacology and Toxicology, University of Veterinary Medicine Budapest, Budapest, Hungary; 2: National Laboratory of Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health and Food Chain Safety, University of Veterinary Medicine Budapest, Hungary; 3: Department of Obstetrics and Food Animal Medicine Clinic, University of Veterinary Medicine Budapest, Budapest, Hungary

Background

In intensive poultry production, feed additives that support intestinal health are receiving increasing attention as potential tools for improving productivity while reducing reliance on antimicrobials. Because perturbations of the gut microbiota may influence animal health, production efficiency, and antimicrobial resistance-related ecological dynamics, the identification of effective non-antibiotic interventions is of growing One Health relevance. This study aimed to evaluate the individual and combined effects of a feed-supplemented antioxidant complex and enrofloxacin treatment on growth performance and caecal microbiota composition in broiler chickens.

Methods

A total of 1,200 Ross-308 male broiler chickens were allocated to six treatment groups and reared for 42 days under intensive production conditions. The antioxidant complex was administered either from the 1st week or from the 3rd week of age, alone or in combination with enrofloxacin treatment. Caecal samples were collected on days 14, 20, and 42. Gut microbiota composition was analyzed using Oxford Nanopore MinION sequencing, and treatment-associated differences were evaluated together with production performance indicators.

Results

Both antimicrobial and antioxidant-based interventions affected microbial community structure and production traits. The group receiving antioxidant supplementation from the 3rd week of age (T4) showed the highest body weight gain among the experimental groups. At the microbiota level, the T4 group, as well as the group supplemented with antioxidants throughout the entire rearing period (T6), exhibited an increased relative abundance of the Lactobacillaceae family, consistent with a more favorable intestinal microbial profile. In contrast, groups receiving combined antibiotic treatment showed higher relative abundances of opportunistic bacterial families, including Helicobacteraceae and Moraxellaceae, indicating a less stable microbial community structure.

Conclusions

Antioxidant supplementation, particularly when initiated from the 3rd week of age, was associated with improved growth performance and a more favorable caecal microbiota composition in broiler chickens. These findings support the relevance of antioxidant-based feeding strategies as promising components of sustainable poultry production. From a One Health perspective, such approaches may contribute to microbiome-supportive flock management and to more prudent antimicrobial use in animal production systems.

672 – Understanding the human behavioural factors that influence bird to human zoonotic disease spread within small-scale poultry flocks in Ontario, Canada

Breanne MURRAY (1), Amy GREER (2), Katherine PAPHITIS (3), Lauren GRANT (1), Kelsey SPENCE (1)

1: Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; 2: Department of Biology, Trent University, Peterborough, Ontario, Canada; 3: Public Health Ontario, Toronto, Ontario, Canada

Background: Public interest in keeping small-scale poultry flocks has increased in Ontario in recent years. Many small-scale poultry keepers have reported a desire to have their own food production system, prioritize homesteading, or keep birds for companionship. Small-scale poultry keepers often engage in frequent direct contact with their birds, which poses risks for pathogen transmission. Several pathogens, such as *Salmonella* and *Campylobacter* bacteria, can be shed through contact with poultry, their feces, and their environment. Small-scale poultry keepers, especially those who do not implement infection prevention and control measures, may be at increased risk of disease. This study aimed to identify Ontario small-scale poultry keeper's perceptions of zoonotic disease and attitudes towards infection prevention and control measures.

Methods: Participants were recruited between September 2024 to February 2025 via convenience sampling through advertisements on social media and email lists of local poultry organizations. Eligible participants were Ontario-residents aged 18 years or older who kept a small-scale poultry flock, which was defined as caring for 1 or more chickens, turkeys, geese, ducks, pheasants, guinea fowl, and/or quail on their property for companionship, personal household use, or other non-commercial purposes. Participation consisted of attending one semi-structured interview held on Zoom, where their experiences as a poultry keeper and perceptions on zoonotic diseases were discussed. Interviews were recorded, transcribed verbatim, and analyzed using a constructivist grounded theory approach.

Results: In total, 21 participants were interviewed and included in the study. Many participants had regular interactions with multiple pets or other livestock, and poultry were just one of the many species present on their property. Infection prevention and control measures were not regularly considered by many participants, but they reported frequently looking for signs of illness or strange behaviours within their flock to protect individual bird health, rather than to reduce the risk of zoonotic disease spread. Participants' infection prevention and control behaviours were primarily shaped by their own past experiences, with the most common practice being regular visual checks of birds to identify early signs of an issue. Participants frequently relied on others, such as their own community networks, for advice about poultry health and management. Participants also reported tensions and mistrust between small flock poultry keeper communities and government authorities, which was thought to lead some keepers to conceal their activities and distance themselves from engagement with government officials and researchers.

Conclusions: Zoonotic pathogens are a significant public health concern, and small-scale poultry keepers may be at increased risk of exposure due to frequent interactions with their birds and limited prevention measures. Public health communication efforts and interventions should account for the already established community networks that small flock poultry keepers have for promoting biosecurity and disseminating knowledge about zoonotic diseases.

678 – Predicting the spectrum of Rift Valley fever virus dynamics across Africa using observed seroprevalence patterns

Melinda K ROSTAL (1,2), Morgan KAIN (1), Peter N THOMPSON (2), Veerle MSIMANG (3), Rebecca F BODENHAM (4), Bruno LOKONON (5), Shruti MURTHY (6), Paul JOHNSON (7), Nichar GREGORY (1), Johana TEIGEN (1), AbdulHamid LUKAMBAGIRE (4), Blandina MMBAGA (4,8), Noam ROSS (9)

1: One Health Research Consulting, United States of America; 2: Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, South Africa; 3: Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, National Health Laboratory Service, South Africa; 4: Kilimanjaro Clinical Research Institute, Moshi, Tanzania; 5: Laboratory of Biomathematics and Forest Estimations, University of Abomey-Calavi, Benin; 6: Centre for International Health, University of Otago, New Zealand; 7: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, UK; 8: Kilimanjaro Christian Medical University College, Moshi, Tanzania; 9: rOpenSci, USA

Background: Rift Valley fever (RVF) is a vector-borne zoonosis of high economic importance. It is well-known for its large, sporadic outbreaks that can result in widespread abortion storms in sheep, cattle, and goats in Africa. Vector life-cycle traits are tightly linked with climate cycles, in particular the El Niño Southern Oscillation phenomenon and abnormally high rainfall, though outbreak prediction remains challenging. We recently challenged the epidemic-centric epidemiology of Rift Valley fever virus (RVFV) and propose that its epidemiological dynamics range from hyperendemic dynamics (with high RVFV circulation and rare or no outbreaks) to highly epidemic dynamics (with large, widespread outbreaks and prolonged interepidemic periods). **Methods:** Using an updated pan-African dataset of animal serological results linked with climate and environmental variables, we fit a quantile random forest model to predict the full conditional distribution of seroprevalence, allowing us to approximate the latent long-term seroprevalence distribution whose shape reflects the underlying transmission regime. Specifically, we clustered predictions made at a 10x10km spatial resolution across Africa into four latent transmission regimes: hyperendemic, intermediate (in the middle of the spectrum), low epidemic (higher seroprevalence with more frequent outbreaks), and high epidemic (lower seroprevalence with infrequent outbreaks). **Results:** We predicted that the East coast of Africa, parts of the Sahel region and central Madagascar are likely to have hyperendemic RVFV dynamics. **Conclusion:** It is critical to investigate the hyperendemic dynamics in these regions to understand the true burden of infection of Rift Valley fever. The tight link between environment and RVFV epidemiological regimes suggests that future climate- and

land use-changes may shift the dynamics of RVFV epidemiology in a given region between epidemic and hyperendemic dynamics.

687 – Community-based Organizations as One Health Partners to Improve Community Uptake of Vector Control Strategies

Kacey ERNST (1), Skyler FINUCANE (1), Jordan ROBINSON (1), Sarah YEO (1), Mary HAYDEN (2)

1: University of Arizona, United States of America; 2: University of Colorado, Colorado Springs, United States of America

Background: Vector-borne diseases (VBDs) are a growing One Health challenge globally. Public engagement in prevention is critical, yet current messaging campaigns are often broad and are not targeted towards individuals at their point of decision making around increased environmental risks. Community-based organizations (CBO) such as hardware stores, community gardens, nurseries, and feed stores, have routine interactions with the public critical moments of decision-making. To date, minimal efforts have been made to partner with CBO to disseminate prevention information across human, animal, and environmental health domains. This study examined the current roles, perceived responsibilities, and partnership potential for VBD education in southern Arizona.

Methods: We conducted key informant interviews with managers, owners, and coordinators from community-facing organizations. Eligible sites including hardware stores (n=28), community gardens (n=10), nurseries (n=12), and feed stores (n=14) were systematically identified and mapped using GIS. Organizations were contacted via phone and screened for eligibility before scheduling semi-structured interviews. Interview domains included VBD awareness, customer inquiries regarding mosquito and tick control, perceived organizational roles in prevention education, and willingness to disseminate information. Interviews were recorded, transcribed, and analyzed using thematic qualitative analysis. Screening data were summarized descriptively.

Results: Thirty-seven CBO have completed screening interviews as of 3/10/2026. We conducted 15 key informant interviews in Pima County (hardware stores n=6, community gardens n=4, nurseries n=2, feed stores n=3). Most screened organizations (78%, 29/37) reported receiving questions from customers about mosquito or tick control, and 84% (31/37) expressed interest in sharing educational materials with their communities. Preliminary thematic analysis identified distinct roles across CBO. Hardware stores served as high-frequency, low-burden touchpoints focused on product guidance for mosquito and tick control. Community gardens emphasized peer learning and environmental management, particularly standing water reduction. Garden centers highlighted nature-based approaches to mosquito prevention that were protective of non-target insect species. Feed stores framed vector control within a One Health perspective, emphasizing livestock and pet health risks. Dissemination strategies identified to date range from training personnel who conducted site visits (feed stores) to posters and short educational videos. Across all groups, participants expressed willingness to support education efforts but emphasized the need for concise messaging, practical prevention guidance, and minimal staff training.

Conclusions: Key informant interviews and in-depth thematic analysis are ongoing. Preliminary findings suggest that CBO represent promising, underutilized partners for expanding VBD prevention messaging. Tailored materials that meet the unique operational realities and perceived roles of each organization type will be needed. Working with these partners may improve community uptake of appropriate strategies to reduce disease vectors while optimizing the health of the environment and non-target organisms. Integrating these partners into public health practice may lead to better public communication regarding One Health risks and mitigation strategies.

Organization Type	Public Interaction	Perceived Role	Messaging Focus
Hardware stores	High-frequency customer contact	Product guidance and decision support	Mosquito control products, yard management
Community gardens	Community engagement	Peer learning and environmental stewardship	Standing water reduction, community prevention
Garden centers	Moderate interaction	Ecological pest management guidance	Habitat management, non-chemical control
Feed stores	Animal-focused interaction	Animal health decision support	Livestock and pet protection, zoonotic disease awareness

692 – Scoping Review: Developing a One Health Surveillance Framework with Community Participatory Approaches for Zoonotic Spillover and Climate Change in African Contexts

Getrude NJOKWE (1,2), Marinda DE VRIES (1), Marike GELDENHUYS (1), Tedson NKOANA (2), Wanda MARKOTTER (1,2)

1: Centre for Viral Zoonoses, Department of Medical Virology, University of Pretoria, Pretoria, Gauteng, South Africa; 2: Future Africa Platform, University of Pretoria, Pretoria, Gauteng, South Africa

Background: Viruses pose growing risks at expanding human-wildlife-environmental interfaces. Although One Health approaches offer holistic prevention potential, climate-integrated and community-driven surveillance frameworks remain limited in resource-constrained African settings. This scoping review maps existing One Health surveillance frameworks and community participatory approaches for zoonotic spillover prevention in Africa and evaluates their integration of climate factors to inform the development of a scalable surveillance framework for resource-constrained settings.

Methods: A scoping review was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) and the Joanna Briggs Institute methodological guidance. Literature searches were performed in major bibliographic databases and grey literature sources without date restrictions. Studies addressing One Health surveillance systems, frameworks, or community participatory approaches relevant to zoonotic spillover prevention in African contexts were eligible for inclusion. Screening and data extraction were conducted using Covidence software. Extracted data included information on surveillance system characteristics, community engagement approaches, cross-sectoral coordination mechanisms, and the integration of climate or environmental considerations. Thematic analysis was used to synthesise patterns across the included studies.

Results: Of 1,639 records identified, 100 studies were included. The findings reveal a fragmented landscape of One Health implementation across African contexts, with uneven coordination between human, animal, and environmental sectors. Community participatory approaches ranged from consultative engagement to empowerment-based models involving community health workers, participatory disease detection, and integration of local knowledge. These approaches support trust-building and may enhance early detection of disease risks in high-exposure communities. However, the integration of climate considerations within surveillance systems was limited, particularly regarding ecosystem change, altered bat ecology, and climate-driven shifts in spillover dynamics. Key gaps identified include weak environmental and climate data integration, limited operationalisation of One Health strategies at the community level, inadequate sustainable financing, and insufficient context-sensitive surveillance tools for rural settings.

Conclusions: The findings highlight important gaps in the implementation of integrated One Health surveillance systems in Africa, particularly regarding climate-informed surveillance and meaningful community participation. This review advances the field by proposing a conceptual, climate-informed One Health surveillance framework that strengthens cross-sectoral governance, embeds community ownership, enhances early warning capacity, and aligns with existing health systems. The framework aims

to support adaptive, prevention-oriented surveillance and improve health security in vulnerable African settings.

696 – Establishing an insectivorous bat model to study MERS-CoV infection dynamics, immune responses and viral persistence

Kaushal BAID (1), Sauhard SHRIVASTAVA (1,2), Akarin ASAVAJARU (1), Arkadeb BHUINYA (1,2), Arianna HURTADO (1), Kim CHIOK (1), Shane SEHEULT (3), Darryl FALZARANO (1), Paul FAURE (3), **Arinjay BANERJEE** (1,2,4,5,6)

1: Vaccine and Infectious Disease Organization (VIDO), University of Saskatchewan, Saskatoon, SK, Canada; 2: Department of Veterinary Microbiology, WCVM, University of Saskatchewan, Saskatoon, SK, Canada; 3: Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, ON, Canada; 4: Department of Biology, University of Waterloo, Waterloo, ON, Canada; 5: Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada; 6: Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada

Background: Middle East respiratory syndrome coronavirus (MERS-CoV) is a zoonotic virus first identified in Saudi Arabia in 2012 and is associated with severe respiratory disease in humans. Vesper bats, which harbor betacoronaviruses, are hypothesized to be ancestral reservoirs of MERS-CoV. Despite the identification of MERS-CoV-related viruses in vesper bats, the infection dynamics of MERS-CoV in these species remain poorly understood. In this study, we experimentally infected *Eptesicus fuscus*, an insectivorous vesper bat with MERS-CoV to investigate viral replication, shedding, clinical symptoms, pathology, and the development of antiviral immune responses.

Methods: *E. fuscus* bats were infected or mock-infected with 10^5 $TCID_{50}$/mL of MERS-CoV. Bats were sampled at 2-, 4-, 7-, and 14-days post-infection. Clinical parameters, including body weight and temperature, were monitored throughout the study. Tissues were examined for gross pathology. We evaluated antiviral gene expression using qPCR and bulk RNA sequencing. Virus-specific neutralizing antibody titers were assessed by micro-neutralization assays.

Results: Infected bats showed no signs of weight loss or elevated body temperature during the study period. MERS-CoV RNA was detected in samples from infected bats, confirming viral replication. Gene expression analyses revealed upregulation of interferon-related genes, indicating activation of an antiviral response. No gross lung pathology or overt tissue damage was observed in infected animals. Infected bats developed virus-specific B cell responses, including the production of neutralizing antibodies.

Conclusions: MERS-CoV can productively infect *E. fuscus* bats without inducing clinical disease or lung pathology, despite evidence of viral replication and antiviral immune activation. These findings support the use of *E. fuscus* as a viable experimental model for studying MERS-CoV and MERS-CoV-related virus infection dynamics, tissue tropism, and host immune responses in bats. This model may provide critical insights into mechanisms of viral tolerance and persistence in reservoir hosts.

709 – Strengthening the community-based surveillance system through the involvement of schools: Experience of a One Health approach in Bambali.

Aminata TOURE (1,2), Yacine CISSE (1,2), **Tracie YOUBONG** (2), Amadou SECK (2), Amadou Yeri CAMARA (5), Daniel YONGA (2), Simone SOSO (4), Somine DOLO (4), Ezechiel Prosper NOALI (3), Thierry Lamare FOUAPON ASSEDI NJATOU (4), Deborah THOMSON (4), Noel Magloire MANGA (1)

1: UFR Sciences de la Santé, Université Assane Seck de Ziguinchor, Sénégal; 2: One Health Lessons®, Dakar, Sénégal; 3: One Health Lessons®, Ouagadougou, Burkina Faso; 4: One Health Lessons®, Washington DC, USA; 5: Regional Health Department of Sedhiou, Sénégal

Background: Involving the educational system could improve community-based surveillance of priority zoonoses in rural areas of Senegal by enhancing knowledge of the One Health (OH) concept. The objective of our study is to implement a strategy to test this hypothesis in a rural community in Senegal.

Methodology: This prospective study aims to evaluate the implementation of a training strategy for teachers, students, and medical personnel in primary and secondary schools within the commune of Bambali, Sédhiou region, Senegal, from April 2025 to May 2026. The training will focus on the concept of

One Health (OH), priority zoonoses, and the digital reporting of zoonotic health events using the RedCap mobile health application.

Results: A total of 754 students, 20 teachers, 4 members of the Community Surveillance and Alert Committee (CVAC), a midwife, and the chief physician of the Bambali health center received training. The comparative analysis of students' knowledge evaluation results indicates that the average percentage of correct answers increased from 68.3% one week after the training to 79.3% one month later. After 4 months of implementation, a total of 529 notifications were recorded in RedCap, including 5 cases of community events related to animal bites and suspected zoonoses. Additionally, one case of human rabies was reported.

Conclusion. Our research highlights the viability of a community-based surveillance reinforcement system for zoonotic diseases, grounded in the One Health approach and incorporating the education system.

721 – Gender-Responsive Climate Adaptation in Andean Rural Communities: A One Health Capacity-Building Approach in Villa de Leyva, Colombia

Natalia CEDIEL-BECERRA (1), Johana REGINO-VERGARA (1), Laura CARREÑO (2), Maria Camila QUERUBIN (1), Jaime PINEDA (1), Alexander NAVAS PANADERO (1)

1: Facultad de Ciencias Agropecuarias, Universidad de la Salle, Colombia; 2: Asociación de mujeres Tierra Digna de Gachantivá

Climate change intensifies environmental, social, and economic vulnerabilities in Andean rural communities, with direct consequences for human, animal, and ecosystem health. As part of a participatory action research, this capacity-building initiative was designed to strengthen community resilience to the climate crisis in rural families in Villa de Leyva through a gender-responsive One Health perspective, by examining how women and men perceive, interpret, and navigate adaptation processes in their everyday lives.

A mixed methods design was conducted with 12 families between September 2024 and June 2025, integrating socioeconomic characterization, participatory workshops (diálogo de saberes), in-depth interviews with women leaders, social cartographies, and a semi-structured survey. The Women's Empowerment in Agriculture Index (WEAI) was adapted for collective assessment across five dimensions: Production (decision-making autonomy), Resources (access and control over assets), Income (use and management of household income), Leadership (community participation and public voice), and Time (distribution of workloads and satisfaction with leisure). Analytical procedures combined descriptive statistics with thematic coding and triangulation of (i) quantitative records on income/expenditure/savings, (ii) qualitative narratives about their life stories, and (iii) community empowerment estrategies. Ethical safeguards included approval by the Universidad de La Salle Ethics Committee (N°216).

Sixty percent of participants were familiar with the concept of climate change, while all respondents reported impacts on family health, animals, and rural livelihoods. Everyday activities affected included animal care (36%), domestic tasks (28%), and agriculture (20%). Key perceived impacts involved crop abandonment due to drought (50%), reduced livestock productivity and schedule adjustments during heat waves (12%), and shifts toward prioritizing harvested foods or reorganizing agricultural labor (13% each). Water-related challenges were critical: 40% stopped cultivation, 40% reported increased water costs, and 20% adopted optimization strategies. Autoconsumption contributes roughly 15–25% of household expenditure, acting as a buffer against climatic and economic variability. Despite strong participation in domestic economic decisions, women face persistent barriers in access to credit, community leadership, and time availability, reflected in an overall WEAI ≈ 60% (acceptable). Women showed stronger autonomy in productive decision-making, access to assets, and control of income, but lower scores in credit access, community leadership, and time use. All women reported daily workloads exceeding 10 hours. Distrust toward credit institutions was widespread due to high interest rates, shifting payment conditions, and limited institutional support for rural women.

Adaptation in rural territories hinges not only on access to resources but also on strengthening women's agency, the economics of care, and community governance. Gender-responsive capacity-building should prioritize: (i) inclusive finance and credit access (e.g., savings groups, guarantees, financial literacy), (ii)

women's leadership and associativity (cooperatives, public-speaking and negotiation skills), and (iii) time-saving infrastructures and shared-care arrangements. Such measures can enhance adaptive capacity, equity, and sustainable climate resilience under a One Health frame.

725 – Outbreak of Salmonella Virchow in South Africa: Whole-genome sequencing used to track the outbreak strain from South Africa to the United States of America

Anthony SMITH (1), Hlengiwe NGOMANE (1), Bolele DISENYENG (1), Tersia KRUGER (1), Shannon SMOUSE (1), Nomsa TAU (1), Morgan SCHROEDER (2), Keeren LUTCHMINARAIN (1), Phuti SEKWADI (1)

1: National Institute for Communicable Diseases, South Africa; 2: Centers for Disease Control and Prevention, United states of America

Background: Whole-genome sequencing (WGS) is transforming communicable disease surveillance globally. The National Institute for Communicable Diseases, South Africa, participates in national laboratory-based surveillance for human isolates of *Salmonella* which includes WGS of isolates. In 2025, an outbreak of *Salmonella enterica* serovar Virchow (*Salmonella* Virchow) was investigated using WGS. We describe how WGS data, supported by epidemiological data, were used to track this outbreak strain from South Africa to the USA.

Methods: WGS of *Salmonella* was performed using Illumina NextSeq technology. WGS data were analysed using multiple bioinformatics tools, including those available at the Center for Genomic Epidemiology and EnteroBase. WGS data analysis allowed for identification and characterisation of isolates. Core-genome multilocus sequence typing (cgMLST) was used to investigate the genetic relatedness and phylogeny of isolates.

Results: In February 2025, a *Salmonella* Virchow cluster of concern was identified in South Africa. Cluster isolates were assigned the EnteroBase cgMLST HC5:527981 identifying number. An outbreak investigation was initiated. The outbreak cluster eventually would include isolates obtained over January-March 2025, from 13 patients that presented with gastrointestinal symptoms. Patient's ages ranged from 1-67 years, with patients located in four provinces across South Africa. Unfortunately, investigations identified no common exposures and no epidemiological links between cases. Interrogation of EnteroBase for global isolates genetically matching the outbreak strain (HC5=527981) identified one isolate match from the USA. Further investigation via the PulseNet International network revealed that the USA isolate was obtained from a 1-year-old child with gastrointestinal illness onset on 11 February 2025. The US family had travelled to South Africa and Ethiopia and returned to the USA on 14 February 2025. The mother of the child and other family members all reported being ill with diarrhoea during this time.

Conclusions: Here we report an example of WGS in action. We show how routine genomic surveillance of *Salmonella* using WGS can lead to the identification of a cluster/outbreak, which then informs targeted

public health investigation. In this instance, the source of the outbreak strain could not be found and no public action or recommendations could be made. We were able to show how global sharing of WGS data and international collaboration through networks such as PulseNet International can track outbreak strains globally and reveal global transmission pathways.

735 – Enhancing surveillance of zoonotic influenza and West Nile Virus in the Netherlands: addressing current gaps

Marloes HEIJNE (1), Pauline LEMPENS (1), Matthijn DE BOER (2), Jolianne RIJKS (3), Lucía DIESTE-PEREZ (4), Christiaan SANDERMAN (4), Evelien GERMERAAD (2), Nikkie THIE (1), Ron FOUCHIER (5), Reina SIKKEMA (5), Gerdien VAN SCHAIK (6), Joke VAN DER GIESSEN (1), Lapo MUGHINI-GRAS (1)

1: National Institute for Public Health and the Environment, Zoonoses and Environmental Microbiology, the Netherlands; 2: Wageningen Bioveterinary Research, Lelystad, the Netherlands; 3: Utrecht University, Dutch Wildlife Health Centre, Utrecht, the Netherlands; 4: Royal GD, Swine department, Deventer, the Netherlands; 5: Erasmus Medical Center, Viroscience, Rotterdam, the Netherlands; 6: Utrecht University, Department of Population Health Sciences, Utrecht, the Netherlands

Background:

Zoonotic influenza viruses and West Nile Virus (WNV) are key pathogens for One Health surveillance in both the Netherlands and across Europe. The Strong1H project (2023–2026) aims to enhance the detection and monitoring of these pathogens by conducting targeted, risk-based sampling in populations that are currently underrepresented in existing surveillance systems.

Methods: Wild boar samples were screened for Influenza A virus (IAV) antibodies using NP-ELISA, with positive samples further characterized via Luminex technology. In addition, samples were collected from domestic outdoor pigs, wild mammals, and environmental sources, and tested for IAV using PCR. Camera traps were used to gain insight into the number and species of scavenging animals with interactions with dead (migratory) birds. For WNV, wild birds and wild mammals were tested by PCR. Both WNV and IAV PCR-positive samples underwent sequencing. IAV sequences were uploaded to a national One Health data-sharing platform, facilitating integrated analysis by comparing sequencing data from domestic indoor pig surveillance with human, avian, and mammalian reference sequences.

Results: With NP-ELISA, antibodies against IAV were detected in 18.5% of the 2585 wild boar samples collected between 2017 and 2025. Further serotyping identified antibodies against Swine Influenza, as well as H5N8 and H5N1 subtypes. Non-invasive saliva samples from 25 outdoor pig farms all tested negative for IAV. In 2025, two red foxes that were tested within the Strong1H project, were positive for H5N1 (DI.2 genotype). Camera trap results confirmed predation on bird carcasses by mammalian carnivores and rodents. Surface water samples from the winters of 2024–25 and 2025–26 frequently yielded pan-influenza PCR positives, though only once an H5-specific positive sample was detected. WNV lineage 2 was detected in two dead wild birds, with sequences clustering alongside other WNV cases (horse, mosquito) in the Netherlands in 2025.

Conclusions: By integrating expertise and data from veterinary, environmental, and human health sectors, and by focusing on under-sampled wildlife and environmental reservoirs, our project strengthens One Health surveillance in the Netherlands. This approach will serve as a basis for the development of a roadmap for sustainable One Health surveillance.

739 – Operational lessons and policy implications from multi-country implementation of a One Health Surveillance and information sharing operational tool (SIS OT) in ECOWAS

Lionel Soléte SOGBOSSI (1), Virgil Kuassi LOKOSSOU (1), Guy Gerard KOUAME (2), Aishat USMAN (1), Tieble TRAORE (3), Félix AGBLA (1), Melchior Athanase AÏSSI (1)

1: West African Health Organisation, Côte d'Ivoire; 2: Private Sector, Côte d'Ivoire; 3: World Health Organisation Regional Office for Africa,Senegal

Background. Effective epidemic intelligence at the human–animal–environment interface requires operational mechanisms for regular, timely, and secure cross-sector information sharing. We synthesized

lessons and policy implications from the West Africa Health Organization (WAHO)-coordinated SIS-OT implementation across six ECOWAS countries to strengthen One Health surveillance.

Methods. SIS-OT guides countries through nine steps grouped into four modules—from planning and information gathering to evaluation, prioritization, roadmap development, and resource selection—culminating in a costed One Health surveillance development plan. Country teams used the standardized Excel-based SIS-OT workbook and annexed tools during facilitated multi-sector workshops to assess capacities and select priority actions. A total of 12 national workshops were conducted across six countries (Guinea, Mali, Senegal, Sierra Leone, Nigeria, and Côte d'Ivoire), engaging approximately 240 participants. We reviewed the cross-country results to extract operational enablers, bottlenecks, and policy levers for scale-up.

Results.Governance and coordination: Political will and advocacy were established at higher levels in Senegal, Guinea, and Côte d'Ivoire, but institutionalization and routine joint working varied. Technical working groups met regularly in Nigeria and Côte d'Ivoire and were fully functional in Guinea. (Implementation I-2: Nigeria/Côte d'Ivoire level 3; Guinea "Complete"). **Legal and policy frameworks**: All countries reported baseline status for legal frameworks governing ethics, confidentiality, and data sharing (Assessment E-3, level 1), indicating the need for formalized cross-sector instruments and standard operating procedures. **Data and interoperability.** Common data elements remained nascent (Planning PL-2; mostly level 1; Guinea level 2). Mechanisms for cross-sector data exchange were advanced in Senegal and Nigeria (I-3, level 3), but analytics/visualization capacities were minimal across all settings (I-10, level 1), limiting near-real-time decision support. **Financing and Human Resources:** Dedicated financing for coordinated surveillance was foundational (I-1, level 1 across countries). Human-resources evaluations were uneven— "Complete" in Senegal and Côte d'Ivoire; level 3 in Mali; and weak elsewhere. **Information sharing practices.** Routine but non-systematic surveillance data sharing (I-7, level 2 in all) was reported across all countries, while risk communication was relatively stronger in Guinea and Nigeria (I-8, level 3)

Conclusions. Multi-country SIS-OT implementation yielded consistent operational lessons: (1) adopt ECOWAS-level model data-sharing MoUs and harmonized common data elements to accelerate interoperability; (2) embed SIS-OT-derived roadmaps within national OH strategies, JEE/NAPHS cycles, and budget lines; (3) invest in interoperable, multi-sector dashboards and data governance (privacy/security) to enable actionable analytics; and (4) institutionalize routine joint simulations and data-quality M&E to drive iterative system strengthening. These lessons are transferable to other regions pursuing scalable OH surveillance.

741 – Prepared for the Unexpected: A Survey of UK Veterinary Surgeons' Engagement with Disaster and Emergency Preparedness

Catherine FINNEGAN

University of Surrey, United Kingdom

Back ground:

Climate change and the increasing frequency and complexity of extreme weather events are introducing a new level of urgency to the One Health imperative: ensuring the resilience of the interconnected systems of human, animal, and environmental health. In the United Kingdom, the rising incidence of natural disasters such as flooding, drought, and wildfires highlights the critical vulnerability of this triad. Within this One Health framework, veterinary surgeons play a pivotal role not only in managing animal health during disasters but also in safeguarding public health. Consequently, veterinarians have a professional duty to be well-informed about disaster management and to actively advise clients on emergency preparedness plans that reflect the interdependence of human and animal welfare in the face of environmental change.

This research study aims to assess veterinary surgeons' perceptions, current practices, and engagement with disaster management through an anonymous survey. By evaluating these factors, the study seeks to strengthen the One Health approach within the UK veterinary community. The findings will inform strategies to enhance cross-sectoral collaboration and emergency readiness, ensuring that the veterinary

profession is equipped to address the evolving challenges posed by climate change across the human-animal-environment interface.

Methods: an anonymous online survey is available to veterinary surgeons in the United Kingdom currently and until the end of April 2026. This research has received a favourable ethical outcome from the University of Surrey.

Results and Conclusions - not yet available, survey is currently running. Data will be available in May 2026 and will be presented at the conference.

744 – Integrating a One Health approach into the assessment of gull and human fecal indicator bacteria in Canadian recreational beach water

Rachel JARDINE (1), Jordan TUSTIN (1), Binyam DESTA (2), Johanna SANCHEZ (1), Shannon MAJOWICZ (3), Tom EDGE (4), David PEARL (2), Teresa BROOKS (5), Andrea NESBITT (6), Sarah ELTON (7), Herb SCHELLHORN (4), Michael SCHWANDT (8), Dylan LYNG (9), Brandon KRUPA (10), Elizabeth MONTGOMERY (11), Mahesh PATEL (12), Ian YOUNG (1)

1: Toronto Metropolitan University, Canada; 2: University of Guelph, Canada; 3: University of Waterloo, Canada; 4: McMaster University, Canada; 5: Health Canada; 6: Public Health Agency of Canada; 7: University of Toronto, Canada; 8: Vancouver Coastal Health, Canada; 9: Manitoba Environment and Climate, Canada; 10: Public Health Niagara Region, Canada; 11: Halifax Regional Municipality, Canada; 12: Toronto Public Health, Canada

Background

Recreational water use at beaches is a popular summer activity amongst Canadians. Swimming and other recreational water activites can increase the risk of acute gastrointestinal illness (AGI) in humans. As climate change continues, the use of recreational waters by both humans and avian populations is likely to occur. This study sought to understand the current level of recreational water exposure amongst human beachgoers in Canada as well as to assess the human and avian microbial sources of fecal indicator bacteria (FIB) in Canadian beaches.

Methods

A prospective cohort study was conducted from 2023 to 2025 across five sites in Canada. Beachgoers were surveyed at the end of their beach day to assess their level of exposure to recreational water and sand along with sociodemographic variables. A follow-up survey was conducted seven days later to document the incidence of acute illnesses. For each recruitment day, water samples were taken to assess FIB levels across six measures: *Escherichia coli*, enterococci DNA, three DNA biomarkers (human sewage, human mitochondria, seagull), and turbidity. Descriptive statistics were calculated to understand the level of sand and water exposure amongst different sociodemographic groups. Bayesian mixed-effects logistic regression models were fitted to evaluate the effects of sand and water contact on the incident risk of AGI, with an interaction included for FIB levels.

Results

From 2023 to 2025, AGI incidence was low (2.6%) amongst the 4085 recruited participants. Children under the age of 14 demonstrated the highest exposure rates to both sand and water. Amongst this age group, 34.4% reported swallowing water as compared to 10.3% of older participants. Across participants, there was a median of 19 excess cases of AGI (95% Credible Interval [CrI]: 4, 68) when swallowing or immersing the body in water as compared to no water contact. *E. coli* levels were generally low across most recruitment days (median = 54 CFU/100 mL). The human sewage biomarker was detected on 47.4% of days, while human mitochondria and seagull markers were found most days (76.0% and 86.0%, respectively). However, only *E. coli* and the seagull biomarker were associated with AGI amongst those who had water contact, especially when swallowing water.

Conclusions

These findings highlight the demographic differences in water and sand exposure at Canadian beaches, with pediatric populations having the greatest exposure. The incidence of AGI was low across our study, indicating success in Canadian beach management. However, increased risks of AGI are associated with *E. coli* contamination. Results from our microbial source analysis suggest seagulls may contribute to this contamination and associated health risks. With the progression of climate change, health authorities

should integrate a One Health lens into beach management which considers the intersection of human, animal and environmental health along shorelines.

747 – Antimicrobial Resistance Transmission Across the One Health Interface: From Surveillance to Action

Bruno GONZALEZ-ZORN, Javier FERNANDEZ-FAVIERES, Andrea ESTUPIÑAN, Natalia MONTERO, Angel F CES, Mario PULIDO-VADILLO

Complutense University of Madrid, Spain

Background Antimicrobial resistance (AMR) is one of the most pressing global health challenges, threatening the effectiveness of modern medicine, food security, and sustainable development. Increasing evidence shows that resistance spreads not only through clinical infections but also through **silent dissemination across interconnected human, animal, food, and environmental systems**, emphasizing the importance of a **One Health approach**. Resistant bacteria, resistance genes, and mobile genetic elements circulate across ecological compartments through complex transmission pathways that often remain undetected until they emerge in clinical pathogens. Advances in genomic technologies and data-driven approaches are transforming our ability to detect and understand these processes, enabling high-resolution tracking of resistance and transmission across sectors.

Methods An interdisciplinary One Health framework integrating **genomic surveillance, epidemiological data, and environmental monitoring** was applied to investigate the dissemination of AMR across human, animal, and environmental compartments. Whole-genome sequencing and comparative genomic analyses were used to characterize bacterial populations, resistance determinants, and mobile genetic elements. Genomic findings were integrated with ecological and epidemiological data to identify potential transmission pathways across sectors. Selected **case studies** including a Oen Health Program in Ronda, Spain, Will be used to illustrate how genomic epidemiology can reveal patterns of cross-sectoral transmission and the movement of resistance genes between reservoirs. Analytical approaches, including computational modeling and data integration, were used to explore the connectivity of AMR across the One Health interface.

Results Integrated genomic and epidemiological analyses revealed substantial connectivity between human, animal, and environmental reservoirs of AMR. Shared resistance determinants and mobile genetic elements were identified across compartments, suggesting frequent cross-sectoral transmission. Genomic case studies demonstrated how specific bacterial lineages, resistance genes, or plasmids can disseminate across ecological niches, highlighting the role of food systems, environmental pathways, and asymptomatic carriage in maintaining reservoirs of resistance. These findings illustrate how genomic surveillance provides unprecedented resolution to track transmission dynamics and detect emerging resistance threats across the One Health system.

Conclusion Addressing AMR requires a systems-based One Health strategy that integrates **genomics, interdisciplinary surveillance, and cross-sectoral governance**. Genomic epidemiology, combined with targeted case studies of transmission across sectors, provides powerful insights into the mechanisms driving the spread of resistance. Strengthening integrated surveillance systems, promoting data sharing, and linking genomic evidence with policy and public health action will be essential to detect emerging threats early and to mitigate the global dissemination of antimicrobial resistance.

763 – Gaps in R&D Funding for Neglected Tropical Diseases: Comparative Analysis of G-Finder Funding and DALYs

Caitlin BUTALA (1,2), Susan WELBURN (1,2), Jenna FYFE (1)

1: University of Edinburgh, United Kingdom; 2: Zhejiang University, Haining, China

Background: Researching funding for neglected tropical disease (NTD) programs is hindered by fragmented, non-transparent reporting: there is no single mandatory repository for donations or government spending. Without a complete funding picture—spanning R&D, prevention, interventions, and

treatment—stakeholders cannot reliably identify gaps addressable by foreign aid, NGOs, or national governments to meet the 2030 SDG targets.

Methods: Annual R&D funding (USD) was extracted from Policy Cures' G-Finder report and International Aid Transparency Initiative (IATI) (data updated 11/03/2026) for 11 NTDs: Onchocerciasis, Taeniasis/Cysticercosis, Trachoma, Leprosy, Lymphatic Filariasis, Chagas, Soil-Transmitted Helminths (combined: whipworm, roundworm, strongyloidiasis, hookworm), Schistosomiasis, Human African Trypanosomiasis, Dengue, and Leishmaniasis. Disease burden was represented by DALYs from the Global Burden of Disease (IHME). Time-series funding was plotted as line graphs per disease; a dual-axis figure juxtaposed annual R&D dollars (orange) with DALYs (blue) to visualize alignment or mismatch between research investment and disease burden.

Results: Visual comparison highlights substantial heterogeneity in R&D investment across NTDs relative to DALYs. Several high-burden diseases show comparatively low R&D funding, while some conditions with lower DALYs receive disproportionate research investment. The absence of consolidated, mandatory reporting likely contributes to obscured funding flows and complicates gap identification.

Conclusions: Current R&D funding for many NTDs does not consistently align with global disease burden. Improving transparency through standardized, centralized reporting of all NTD-related funding (including governmental, philanthropic, and private sector contributions) is critical to inform resource allocation and accelerate progress toward 2030 SDG goals. G-Finder remains a key resource for R&D tracking but cannot substitute for comprehensive, mandatory financial disclosure and does not track for control programmes or interventions.

767 – Ecological Drivers of the Global Spatiotemporal Distribution of Coronavirus Prevalence in Bats

Marina VOINSON (1), Lea JOFFRIN (1), Cedric MARSBOOM (2), Vincent SLUYDTS (1), Herwig LEIRS (1), Julien CAPPELLE (3)

1: University of Antwerp, Belgium; 2: Avia-GIS, Agro-Veterinary Information and Analysis, Zoersel, Belgium; 3: ASTRE, CIRAD, INRAE, Univ Montpellier, Montpellier, France

Background: Bats host a remarkable diversity of viruses, including coronaviruses, whose prevalence varies markedly across space and time. This variability likely results from a complex interplay of ecological conditions, species assemblages, land-use change, and human pressures. However, despite numerous local studies, the large-scale drivers shaping coronavirus prevalence across bat species remain poorly understood. Here, we aim to identify the ecological, socio-demographic, climatic, land-cover, and biodiversity factors associated with coronavirus prevalence in bats at the global scale.

Methods: We developed a global analytical framework combining two complementary datasets: a newly compiled global database of coronavirus detections in bats and a large-scale ecological dataset describing species traits such as lactation period, birthing seasons, colony size etc. These datasets were further integrated with field data generated through the BCOMING project. Using a probabilistic modeling approach based on Integrated Nested Laplace Approximation (INLA) and incorporating spatial and temporal structure, we quantified how environmental and anthropogenic gradients influence viral prevalence across bat species and regions worldwide.

Results: Preliminary analyses highlight the birthing season as a key driver of coronavirus prevalence in bats globally, likely reflecting increased susceptibility and transmission associated with reproductive aggregations and juvenile recruitment.

Conclusions: By integrating wildlife ecology, environmental change, and zoonotic risk assessment, this study contributes to a One Health perspective. Our framework provides scalable tools to better understand the ecological conditions that favor viral circulation in bat populations and to improve the assessment of spillover risk at the human–animal–environment interface.

769 – Biodiversity and ecosystem conservation as primary prevention of zoonotic spillover: developing a multi-disciplinary systems analysis framework for finding win-win solutions for public and environmental health

Elisa Zofia STEFANIAK, Michael FREIBERGER, Gemma GERBER, Juliette MARTIN, Christopher WONG, Stefan WRZACZEK, Piotr ZEBROWSKI

International Institute for Applied Systems Analysis, Austria

Background: By the principles of One Health improving ecosystem function such as biodiversity, nutrient cycling or habitat connectivity can have a positive effect on human health while human action can in turn severely affect ecosystem health for example through land use change or pollution. While there is large complexity in how these systems interconnect there are many examples of successful one health interventions and ecosystem conservation efforts showcasing their contributions to reduction of the burden of zoonotic diseases.**The lack of integrated quantitative frameworks and modelling approaches within the space of One Health poses a barrier for the evaluation of potential conservation interventions and for policy implementations. Methods:** We develop **a quantitative systems analysis framework** which explores the potential impact of conservation policy measures both on the ecological and human systems. We focus on the potential of zoonotic spillovers and highlight how conservation implementations can affect the risk of disease outbreak and disease burden on the one hand and the potential effects on social, economic, and conservation objectives.**Results:** Wepresent and discuss the process of applying the framework to country-level conservation measures in West Africa to limit the risk of Ebola spillover using interim results for a subregion of interest.**Conclusions:** We demonstrate the benefits of a multi-disciplinary framework for the examination of policy and climate scenarios by illustrating its substantial additional insights of holistic effects of conservation based One Health approaches in the human- and ecosystem. We hope that as One Health becomes more ingrained in public health discourse and policy, quantitative systems analysis methodologies can aid in bridging conservation and public health objectives.

---

778 – Genomic characterization of vancomycin- and linezolid-associated resistance in multidrug-resistant Enterococcus spp.

Levente RADNAI (1,2), Ákos JERZSELE (1,2), Ádám KEREK (1,2)

1: Department of Pharmacology and Toxicology, University of Veterinary Medicine Budapest, Hungary; 2: National Laboratory of Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health and Food Chain Safety, University of Veterinary Medicine Budapest, Hungary

Background

Antimicrobial resistance (AMR) in *Enterococcus* spp. is of growing One Health concern because poultry-associated strains may serve as reservoirs of resistance determinants relevant to animal health, food safety, and human medicine. In particular, resistance linked to glycopeptides and oxazolidinones warrants close attention due to the critical role of vancomycin and linezolid in human therapy. This study aimed to characterize the genomic background of vancomycin- and linezolid-associated resistance in phenotypically prescreened multidrug-resistant *Enterococcus* isolates from Hungarian poultry.

Methods

A total of 73 *Enterococcus* isolates recovered from large-scale poultry farms in Hungary were selected after phenotypic prescreening based on minimum inhibitory concentration testing according to CLSI guidelines. Whole-genome sequencing was performed using the Illumina NextSeq platform. Bioinformatic analyses were used to identify antimicrobial resistance genes, resistance-associated chromosomal mutations, and the putative chromosomal, plasmid, phage, or mobile genetic element localization of relevant determinants.

Results

The sequenced collection comprised *Enterococcus faecalis* (60.3%), *E. faecium* (35.6%), *E. casseliflavus* (2.7%), and *E. mundtii* (1.4%). Overall, 179 resistance gene types and 1,227 total gene hits were identified, indicating a broad resistome background. Twelve glycopeptide resistance genes were detected with 56 total occurrences, dominated by vanC-cluster elements; no *vanA* gene was found. A plasmid-associated

vanW gene was identified in one isolate, indicating the potential mobility of clinically relevant glycopeptide resistance determinants. Classical transferable linezolid resistance genes (*optrA, poxtA, cfr*) were not detected. Instead, linezolid-associated efflux and ribosomal protection-related genes were frequent, including *efrA* (90.4%), *lsaA* (78.1%), *efrB* (78.1%), and *emeA* (68.5%). In addition, a G2576T mutation in 23S rRNA was identified in seven isolates originating from the same breeder flock, suggesting localized dissemination of a target-site-associated linezolid resistance mechanism. Other prominent resistance determinants included *dfrE* (76.7%), *tetL* (46.6%), *tetM* (43.8%), and *ermB* (32.9%).

Conclusions

Hungarian poultry-associated *Enterococcus* spp. carried a diverse multidrug resistome dominated by vanC-type glycopeptide resistance determinants and multifactorial linezolid resistance-associated mechanisms rather than classical transferable oxazolidinone resistance genes. The detection of a plasmid-associated *vanW* gene and a flock-linked 23S rRNA mutation highlights the importance of integrated genomic surveillance of poultry-associated enterococci within a One Health framework.

---

789 – Elements of the only County One Health Unit in Kenya with successful community-based and county-level activities

John VANLEEUWEN (1), **Erastus KANGETHE** (2), Brian BEDARD (2), Colleen WALTON (3), Christopher YEOMANS (2), Morag HUMBLE (2), Fredrick OBONYO (4)

1: UPEI, Canada; 2: Alinea International; 3: Farmers Helping Farmers; 4: Meru University of Science and Technology

Background:

Methods:

Results:

Conclusions:

The strong backgrounds of the key stakeholders and their trusted partners have led to the only COHU in Kenya with successful community-based and county-level activities.

---

792 – Engaging citizens in research to enhance tick-borne diseases prevention and ecosystem conservation in Canadian peri-urban nature parks.

Manon BOITEUX (1,2), Geneviève BARON (3), Catherine BOUCHARD (4), Heather BRAIDEN (5), Frédéric BUSSIÈRE (6), Céline CAMPAGNA (7), Fredrick CHARBONNEAU (8), Evelyne DE LEEUW (9,2), Charles DUPRAS (9,2), Sara TEITELBAUM (10), Katrine TURGEON (11), Cécile AENISHAENSLIN (1,2)

1: Groupe de Recherche en Épidémiologie des Zoonoses et Santé Publique (GREZOSP), Département de Pathologie et Microbiologie, Faculté de Médecine Vétérinaire, Université de Montréal, Saint-Hyacinthe, QC, Canada.; 2: Centre de Recherche en Santé Publique de l'Université de Montréal, Montréal, QC, Canada.; 3: Département des sciences de la santé communautaire, Faculté de médecine et des sciences de la santé, Université de Sherbrooke et Direction de la santé publique de l'Estrie, CIUSSS de l'Estrie-CHUS; 4: Modelisation Hub Division, Public Health Agency of Canada, St. Hyacinthe, QC, Canada.; 5: Ecole d'urbanisme et d'architecture du paysage, Faculté d'aménagement, Université de Montréal, Montréal, QC, Canada.; 6: Service des grands parcs, du Mont-Royal et des sports, Ville de Montréal, Montréal, QC, Canada; 7: Équipe de coordination de la science de l'adaptation, Ouranos, Montréal, QC, Canada; 8: Direction régionale de santé publique du CIUSSS du Centre-Sud-de-l'Île-de-Montréal; 9: École de santé publique de l'Université de Montréal, Montréal, QC, Canada; 10: Département de sociologie, Faculté des arts et des sciences, Université de Montréal, Montréal, QC, Canada.; 11: Institut des Sciences de la Forêt Tempérée (ISFORT), Département des Sciences Naturelles, Université du Québec en Outaouais (UQO), Ripon, QC, Canada

Background Exposure to nature in peri-urban parks benefits human well-being and health, especially for city dwellers. However, climate change, habitat fragmentation and deer overpopulation increase risks of tick-borne diseases (TBDs) in Canada. In a One Health (OH) perspective, preventive behaviors such as wearing long clothing, body checks or staying on trails are the main way to reduce transmission, while some also support ecosystem conservation, allowing for co-benefits. Yet, adoption in Canadians remains limited, and awareness campaigns have had modest impact. Citizen science (CS) in nature may enhance knowledge and practices regarding TBDs prevention while fostering ecosystem health.

Objectives This study aims to: 1) Evaluate the effects of participation to a citizen science initiative implemented in peri-urban natural parks on knowledge, attitudes, and practices (KAP) towards TBDs and ecosystem conservation; 2) identify factors influencing participation and the effects of the initiative.

Methods We use a quasi-experimental design with intervention (I) and control (C) groups, applying mixed methods to evaluate scientific, participant, and socio-ecological outcomes using a OH approach. Qualitative data complement quantitative findings, enabling analysis of both outcomes and processes. In May 2025, 305 citizens were recruited from five peri-urban parks in Quebec and randomly assigned to I or C. In summer 2025, group I participated in CS activities (tick sampling, three workshops and online tools). For objective 1, KAP are measured with surveys administered pre-intervention (2025), and one (2026) and two years post-intervention (2027). Multivariate analyses will be used to estimate the effects of CS participation. Then, participants selected from group I in function of KAP change and participation rate (n=40) will be invited to semi-structured interviews in fall 2026. Interviews will be thematically analyzed to identify facilitators and barriers to participation and behavior changes.

Results Study participants are mostly women (80%), with a median age of 50–64 years. Baseline results show high biodiversity knowledge score and average tick knowledge score. Presence of ticks impacts well-being with 60% of respondents reporting being worried about the idea of contracting a TDB and 25% enjoying nature less. Regarding preventive behaviors, only 40% report adopting these behaviors with an important variability by parks. There were no significant differences in KAP between groups I and C at baseline. The study is ongoing. Post-intervention KAPs will be assessed in May 2026 and further analyses will provide quantitative results about the intervention's effectiveness.

Conclusion At the municipal level, this project aims to promote preventive behaviors against TBDs while supporting ecosystem conservation in peri-urban parks. With a concrete initiative, it will explore how citizen science can contribute to implement key principles of OH such as equilibrium, intendancy, equity and transdisciplinarity. It will provide practical mechanisms to implement and evaluate OH intervention through a participatory approach.

797 – ESTIMATED PREVALENCE OF BARTONELLA SPP. DNA IN INDONESIA SHELTER CATS

Nadya W, Jennifer HAWLEY, Michael R LAPPIN
Colorado State University, United States of America

Background: Several *Bartonella* spp. use cats as a reservoir and fleas as a vector and can induce clinical illness in both humans (cat scratch disease; endocarditis; neurological signs) and cats (fever, bacteremia). A recent study assessing fleas from cats living in several countries in East and Southeast Asia, including Indonesia, identified *Ctenocephalides felis* as the most frequently observed flea, and *Bartonella henselae* as the most common pathogen. However, the estimated prevalence of *Bartonella* spp. in the blood of cats in Indonesia animal shelters has not been studied. This study aims to estimate the prevalence rates of *Bartonella* spp. in cats housed in Indonesia shelters and characterize the genetic diversity of detected strains and compare to sequences reported from different countries including the USA

Methods: A study using stratified convenience sampling based on case availability during field collections was carried out in Yogyakarta (7.8014° S, 110.3648° E) and Medan (3.5952° N, 98.6722° E), Indonesia.A total of 104 feline blood in EDTA samples was collected from 50 cats in Medan and 54 cats in Yogyakarta, packaged, and shipped to our laboratory. DNA was extracted from blood and assayed by PCR for *Bartonella* spp. Genetic sequencing was used to genotype positive amplicons.

Results: *Ctenocephalides felis* were identified at the time of sampling on 1 of 104 cats (1%).

Bartonella spp. DNA was amplified from 33 of 104 (31.7%) samples. Adequate DNA for sequencing was present in 32 samples identifying *B. henselae* (21 cats; 65.6%), *B. clarridgeiae* (7 cats; 21.9%), or *B. koehlerae* (4 cats; 12.5%). Co-infection with *B. henselae* and *B. clarridgeiae* was detected on 2 of 104 cats (2%). Experiments to compare these *Bartonella* spp. genetically to those in China, Thailand, and the USA are ongoing. These findings confirm multiple flea-borne feline associated *Bartonella* species in shelter cats in Indonesia, with *B. henselae* being the most common in this population.

Conclusions: The *Bartonella* spp. estimated prevalence rates suggest that exposure to fleas commonly occurred in the sampled cats. Overall, these results reinforce One Health recommendation emphasizing the importance of consistent flea control to reduce zoonotic infection risk for both cats and humans.

802 – Climate-Driven Seafood Future and Nutrition: A One Blue Health Case Study in Mexican Small-Scale Fisheries

Marina BANUET MARTINEZ (1), William CHEUNG (2), Arturo J. HERNANDEZ VELASCO (3), Carlos A. DOMINGUEZ SANCHEZ (4), Maria J. ESPINOSA ROMERO (5), James FORD (6), Shelby YAMAMOTO (7), Sherilee HARPER (1)

1: University of Alberta, Canada; 2: University of British Columbia, Canada; 3: Comunidad y Biodiversidad, A.C. (COBI), Mexico; 4: CADS Science Documentary; 5: Comisión Nacional de Acuacultura y Pesca (CONAPESCA), Mexico; 6: University of Leeds, UK; 7: University at Buffalo, USA

Background: Climate-driven shifts in marine ecosystems threaten both ocean and human health, especially in small-scale fishing communities where seafood is integral to culture and public health nutrition. The One Health approach conceptualizes these interdependencies by linking climate, marine ecosystems, and human well-being. We adopted this perspective and introduced a One Blue Health framework that explicitly centers ocean–human linkages. This framework was used to quantify how projected climate-related changes in species distributions and catches may affect seafood-derived nutrition, reshape diets, and to examine whether locally perceived adaptation strategies align with ecological projections.

Methods: We conducted an interdisciplinary, community-based mixed-methods study with two small-scale fishing communities in the Mexican Pacific. We integrated community dietary data and seafood intake patterns through retrospective dietary recalls and nutrient composition analysis. We then linked nutritional data with climate projections of seafood species catch potential and habitat suitability for 2010–2090 under both low and high-emissions scenarios. We estimated the trajectories of seafood contributions to dietary requirements for protein and key micronutrients. To understand behavioural responses and adaptation pathways within local food systems, we developed qualitative climate disruption scenarios and conducted interviews with fishers and community members.

Results: Projected changes in marine ecosystems indicate divergent futures for seafood species that currently support fisheries livelihoods and household nutrition. Several key species are expected to decline substantially by mid-century under both climate scenarios, while others may remain stable or increase. These ecological changes are likely to reshape dietary patterns. Analysis of climate disruption narratives revealed that households anticipate coping by increasing seafood intake and switching among familiar species; however, these strategies do not consistently align with projected species availability, highlighting tensions between perceived and ecologically feasible adaptation pathways. Across scenarios, these changes are projected to reduce dietary diversity and decrease the contribution of seafood to recommended intakes of key nutrients essential for immune and metabolic health. Qualitative findings further indicate that behavioural responses to climate disruptions, including economic pressures and changes in fishing practices, may intensify these nutritional transitions.

Conclusions: Framing these findings within our One Blue Health framework demonstrates that climate-driven transformations of marine ecosystems can directly compromise public health nutrition and widen health risks. This case study illustrates the value of pairing climate-impact modelling with local dietary data and qualitative narratives to identify place-specific adaptation pathways that protect both ecosystem integrity and human health. As climate pressures intensify across marine systems, connecting ocean health to human health will be critical for developing fisheries and food policies that support both ecosystems and coastal communities. Our One Blue Health framework offers a scalable approach for fostering collaborations at the intersection of ocean science, public health, and climate adaptation.

811 – One Health Risk Assessment of Transboundary Introduction of a Novel Avian Influenza Variant in Ubon Ratchathani Province, Thailand

Kittichai UNJIT (1), **Pusana RODSOM** (2), **Peeriya WATAKULSIN** (2), **Ariya BUNNGAMCHAIRAT** (3), **Serge MORAND** (4), **Soawapak HINJOY** (2)

1: National Institute of Animal Health, Department of Livestock Development, Bangkok, Thailand; 2: Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand; 3: Faculty of Public Health, Mahidol University, Bangkok, Thailand; 4: Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand

Background:

The highly pathogenic avian influenza (HPAI) H5N1 virus continues to evolve into genetically diverse clades with enhanced virulence and increased cross-species transmission potential, leading to the emergence of novel avian influenza variant strains. Ubon Ratchathani Province is considered a high-risk area for avian influenza outbreaks because of its transboundary location shared borders with neighboring countries, where avian influenza activity has been reported, dense small-scale poultry production, cockfighting activities and close human–poultry interactions. This study aimed to assess the joint risk assessment (JRA) under a One Health framework to systematically identify risk of emergence, transmission pathways, quantify risk levels, and support evidence-based preparedness planning for novel avian influenza variant in Ubon Ratchathani Province, Thailand, a border area vulnerable to transboundary zoonotic diseases.

Methods:

The Joint Risk Assessment was conducted under the PREZODE-ASAMCO Project using a methodology adapted from the Department of Livestock Development Rapid Risk Assessment Tool (Version 25AUG2025). Participants representing public health, animal health, environmental sectors, and local authorities collaboratively defined the risk question, identified transmission pathways, and evaluated likelihood, consequences and uncertainties within a One Health framework. The participatory JRA process enabled shared understanding of cross-sectoral risks and joint prioritization of mitigation actions.

Results:

Ten potential introduction and transmission nodes were identified, including brokers, animal transporters, vehicles (boats), natural water sources, households, communities, cock training grounds, cockfighting arenas, shelters, and fresh markets. Likelihood and uncertainty levels were scored using expert consensus and available sectoral data. High-likelihood nodes were primarily associated with illegal cross-border poultry movement and cockfighting activities. Consequence assessment across public health, animal health, and environmental domains indicated high potential impacts, alongside risks to food security and environmental contamination. Risk estimation integrating likelihood and impact severity identified three highest-risk pathways linking imported native chickens to cock training grounds and cockfighting arenas. Individuals with close occupational exposure, particularly fighting cock owners and referees, were classified as very high-risk groups.

Conclusions:

This study demonstrated that participatory Joint Risk Assessment under a One Health framework was an effective tool for identifying high-risk transboundary introduction pathways and prioritizing risk-based mitigation strategies. The findings highlighted the critical role of informal animal movement networks and high-contact poultry activities in driving local amplification risks. Priority risk management measures include strengthening biosecurity and registration systems in cockfighting settings, enhancing surveillance and law enforcement to prevent illegal cross-border animal movement, and updating the provincial One Health preparedness and response plan.

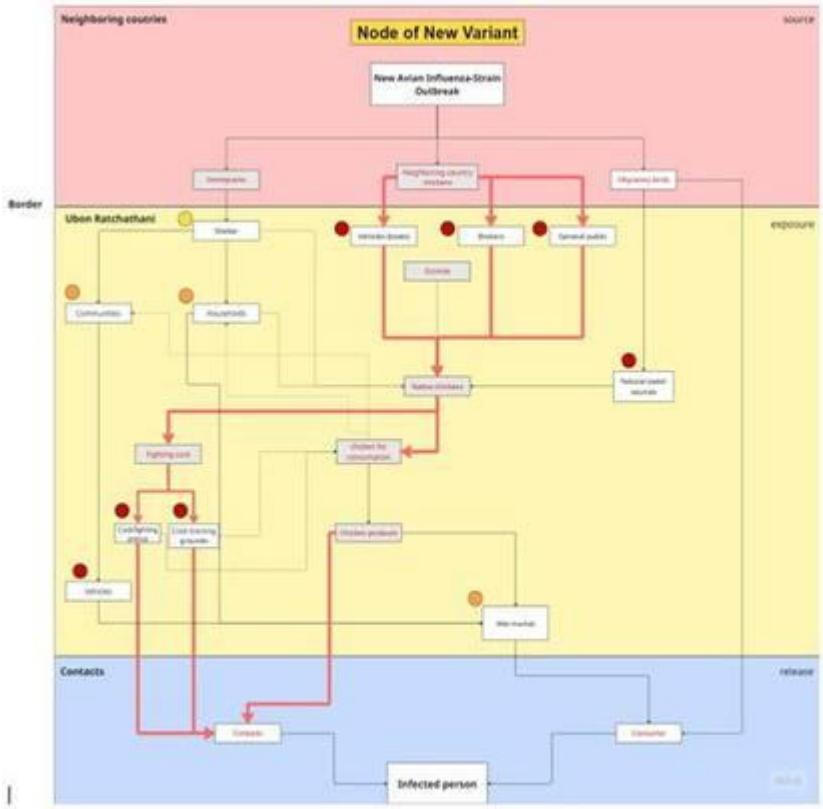


Figure1 Risk Pathway of the potential likelihoods avian influenza virus through native chickens imported from neighboring countries in Ubon Ratchathani Province

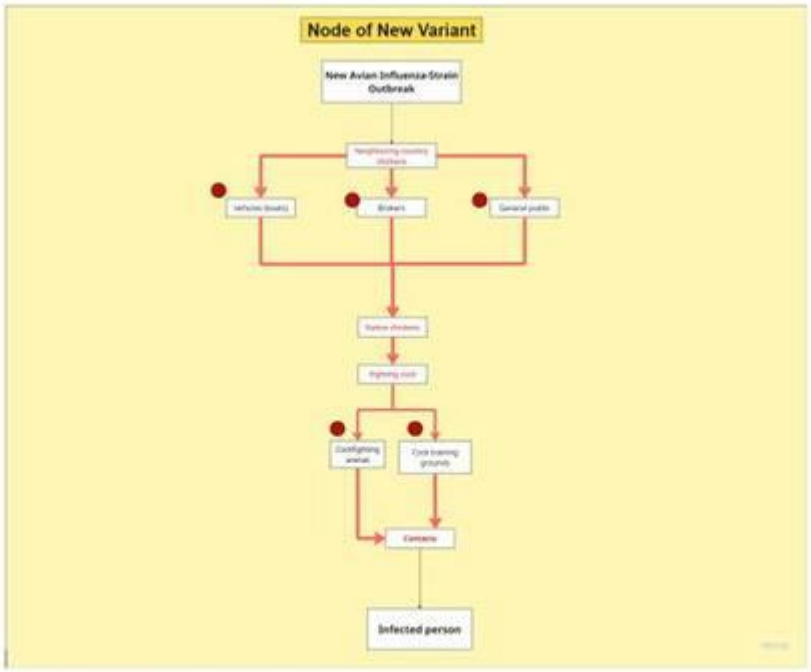


Figure 2 Selected Nodes with high risk level

816 – From Model to Intervention: A One Health Approach to Wild meat Value Chains and Zoonotic Risk in the Democratic Republic of the Congo

Ismaël Dognimin COULIBALY (1,2), Arlette Olaby DINDE (2), Marie Jeanne ATUL (3), Mare GERAERTS (4), Bognan Valentin KONE (2,5), Patrick MPOYO (3), Matthew BAYLIS (6), Justin MASSUNU (3), Katharina KREPPEL (4), Bassirou BONFOH (1)

1: Université Peleforo Gon Coulibaly; 2: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Côte d'Ivoire; 3: Institut National de Recherche Biomédicale, Kinshasa, République démocratique du Congo; 4: Institute of Tropical Medicine, Antwerp, Belgium; 5: Institut National de Santé Publique, Abidjan, Côte d'Ivoire; 6: University of Liverpool, Liverpool, UK

Background

Human–wildlife interactions associated with hunting, trading and consumption are recognized drivers of zoonotic disease emergence, particularly in Central Africa. Wild meat represents an important source of income and protein for many communities but also constitutes a reservoir of multiple zoonotic pathogens. Despite growing evidence on zoonotic risks from wild meat, translation into context-specific intervention strategies remains limited. This study examined how hunting, handling, and consumption practices involving wild meat contributes to livelihoods, zoonotic risks and identified priority intervention pathways to strengthen community resilience within a One Health framework.

Methods

A qualitative participatory study was conducted in Kinshasa, surrounding the wild meat supply chain in the DRC. Seventeen participants were purposively selected to represent direct actors (hunters, vendors, and consumers) and indirect stakeholders (veterinary services, public health professionals, environmental specialists, and researchers). Data collection combined a participatory situational analysis with a SWOT (strengths, weaknesses, opportunities, threats) framework of risk mitigation, followed by stakeholder analysis and a Group (intervention) Model Building (GMB). The situational analysis identified structural drivers of zoonotic risk along the wild meat value chain and the prioritization of interventions based on their perceived effectiveness and feasibility. The GMB method mapped wild meat value chain actors and their interactions and power relations, identified the core problem, and co-developed causal diagrams considering practices, environment and socio-economic drivers, and health impact outcomes. Data were synthesized through thematic analysis, causal loops and systems analysis to identify priority interventions towards zoonosis mitigation.

Results

Participants identified recurrent Ebola, Mpox outbreaks associated with wild meat as the main threat to health within the wild meat value chain. Direct risk factors included close human exposure to wild animals during hunting and processing of carcasses with limited use of personal protective equipment. Structural drivers of zoonotic risk identified included strong economic dependence on wild meat, food insecurity, weak regulatory enforcement and informal trade networks. Dense economic power interdependencies between hunters, vendors, intermediaries, and consumers were recorded. Sanitary oversight of wild meat was reported as centralized, with limited inspection and regulatory capacity at decentralized levels. Causal loop analysis highlighted reinforcing feedback mechanisms whereby income losses and market restrictions particularly during outbreaks contributed to clandestine trade, increasing exposure risks. Priority interventions identified from the GMB were community-based risk communication on zoonosis risks, diversification of livelihoods of wild meats dependants, sustained monitoring, surveillance and control system, and improved governance of wild meat trade.

Conclusion

Zoonotic risks associated with wild meat value chains arise from complex and interconnected interactions among wildlife commodities, livelihoods, and integrated human–animal health systems. These interdependencies require integrated strategies and collective action. Risk communication, income diversification, enhanced surveillance systems, and One Health governance are essential to mitigate zoonotic outbreaks while strengthening community resilience at the wildlife–nutrition–health interface.

---

827 – Prioritising climate-sensitive infectious diseases in India: integrating climate hazards, pathogen transmissibility and health outcomes using a multicriteria decision analysis framework

Ricardo SOARES MAGALHAES (1), Kei OWADA (1), Adam CHARETTE-CASTONGUAY (2), Uttara KENNEDY (1), Bente SCHRIJVER (3), Remco SCHRIJVER (3), Mudassar CHANDA (4), Baldev GULATI (4), Debdutta BHATTACHARYA (5), Sanghamitra PATI (5), Hikuepi KATJIUONGUA (6)

1: The University of Queensland, Australia; 2: CSIRO; 3: VetEffect; 4: ICAR-NIVEDI; 5: ICMR-RMRC; 6: World Bank

Background: Climate change is increasingly recognised as a major driver of emerging and re-emerging infectious diseases affecting human, animal, and environmental health systems. To support evidence-based prioritisation of climate-sensitive infectious diseases in India, a structured One Health prioritisation process was implemented across three states (Kerala, Assam, and Odisha) through a series of multi-sectoral expert workshops.

Methods: The prioritisation protocol combined systematic evidence review, expert consultation, and multi-criteria decision analysis using the Fuzzy Analytic Hierarchy Process (FAHP). Initially, a scoping review of climate-sensitive infectious diseases in India identified candidate pathogens and informed the development of disease fact sheets and prioritisation criteria. State-level workshops were conducted in October 2025 involving 78 experts from animal, human, and environmental health sectors. Experts refined disease lists, selected relevant climate hazard criteria, and weighted the importance of climate hazards, transmission mechanisms, and health outcomes. Diseases were then scored in real time using a web-based interface in R-Shiny based on predefined questions linking climate hazards to disease transmission pathways and impacts.

Results: Across the three states, experts consistently identified flooding, warming, and seasonal variability as the most influential climate hazards shaping disease transmission. However, regional hazard profiles differed, with humidity emphasised in Assam and cyclones highlighted in Odisha. For human diseases, prioritisation results varied by state: cholera and typhoid ranked highest in Kerala, dengue and malaria in Assam, and malaria followed by dengue and cholera in Odisha. Among animal diseases, foot-and-mouth disease was prioritised in Kerala and Odisha, whereas African swine fever ranked highest in Assam. Key zoonoses identified included amoebic meningoencephalitis and leptospirosis in Kerala, Japanese encephalitis in Assam, and leptospirosis in Odisha.

Conclusion: In this study we demonstrate that priority climate sensitive zoonotic and non-zoonotic infections are heterogenous at subnational level in India. The outputs provide a transparent evidence base to guide geospatial modelling and spatial suitability mapping for selected priority zoonotic diseases to support climate-informed surveillance and preparedness strategies in India.

829 – Provincial One Health Joint Action Plan for Crimean–Congo Hemorrhagic Fever Prevention and Control in Balochistan, Pakistan

Mumtaz Ali KHAN, Majid Ali TAHIR, Muazam Abbas RANJHA, Muhammad SALMAN

National institute of Health, Pakistan

Background

Crimean–Congo Hemorrhagic Fever (CCHF) remains a recurrent zoonotic threat in Balochistan, Pakistan, particularly in districts with extensive livestock movement and cross-border trade. During the Provincial Risk Profiling Workshop held in Quetta in July 2024, CCHF was prioritized as a high-risk hazard due to seasonal outbreaks, high case fatality, and occupational exposure among farmers, butchers, and health workers. In line with recommendations from the Joint External Evaluation-2023, a provincial hazard-specific preparedness and response plan was developed using a multisectoral One Health approach.

Methods

A multisectoral planning workshop was conducted on 04-07 August in Quetta, Balochistan. Subject matter experts (SMEs) who participated in the risk assessment were engaged in the planning process to maintain technical continuity. SMEs were nominated from human health, livestock and veterinary services, environmental protection, agriculture, municipal and local government authorities, border health services, and disaster management agencies. Nominations were requested to have prior experience in zoonotic disease preparedness, surveillance, or response. Technical groups reviewed risk profiles, surveillance data, and previous outbreak patterns. Using a One Health framework, experts developed outbreak scenarios, rapid risk assessment tools, response triggers, and sector-specific operational

responsibilities. Planning outputs were refined through joint discussions and validated with provincial departments and partner organizations.

Results

The planning process produced a provincial CCHF preparedness and response framework covering twelve high-risk districts. Three outbreak scenarios were defined to guide response operations. Level 1 (Alert/Monitoring) is triggered by a single suspected or confirmed case in one district within two weeks and involves routine surveillance, verification by the Surveillance and Response Unit, and coordination between district health offices and livestock surveillance teams. Level 2 (Localized Outbreak) is activated when at least five confirmed cases or one death occur within two weeks, requiring deployment of district Rapid Response Teams, epidemiological investigation, joint human, animal surveillance, laboratory confirmation, and targeted tick control measures. Level 3 (Public Health Emergency) is triggered when multiple districts report sustained transmission. At this stage the Provincial Public Health Emergency Operations Center is fully activated. Response branches include health services, livestock and veterinary services, municipal sanitation, agriculture departments, border health services, Eid livestock market administration, and disaster management authorities to coordinate vector control, safe animal handling, case management, and community risk communication.

Conclusion

Risk-based planning can be translated by assessment findings into practical multisectoral preparedness and response strategies. Clearly defined outbreak levels, operational roles, and coordination mechanisms strengthened collective readiness under a One Health framework. Risk-informed joint planning offers a practical pathway for countries to enhance coordinated disease emergency preparedness and response across human, animal, environmental, and administrative sectors.

---

833 – Operationalizing a One Health Approach for Antimicrobial Resistance Containment in Pakistan: A National Implementation Framework from NAP-AMR 2.0

Mumtaz Ali KHAN, Zurva ASHRAF, **Muhammad SALMAN**
National institute of Health, Pakistan

Background

Antimicrobial resistance (AMR) is a rapidly escalating global health security threat increasing morbidity, mortality, and healthcare costs. The spread of resistant pathogens across human, animal, food, and environmental systems threatens poses risks to health systems, food security, and pandemic preparedness. Pakistan is experiencing a growing burden of drug-resistant infections. Pakistan developed the National Action Plan on AMR 2024–2028 using a national One Health approach. This study examines the operationalization of NAP-AMR, focusing on multisectoral approach and implementation priorities.

Methods

A multisectoral policy and implementation review was conducted during the formulation of NAP-AMR-2 between May 2024 and February 2025. The process was coordinated by National Institute of Health Pakistan. Stakeholders included federal ministries responsible for health, livestock, agriculture, water resources, and environment; provincial health departments; academic institutions; and international partners.

Evidence sources included national AMR surveillance reports, Joint External Evaluation findings, the Tripartite AMR Country Self-Assessment Survey (TrACSS), and implementation reviews of the previous national AMR action plan. Sector-specific SWOT analyses and provincial consultations identified priority gaps and interventions. Strategic activities were costed using the WHO-AMR-NAP costing tool and aligned with global AMR governance frameworks. A monitoring and evaluation framework with measurable indicators was incorporated to support accountability and implementation tracking.

Results

Pakistan has established national AMR Sentinel surveillance system through 35 sentinel laboratories integrated AMR data from public and private laboratories and health facilities and reports annually to the GLASS-WHO. Sentinel surveillance enables monitoring of resistance trends across the country. Data are

analyzed at NIH and disseminated through annual national AMR surveillance reports to relevant stakeholders. Findings indicate rising resistance to several broad-spectrum antibiotics, reinforcing the need for strengthened stewardship and regulatory oversight.

NAP-AMR 2.0 builds on this surveillance platform to expand integrated One Health monitoring, strengthen laboratory and genomic surveillance capacity, and scale antimicrobial stewardship across healthcare and livestock sectors. Interventions also prioritize infection prevention and control (IPC), vaccination, water, sanitation and hygiene (WASH), and environmental monitoring addressing pharmaceutical waste, agricultural runoff, and wastewater-related AMR drivers.

Implementation aims to expand the national AMR surveillance network beyond the current 35 sentinel laboratories and strengthen real-time detection of resistance trends. With support from the Pandemic Fund, Pakistan is advancing interoperable surveillance and data-sharing systems linking human, animal, food, and environmental sectors, operationalizing a national One Health data architecture.

Conclusions: NAP-AMR 2.0 establishes a national implementation framework for AMR containment through an integrated One Health approach. Pakistan's surveillance platform, sentinel laboratory network, and routine reporting to GLASS provide a critical evidence base for policy action. Strengthening surveillance, stewardship, infection prevention, environmental monitoring, and sustainable financing can significantly enhance AMR containment and health security. Sustained political commitment and multisectoral collaboration will be essential to translate this strategy into measurable public health impact.

849 – Health Literacy, Environmental Sanitation, and Dengue Prevention Behavior in Urban Households: A One Health Study from Makassar, Indonesia

Nasrah NASRAH, Syamsuar MANYULLEI, Ridwan Mochtar THAHA, Andi Putri Cahaya NINGRUM
Hasanuddin University, Indonesia

Background: Dengue remains a major public health threat in Indonesia, particularly in densely populated urban settings where transmission is shaped by the interaction of human behavior, household environmental conditions, and social determinants. In Makassar, South Sulawesi, increasing dengue incidence and suboptimal larva-free indicators in the Kassi-Kassi area highlight the need for more integrated prevention strategies. From a One Health perspective, dengue prevention at household level cannot be understood solely through biomedical risk, but must also consider how health literacy and environmental sanitation influence community behavior. This study aimed to analyze the association between sociodemographic characteristics, health literacy, environmental sanitation, and dengue prevention behavior among urban households in Makassar.

Methods: A community-based cross-sectional study was conducted in Kassi-Kassi, Makassar, Indonesia. Data were collected from 168 household respondents using a structured questionnaire assessing sociodemographic characteristics, health literacy, and dengue prevention behavior, complemented by direct observation of household environmental sanitation conditions. Bivariate analysis was used to identify variables associated with dengue prevention behavior, followed by multivariable logistic regression for variables meeting selection criteria.

Results: Of 168 respondents, 57.7% demonstrated poor dengue prevention behavior, while 42.3% showed good preventive behavior. At bivariate level, health literacy was significantly associated with dengue prevention behavior (p=0.031), whereas sanitation status met the criterion for multivariable analysis (p=0.146); other sociodemographic variables were not significantly associated. In the multivariable model, health literacy and sanitation status were jointly associated with dengue prevention behavior (Omnibus test p=0.018), although the model explained a modest proportion of variance (Nagelkerke R Square=0.078). In partial regression, health literacy emerged as the strongest determinant, while sanitation status was not independently significant. These findings suggest that the capacity to access, understand, and apply health information may be more influential for household dengue prevention behavior than sociodemographic background alone.

Conclusions: This study supports a One Health framing of dengue prevention in urban communities by showing that household behavior is shaped by the intersection of human informational capacity and environmental context. Strengthening health literacy, while simultaneously improving household

sanitation, may provide a more effective pathway for community-based dengue prevention in endemic urban areas such as Makassar.

851 – Molecular Identification and Characterization of Mobatvirus (Hantaviridae) in Lao PDR

Chittaphone VANHNOLLAT (1), David SAFRONETZ (2), Philippe BUCHY (1)

1: Institut Pasteur du Laos, Lao People's Democratic Republic; 2: National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg Canada

Background

Hantaviruses pose a significant global public health threat, with bat-associated lineages challenging traditional rodent-reservoir paradigms. Southeast Asia has emerged as an important region for hantavirus discovery, yet the genetic diversity of *Mobatvirus* remains largely underexplored in Lao People's Democratic Republic (Lao PDR). This study aimed to expand surveillance efforts and characterize the genomic diversity, phylogenetic relationships, and potential zoonotic risk of bat-borne hantaviruses at the wildlife-human interface in Lao PDR.

Methods

An expanded surveillance program was conducted from May 2023 to October 2025 across three sites in Lao PDR: Khounkham district (Khammouane Province), Viengthong district (Bolikhamxay Province), and Kasi district (Vientiane Province). Live-captured bats were collected using harp traps and mist nets, while wild animals from local wet markets were surveyed with vendor permission. Biological samples including tissues, intestines, anal swabs, and saliva were screened using nested PCR targeting hantavirus RdRp gene. Positive samples underwent high-throughput sequencing. Phylogenetic and comparative analyses were performed to characterize the identified hantaviruses.

Results

Samples collected from bats and wild animals from wet markets, representing 34 genera and 59 species. Of all samples tested, 20 were positive for hantavirus: 17 from tissue samples, 2 from saliva swabs, and 1 from an anal swab. Positive samples originated from four bat species: *Aselliscus stoliczkanus*, *Hipposideros gentilis*, *Rousettus amplexicaudatus*, and *Macroglossus sobrinus*. Coding-complete genomes were recovered for multiple novel variants. Phylogenetic analysis confirmed these viruses form a monophyletic group within Mobatvirus, resolving into two major subclades: one clustering with Quezon and Robina viruses from fruit-eating bats, and another bifurcating into lineages corresponding to Đakrông and Xuân Sơn viruses associated with trident and leaf-nosed bats, respectively. Strong host specificity was observed with no evidence of host switching. Notably, two positive samples were collected from a bat found within a local wet market. Natural selection analysis revealed extremely low dN/dS ratios across all genome segments, indicating strong purifying selection with only limited episodic positive selection at specific codon sites.

Conclusions

This study significantly expands the known diversity of Mobatvirus in Lao PDR, identifying novel variants across multiple bat species and documenting endemic circulation at surveillance sites. The detection of these viruses in a wet market, a critical interface for human-wildlife contact, indicates a tangible zoonotic risk despite strong purifying selection, suggesting viral stability within bat reservoirs. These findings highlight the urgent need for serological surveillance in at-risk human populations, including market workers and communities that consume bushmeat, to assess the actual spillover potential. Future research should focus on the functional characterization of these mobatviruses and development of reservoir-derived cell culture models to better understand their pathogenicity and zoonotic implications.

854 – Evidence of interepidemic Rift Valley fever circulation in humans and livestock in northern Kenya; estimation of interepidemic Rift Valley fever incidence rates in human and livestock

Mathew MUTURI (1,2), Athman MWATONDO (1)

1: Zoonotic Disease Unit Kenya, Kenya; 2: Freie University, Berlin, Germany

Unraveling the complexity of where and how Rift Valley fever virus (RVFV) is maintained inendemic areas during interepidemic periods (IEP) is critical to improving the early detectionand response capacity of vulnerable communities in Sub-Saharan Africa. Unfortunately, dataon key epidemiological parameters—such as the force of infection and its determinants,crucial for designing tailored interventions—are almost nonexistent. We conducted ahousehold-based longitudinal study of pastoral cattle (n = 687), sheep (n = 622), and goats(n = 629), and 814 livestock keepers in an endemic region of northern Kenya between March 2022 and May 2023 to estimate the incidence rate of RVFV and determine risk factors for infection. Exposure to RVFV was assessed using an anti-RVF Immunoglobulin enzyme- linked immunosorbent assay. An interval-censored regression model for survival data analysis was used to estimate incidence and identify risk factors, with hazard ratios used to quantify the risk of exposure. Seropositivity in the baseline survey to identify naïveanimals for follow-up were highest in cattle at 31.73% (95% CI 28.24% - 35.33%), followed bygoats at 28.77% (95% CI 25.28% - 32.44%) and sheep at 25.88% (95% CI 22.51% -29.43%). The human prevalence was 7.37% (95% CI 5.77 – 9.17%). We observed 113 newlivestock infections over 805 animal-years, translating to an annual livestock incidence rate of14% (95% CI 11.56%–16.87%), however, cattle had a significantly higher incidence rate of20% (95% CI 15.38% – 26.18%). There was homogeneity of exposure across all ages andsexes, but insecticide use was associated with a lower hazard of infection, underlining theimportance of routine vector control in RVF prevention. We detected 15 humanseroconversions over 629 human-years, giving an incidence rate of 2.38 % (95% CI 1.33% -3.93%). The high incidence rate in all livestock age groups and evidence of seroconversionsupport the proposition that cryptic transmission could be the primary mode of viralpersistence in endemic areas. In contrast, the low incidence in humans indicates limitedcross-species transmission during non-outbreak periods. Nearly a century since RVF wasreported in the country, this is the first linked study to report field-based estimations on theincidence rate of RVFV in humans and livestock in Kenya, highlighting the critical need formore systematic studies to provide robust data to inform surveillance and mitigationstrategies adaptable to endemic areas in Sub-Saharan Africa.

864 – Virome analysis reveals ORF7 sequences of Type 2 Porcine Respiratory and Reproductive Syndrome Virus (PRRSV) for the first time in a rodent host (Microtus pennsylvanicus)

Elena SGARABOTTO (1,2), Nicola ZADRA (2,3), Jacob A. TYRELL (4), Chiara ROSSI (1), Ian HEWSON (5), Jeremy B. SEARLE (4), Heidi C. HAUFFE (1,3)

1: Conservation Genomics Research Unit, Research and Innovation Centre, Fondazione Edmund Mach, Via Edmund Mach 1, 38098 San Michele all'Adige (TN), Italy; 2: Università degli Studi di Ferrara, via Ludovico Ariosto 35, 44121 Ferrara, Italy; 3: NBFC, National Biodiversity Future Center, Palermo, Italy; 4: Department of Ecology and Evolutionary Biology, Corson Hall, Cornell University, Ithaca, NY 14853, USA; 5: Department of Microbiology, Wing Hall, Cornell University, Ithaca, NY 14853, US

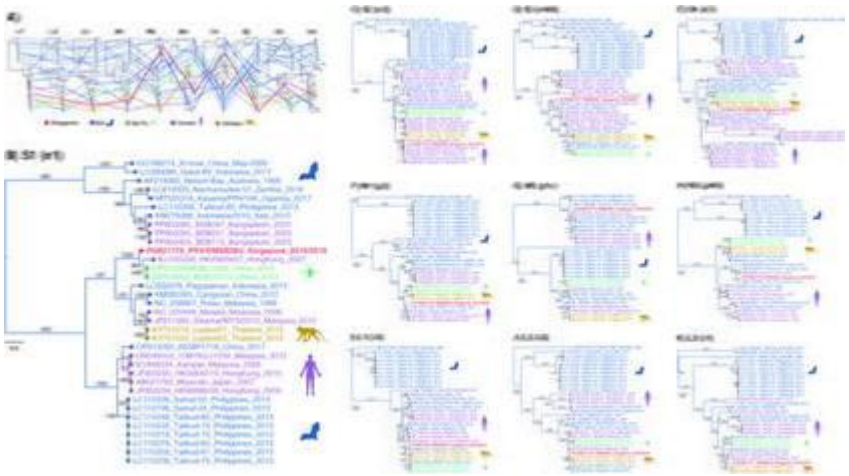
Background: Rodents are well-recognized reservoirs of zoonotic pathogens of public health relevance, including those that have affected the pig industry. However, the contribution of wild rodent populations to zoonotic outbreaks in pigs (*Sus scrofa*) and other livestock deserves more attention**.** One example of an abundant wild rodent is the meadow vole (*Microtus pennsylvanicus*) found widely across northern North America that moves between natural and human-modified habitats and is host to a range of zoonotic pathogens. It has previously been suggested that this rodent species could be linked to farm-to-farm transmission of pathogens affecting livestock but to our knowledge this hypothesis has not been tested**.** One particularly important pathogen affecting pigs is the Porcine Respiratory and Reproductive Virus (PRRSV). PRRSV has the highest economic impact on the pig husbandry industry of any pathogen, but up to now, farm-to-farm transmission of this virus has been assumed to be associated with movement of and contact with infected pigs and fomites. **Methods**: The lung virome of meadow vole (*Microtus pennsylvanicus)* from six neighbouring locations in New York State, USA was investigated using metagenomics and a novel de novo assembly virus discovery pipeline, Lazypipe v 3.1, to determine the circulation of potentially zoonotic viruses in a common wild rodent. **Results**: This study provides the first evidence of the occurrence of Type 2 Porcine Respiratory and Reproductive Syndrome Virus (PRRSV2) in a rodent, or indeed in any species apart from wild and domestic pigs (*Sus scrofa*). Our results showing the natural occurrence of this virus in potential transmission hosts other than wild or domestic pigs challenge the common farm-to-farm transmission scenario. Phylogenetic analysis of assembled partial

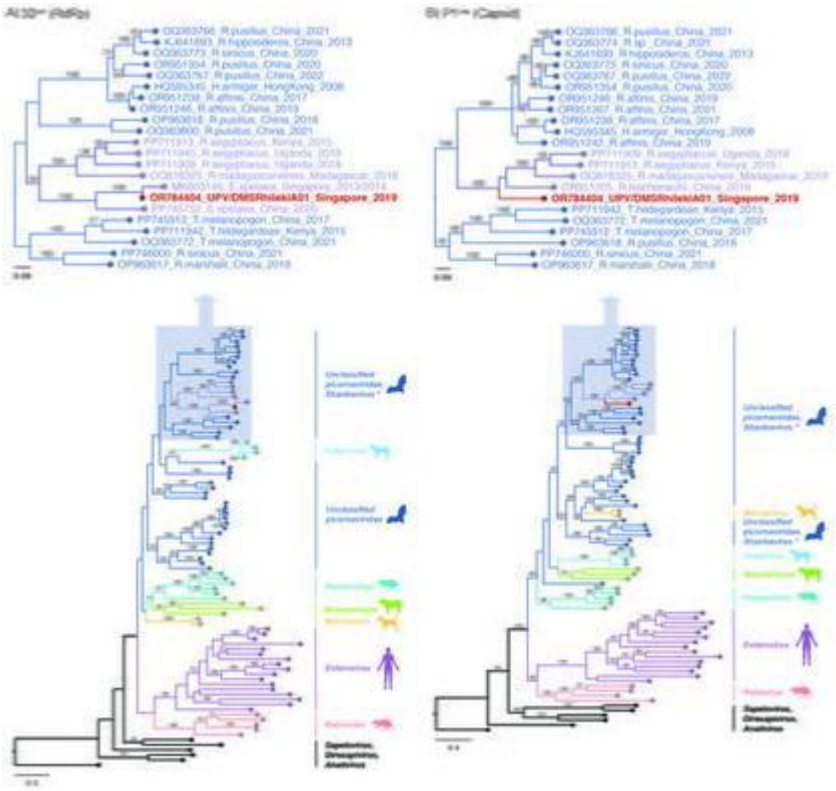
genomes from four of our pooled samples and all other nucleocapsid protein (ORF7) sequences available in Genbank showed that the sequences recovered from meadow voles unambiguously clustered within the PRRSV2 clade together with sequences derived from wild and domestic pigs. **Conclusions**: Historical research suggests that spillover from voles to domestic pigs may be the most parsimonious explanation for these results; however, we cannot rule out the reverse: that the source of PRRSV2 in these wild voles derives from pigs. Our results reinforce the importance of characterizing wildlife viromes to survey possible sources of zoonotic pathogens, which is vital for making evidence-based decisions regarding potential threats to the health of humans, livestock and wild fauna.

868 – Characterization of a novel Pteropine Orthoreovirus and an unclassified Picornavirus from cave nectar bats (Eonycteris spelaea), Singapore

Dolyce LOW, Lena CH'NG, Yan ZHUANG, Peter CRONIN, Yvonne SU, Ian MENDENHALL, **Gavin SMITH**
Programme in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

The cave nectar bat (*Eonycteris spelaea*) is a widespread pollinator of economically important crops such as durian and petai in Southeast Asia. It roosts in large colonies and shows strong site fidelity, traits that can support viral persistence and transmission. While several medically important virus families, including coronaviruses, filoviruses and paramyxoviruses have been reported from this species, the diversity and evolutionary dynamics of pteropine orthoreovirus (PRV), a bat-borne, segmented double-stranded RNA virus with documented zoonotic spillover, and bat picornaviruses remain incompletely characterized. A complete genome (ten full-length segments) of a Singapore *E. spelaea* PRV (PRV/DMSB26U/Singapore) was assembled from a dataset generated from pooled urine samples collected between 2015–2016 using the Twist Comprehensive Viral Research Panel on an Illumina MiSeq platform. Segment-specific maximum-likelihood phylogenies and tanglegram comparisons indicated extensive reassortment, with different segments clustering with PRVs from China, Thailand, Indonesia, and Malaysia. Whole-genome similarity ranged from 78.3–90.7% nucleotide identity, with the highest divergence in the S1 segment, consistent with antibody-driven selection. Separately, an unclassified picornavirus (UPV) was isolated from freshly collected pooled urine (2020) following blind inoculation on Rhileki cells (*Rhinolophus lepidus* primary kidney cells). Cytopathic effect was observed and nanopore sequencing was performed on culture supernatant and cell fractions, generating a 6,909 bp genome encoding 13 proteins. The Singapore *E. spelaea picornavirus (*UPV/DMSRhilekiA01/Singapore) groups within a monophyletic clade of frugivorous and nectivorous bat picornaviruses, which in turn fall within a clade of insectivorous bat UPVs. It is most closely related to the Chinese *E. spelaea* and *Rousettus leschenaultii* picornaviruses with 75.1% nt (88.7% aa) and 66.7% nt (73.2% aa) similarity in the RdRp and capsid genes, respectively, followed by the African bat picornaviruses (60.9–62.3% nt, 61.3–63.1% aa). The identification of genetically related viruses in geographically distant bat populations, suggests these bat populations are more interconnected than currently understood, highlighting a knowledge gap in our understanding of the ecology of *E. spelaea and their viruses.* Although their zoonotic risk is unknown, continued genomic and serological surveillance studies are warranted, given repeated spillover of PRV to humans.





871 – Title: AMR at the Human–Animal–Environment Interface: Multi-Drug Resistant E. coli in Nigerian Live Bird Markets

Annelies VAN BOHEMEN (1), Ben SWIFT (1), Kennedy CHAH (2), Andrew MEAD (1), Lucy BRUNTON (1)
1: Royal Veterinary College; 2: University of Nigeria, Nsukka

Live Bird Markets (LBMs) represent critical interfaces where human, poultry, and environment interact, facilitating the emergence and spread of Antimicrobial Resistance (AMR). *Escherichia coli* is widely used as an indicator organism for One Health AMR surveillance due to its ubiquity and capacity to acquire and disseminate resistance determinants. Despite growing concern over the spread of Multi-Drug Resistant (MDR) bacteria, particularly in low- and middle- income countries, data describing resistance patterns across the human-animal-environment interface in LBMs remain limited. This study aimed to characterise AMR patterns among *E. coli* isolates across human, poultry, and environmental sources in Nigerian LBMs.

A cross-sectional study was conducted in four LBMs across Southeast Nigeria between October and December 2024. A total of 487 samples were collected from live bird sellers (hand swabs, n = 47), poultry (cloacal swabs, n = 187), and environmental sites (soil, water, slaughter table swabs, cage swabs, n = 253). *E. coli* isolates (n = 224) were identified using standard biochemical methods. Antimicrobial susceptibility testing to 16 antibiotics representing 12 antimicrobial classes was performed using the Kirby-Bauer disc diffusion method and interpreted according to the CLSI 2025 guidelines. Proportions of resistant isolates were compared across sources using Fisher's exact test. Logistic regression was applied to estimate odds ratios (ORs) and 95% confidence intervals for MDR across sources. MDR was defined as resistance to ≥1 agent in ≥3 antimicrobial classes.

Among the 224 *E. coli* isolates tested, the highest resistance was observed for tetracycline (85%), followed by ampicillin (80%) and sulfamethoxazole-trimethoprim (68%). The lowest resistance occurred for imipenem (1%), and no resistance to ertapenem was observed. Resistance to ciprofloxacin was observed in 41% of isolates, and resistance to third-generation cephalosporins was rare (3%) (Figure 1). Resistance patterns were highly diverse, with 24% of isolates (54/224) having unique combinations (Table 1). The median number of antibiotics to which isolates were resistant was 5 (IQR 3 – 6).

MDR prevalence was 83% overall, highest in poultry (85%), followed by the environment (82%) and humans (40%) (Figure 2). There was weak evidence against the null hypothesis that there were no

differences in MDR prevalence between sources (Fisher's exact test, p = 0.055). Logistic regression indicated that human isolates had lower odds of MDR compared with environmental isolates (OR 0.15, 95% CI 0.02-0.96, p = 0.046), while MDR odds in poultry isolates were similar to those in environmental isolates (OR 1.26, 95% CI 0.61-2.59, p = 0.53).

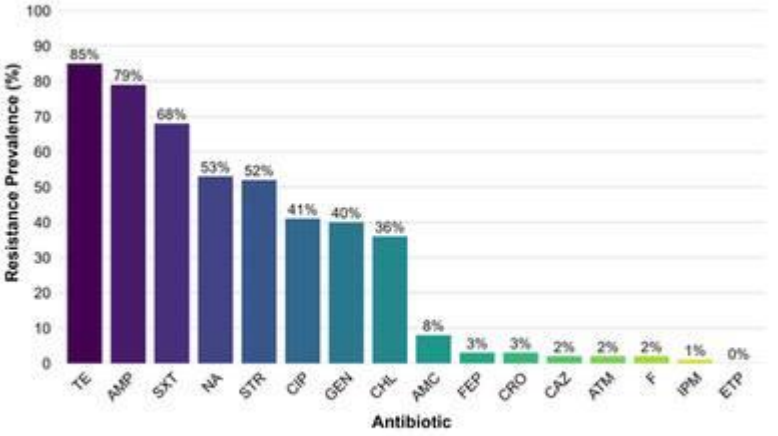
The high prevalence of MDR *E. coli* in both poultry and environmental samples highlights LBMs as potential reservoirs for AMR at the human-animal-environment interface. Strengthening interdisciplinary One Health surveillance and biosecurity practices in these settings may be critical to mitigating the spread of AMR.

Table 1: Most frequent antimicrobial resistance patterns among *Escherichia coli* isolates recovered from Live Bird Markets in Southeast Nigeria

Resistance pattern	Count	Percent (%)
GEN, STR, AMP, CIP, SXT, CHL, NA, TE	17	7.6
AMP, SXT, TE	11	4.9
STR, AMP, SXT, TE	11	4.9
STR, AMP, CIP, SXT, NA, TE	7	3.1
GEN, AMP, CIP, NA, TE	6	2.7
STR, AMP, SXT, CHL, TE	6	2.7
TE	6	2.7
GEN, AMP, SXT, TE	5	2.2
GEN, STR, AMP, CIP, SXT, NA, TE	5	2.2
GEN, STR, AMP, SXT, CHL, NA, TE	5	2.2
SXT, TE	5	2.2
Other patterns	131	58.5
Pan-susceptible	9	4

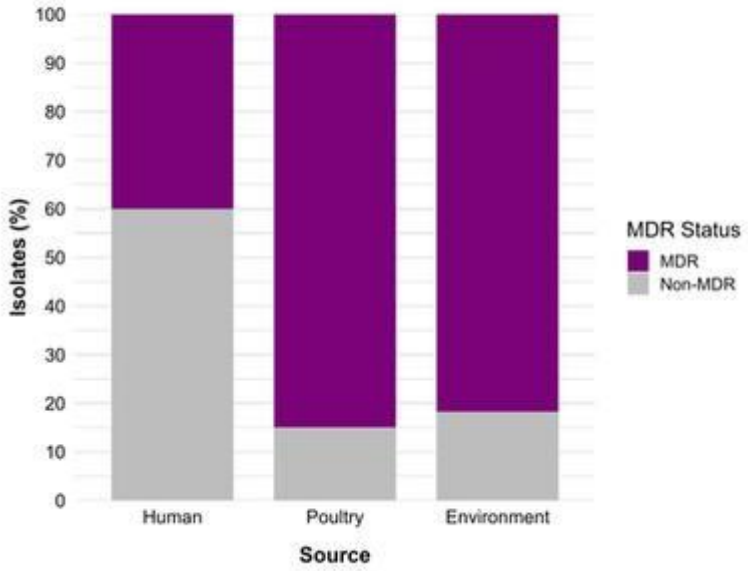
Resistance patterns represent combinations of antibiotics to which isolates were resistant. Patterns occurring in ≤4 isolates were grouped as "Other patterns." Pan-susceptible isolates showed no resistance to any of the antibiotics tested. Antibiotic abbreviations: AMP, ampicillin; ATM, aztreonam; CAZ, ceftazidime; CHL, chloramphenicol; CIP, ciprofloxacin; CRO, ceftriaxone; F, nitrofurantoin; FEP, cefepime; GEN, gentamicin; IPM, imipenem; NA, nalidixic acid; STR, streptomycin; SXT, sulfamethoxazole–trimethoprim; TE, tetracycline; ETP, ertapenem.

Fig 1: AMR prevalence among *Escherichia coli* isolates recovered from Live Bird Markets in Southeast Nigeria



Antibiotic abbreviations: AMP, ampicillin; ATM, aztreonam; CAZ, ceftazidime; CHL, chloramphenicol; CIP, ciprofloxacin; CRO, ceftriaxone; F, nitrofurantoin; FEP, cefepime; GEN, gentamicin; IPM, imipenem; NA, nalidixic acid; STR, streptomycin; SXT, sulfamethoxazole–trimethoprim; TE, tetracycline; ETP, ertapenem.

Fig 2 Distribution of multidrug-resistant *E. coli* isolates by source



876 – SeroPrevalence of dengue and chikungunya – Findings from an Acute Febrile Illness (AFI) surveillance in a rural cohort of Odisha, India

Subrata Kumar PALO, Srikanta KANUNGO, Debdutta BHATTACHARYA, Sanghamitra PATI
ICMR Regional Medical Research Centre, Bhubaneswar, India

Introduction: Dengue and chikungunya are important mosquito-borne viral diseases that contribute significantly to the burden of acute febrile illness (AFI) in tropical regions. In India, periodic outbreaks and endemic transmission highlight the need for community-based surveillance to better understand the prevalence and transmission dynamics of these infections, particularly in rural populations where diagnostic data are often limited.

Rationale: Despite the endemicity of arboviral diseases in eastern India, evidence on their prevalence in rural community cohorts remains limited. Surveillance through AFI platforms provides an opportunity to

detect active infections and understand the underlying seroprevalence, which can guide early diagnosis, vector control, and public health preparedness.

Methodology: An AFI surveillance study was conducted in a rural cohort in Odisha. At baseline, blood samples were collected from 755 participants to assess exposure to dengue and chikungunya using serological testing. Participants were followed for febrile episodes, and individuals presenting with fever were further evaluated. Acute and convalescent samples from AFI cases were tested to detect recent infections.

Results: Among the 755 participants, 280 (37.1%) were positive for dengue IgG antibodies and 33 (4.3%) for chikungunya IgG, indicating prior exposure. During surveillance, 428 (56.6%) individuals reported fever episodes, of which 149 (19.7%) met the criteria for acute febrile illness. Laboratory analysis identified 24 dengue infections, including 15 cases in the acute phase, 7 in the convalescent phase, and 2 IgG seroconversions. No chikungunya cases were detected during the surveillance period.

Conclusion: The findings demonstrate substantial prior exposure to dengue in the rural cohort and confirm ongoing dengue transmission through AFI surveillance. Continued community-based monitoring and strengthened vector control measures are essential to reduce the burden of dengue and improve early detection of arboviral diseases in rural Odisha.

879 – Vaccination of Foals Induces Functional Humoral and Th1-Biased Cellular Immunity to Hendra Virus Under Field Conditions

Gervais HABARUGIRA (1), Mitchell P. COYLE (2), Ilona TUREK (1), Adriana PLIEGO ZAMORA (3), Siying YE (1), Emma MCGOWAN (1), Jennifer BARR (1), Nagendra Singanallur BALASUBRAMANIAN (1), Grantley R. PECK (1), Helle BIELEFELDT-OHMANN (3,4), Kim HALPIN (1)

1: CSIRO Australian Centre for Disease Preparedness, Geelong, VIC 3219, Australia; 2: Equine Unit, Office of the Director Gatton Campus, The University of Queensland, Gatton, QLD 4343, Australia; 3: School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, QLD 4072, Australia; 4: Australian Infectious Diseases Research Centre, The University of Queensland, Brisbane, QLD 4072, Australia

Background: *Henipavirus hendraense,* commonly known as Hendra virus (HeV), is a highly pathogenic, enveloped, negative-sense single-stranded RNA virus belonging to the genus *Henipavirus* within the family *Paramyxoviridae*. The virus is a zoonotic pathogen that poses a threat at the animal–human interface, with infected horses acting as the principal amplification host for human infection. Vaccination of horses is therefore a cornerstone of One Health strategies to prevent infection of humans. However, evidence to inform vaccination policy in foals remains limited, particularly regarding early-life immunisation, and the influence of passive immunity under field conditions.

Methods: In this longitudinal field study, nine foals born to vaccinated mares and housed under standard farming conditions were vaccinated with Equivac® HeV (Zoetis Inc.) and followed for nine months. Blood samples were collected prior to vaccination and at monthly intervals thereafter. Vaccine-induced humoral immunity was assessed using serum neutralization assays to measure functional neutralizing antibodies and a microsphere immunoassay to quantify total anti-HeV IgG. T-cell memory responses were characterised using ELISpot assays detecting HeV-specific interferon-gamma (IFN-γ) and interleukin-4 (IL-4), alongside cytokine profiling of peripheral blood mononuclear cells following stimulation with recombinant HeV glycoprotein.

Results: All foals mounted detectable antibody responses following vaccination, irrespective of the presence of maternal antibodies at baseline. Neutralising antibody responses increased with successive vaccine doses, consistent with the development and maturation of functional humoral immunity. ELISpot demonstrated robust IFN-γ responses in the absence of IL-4 production, indicating a Th1-biased cell-mediated immune profile. Cytokine secretion profile corroborated these findings, with IFN-γ, IP-10 (CXCL10) and interleukin-2 identified as the predominant mediators. Both humoral and cell-mediated immune responses increased progressively over time, demonstrating sustained immune maturation under field conditions.

Conclusions: This study provides the first evaluation of vaccine-induced cell-mediated immunity alongside humoral immunity against Hendra virus in foals under field conditions. This addresses a critical knowledge gap relevant to equine vaccination policy. The demonstration of effective early-life immunity, irrespective of the presence of passive maternal antibodies, supports early and widespread equine

vaccination as a practical One Health intervention to prevent HeV transmission risk and protect both animal and human health.

888 – Surveillance of Vector-Borne and Emerging Pathogens in Finnish Reindeer

Kirsi AALTONEN (1), Eda ALTAN (1), Minttu HUTTUNEN (1), Laura ITKONEN (2), Ruut JOENSUU (1), Heli NORDGREN (1), Anu NÄREAHO (1), Antti OKSANEN (2), Jenni PETTERSSON (1), Maij T. SUVANTO (1), **Essi M. KORHONEN** (1)

1: University of Helsinki, Finland; 2: Finnish Food Authority, Finland

Background

Reindeer (Rangifer tarandus tarandus) husbandry is an important livelihood in northern Finland. Climate change is expected to facilitate the northward expansion of arthropod vectors such as ticks and mosquitoes, potentially increasing the risk of vector-borne pathogens in northern ecosystems. Due to their extensive grazing and close interaction with wildlife, vectors and also humans, reindeer may also act as sentinel animals for monitoring emerging vector-borne diseases.

The aims of this study are to assess reindeer exposure to vector-borne and emerging pathogens and evaluate their disease burden, to develop improved diagnostic tools for key pathogens identified, and to establish a biobank of samples collected across the Finnish reindeer herding area.

Methods

Samples are collected from reindeer at slaughterhouses during routine slaughter across the Finnish reindeer herding region. Blood, fecal samples, and swabs from suspected poxvirus lesions will be obtained. Blood samples will be examined for parasites and screened for antibodies against selected vector-borne pathogens, including tick-borne encephalitis virus (TBEV), Babesia, Anaplasma, and orbiviruses. Diagnostic tools will be developed for pathogens detected in the study, including a PCR assay for the detection of reindeer poxvirus. Vectors, including ticks, mosquitoes and biting midges, will also be collected and screened using molecular methods.

Results

Preliminary analyses indicate a 33–50% positivity rate for microfilariae in reindeer blood samples. Further investigations of the filarial findings, as well as serological screening for antibodies against vector-borne viruses and bacteria, are ongoing, and updated results will be presented at the conference.

Conclusions

This study will provide new insights into infectious diseases affecting reindeer and support the development of improved diagnostic methods. The outcomes will strengthen the capacity to detect and manage emerging pathogens within the reindeer husbandry sector. The comprehensive sample collection and resulting biobank will form a long-term resource for future research, including microbiome studies and investigations into the impacts of environmental change.

895 – Operationalizing One Health at the Municipal Level: Evidence, Power, and Local Stewardship in the Philippines

Nai Rui CHNG (1), Geminn Louis C. APOSTOL (2), Duane Raphael MANZANILLA (3), Noelle CUBACUB (2), Percival Ethan LAO (2), Veincent Christian F. PEPITO (2), Katie HAMPSON (1), Mary Elizabeth MIRANDA (3), Jobin MAESTRO (4), Noel MIRANDA (2)

1: School of Biodiversity, One Health & Veterinary Medicine, College of Medical, Veterinary & Life Sciences, University of Glasgow; 2: Ateneo Center for Research & Innovation, Ateneo School of Medicine & Public Health, Ateneo de Manila University; 3: The Field Epidemiology Training Program Alumni Foundation, Inc. (FETPAFI); 4: Alcantara Rural Health Unit, Municipality of Alcantara

Background: Despite access to regional and national One Health frameworks, evidence on how these are operationalized by local governments remains limited. This study examines Alcantara Municipality in Romblon Province, which enacted one of the Philippines' first municipal One Health ordinances in 2024

following a rabies outbreak, to understand the drivers of policy adoption and multisectoral implementation challenges in a decentralised health system.

Methods: We employed an evidence-informed policymaking (EIPM) framework (Sempé et al., 2025), analyzing qualitative interviews (n=12), focus group discussions (n=3), and co-produced LGU outputs—an Action Review, Theory of Change, and Implementing Rules and Regulations—alongside observation notes from November 2024 to March 2025. Our team engaged in co-production, facilitating operational instrument development with local interest-holders.

Results: Key findings reveal four insights about evidence and power in local One Health governance. First, while policy champions and external experts catalyzed ordinance enactment, reliance on a small number of individuals risks undermining collective ownership and sustained implementation. Broader coalitions from the outset appear essential for long-term durability. Second, systematic mechanisms for collecting local One Health data remain limited. Rabies surveillance data exists but is not integrated within a coherent local knowledge system, while informally gathered community knowledge is not formally recognized as evidence. For Local Government Units (LGUs) such as Alcantara, “evidence” extends well beyond scientific data to include community narratives, social media discourse, and political feedback—information that often carries greater persuasive power than research findings. Third, transitioning from adoption to operationalization exposed critical gaps. Epidemiologic evidence justified the ordinance and supported establishment of a Multi-Sectoral One Health Council, but proved insufficient for decisions around coordination mechanisms, resource allocation, and collaboration intensities. Operationalization required governance evidence, organizational knowledge, and understanding of local capacity and political economy—largely absent from traditional health information systems. Executive Orders and supplementary ordinances were needed to translate national frameworks into locally actionable steps. Fourth, co-production revealed that local interest-holders possess valuable experiential knowledge about human-animal-environment interactions, preferring locally generated information over national directives, yet lacking accessible frameworks to organize it into coordinated action.

Conclusions: Our findings demonstrate that effective One Health operationalization at the municipal level requires a broader conception of what counts as “evidence” and who stewards it. Moving beyond top-down technocratic models, we argue for building local data stewardship capacity—enabling LGUs to document, analyze, and own their One Health intelligence, including monitoring systems that capture community-relevant indicators alongside traditional surveillance metrics. Sustainable implementation in devolved systems should depend less on technical blueprints from above and more on strengthening local capacity to generate, interpret, and act on context-specific evidence—including the lived experience of diverse interest-holders—while maintaining connections to broader frameworks. These findings have implications for how national and international partners support One Health operationalization in decentralized contexts.

899 – Developing Synergistic, Cross-Faculty One Health Education at the University of Helsinki and with Una Europa Partners

Topi TANSKANEN, Pyry KOSKINEN, Annamari HEIKINHEIMO, Sarah GREEN, Riikka KETO-TIMONEN, Olli PELTONIEMI, Tarja SIRONEN

University of Helsinki, Finland

Addressing complex One Health challenges requires professionals who can integrate perspectives across human, animal and environmental health, and collaborate effectively with policy actors and communities. To meet this need, the University of Helsinki is developing a coherent One Health education pathway across three training levels. This pathway is genuinely cross-disciplinary, grounded in institutional strengths and ongoing research, and resource-efficient. It brings together expertise from six faculties to create a Master of Science (MSc) in One Health, a One Health Doctoral Programme, and—together with the Una Europa university alliance—a lifelong learning microcredential One Health in Governance for working professionals.

We reviewed existing One Health master’s programmes and compared them with societal needs and institutional strengths. While many programmes are anchored in infectious diseases or population health, our design adopts a broader perspective, emphasising integrated One Health approaches, cross-disciplinary literacy, and communication and collaboration across disciplinary and national boundaries.

Building on the Helsinki One Health research network (established 2018), a cross-faculty curriculum team consolidated teaching expertise and content from the Faculties of Veterinary Medicine; Medicine; Pharmacy; Agriculture and Forestry; Biological and Environmental Sciences; and Social Sciences. To foster transdisciplinarity, the MSc incorporates cross-disciplinary co-teaching; an applied capstone project tackling real-world challenges; paired master's theses (cross-disciplinary where feasible); a joint thesis seminar; and workshops for teaching staff to support learning across disciplinary interfaces.

In parallel, the University of Helsinki is merging field-specific doctoral programmes into a One Health Doctoral Programme, and co-developing learning materials with Una Europa for government, NGO and other sectoral professionals.

The integrated approach strengthens educational pathways from master's level to doctoral training, expands interdisciplinary teaching and supervision, and enhances internationalisation by enabling globally recruited staff to teach beyond programmes tied to national language requirements.

Shared modules covering core One Health concepts and transferable academic and professional skills are being designed for reuse across the MSc, doctoral programme and microcredential, improving resource efficiency. Newly developed teaching also contributes to existing curricula in sustainability, microbiology and ecology, agriculture and nutrition, and medicine and veterinary medicine.

A modular, synergistic One Health education pathway can expand cross-faculty capacity without creating disproportionate teaching demands. It enables graduates and professionals to address complex, cross-disciplinary health challenges while maintaining a distinct One Health identity rooted in systems thinking and collaboration. Addressing differences between scientific traditions, particularly across the life and social sciences, has shown that sustained collaboration can transform cross-disciplinary challenges into shared strengths.

907 – Different forms of One Health: Insights from Eight Years of Fleming Fund Engagement

Syed ABBAS (1), **Rebecca MAUDLING** (2), Tim SHORTEN (2)
1: Institute of Development Studies, United Kingdom; 2: independent consultant

Background Although the One Health (OH) approach has gained global prominence as a framework for addressing complex health challenges such as antimicrobial resistance (AMR), there remains limited practical guidance on how to adapt OH implementation across diverse country contexts. Efforts to institutionalise OH often confront differing political, ecological and organisational realities, making it difficult for countries to operationalise the concept in ways that are both effective and sustainable. The UK Fleming Fund programme, which positions OH as a core organising principle for strengthening integrated AMR surveillance and evidence-based policy across human, animal and environmental sectors, offers a valuable opportunity to examine context-sensitive pathways for OH implementation.

Methods This analysis draws upon a multi-country evaluation of Fleming Fund activities conducted between 2019 and 2024. Evidence was synthesised from four rounds of country visits, a targeted literature review, semi-structured interviews with key informants involved in AMR and OH initiatives and comparative cross-country analysis. Preliminary findings were subsequently refined through structured discussions with technical experts working across AMR, surveillance and OH policy. The combined dataset enabled identification of recurring challenges, context-specific strategies and design principles relevant to strengthening OH implementation at national level.

Results The study proposes a “menu of options” to support countries in tailoring OH programmes to their institutional, ecological and political contexts. This framework comprises three interlinked dimensions:**(1) Outcomes:** Broadening OH ambition beyond health-sector improvements to encompass food safety, livelihoods, environmental integrity and biodiversity, thereby aligning OH with nationally salient priorities.**(2) Entry Points:** Grounding OH in concrete AMR-related activities, including infection prevention and control, integrated surveillance, antimicrobial stewardship and cross-sector governance. These technical entry points help establish feasible and sector-specific starting positions for collaboration.**(3) Structures:** Allowing for flexible governance arrangements that reflect local institutional cultures. Options range from formal interministerial committees and working groups to informal networks, distributed leadership models, or hybrid approaches. Countries may select arrangements suited to their administrative capacity, political incentives and sectoral relationships.

Conclusions The proposed framework provides a practical tool for countries seeking to adapt and institutionalise OH approaches in ways that are both acceptable and sustainable. By offering modular options rather than prescriptive models, it supports the development of OH programmes that align with national priorities and existing systems. This adaptability is especially important for AMR, where effective responses require contextually grounded coordination across sectors. The framework therefore contributes to more operationally relevant OH guidance for policy, practice and future research.

912 – Strengthening Veterinary Laboratory Systems for Pandemic Preparedness: Zambia’s One Health Experience under the Pandemic Fund

Mwape FANDAMU (1), Frank BANDA (2)

1: Central Veterinary Research Institute, Zambia, Zambia; 2: Food and Agriculture Organization of the United Nations, Zambia

The Department of Veterinary Services in Zambia, through the Central Veterinary Research Institute (CVRI) and its network of provincial and district laboratories, plays a critical role in safeguarding animal and public health. However, limited pandemic preparedness has historically constrained the veterinary laboratory network's effectiveness. Gaps identified through the 2023 Joint External Evaluation, Performance of Veterinary Services assessments and FAO laboratory mapping tools highlighted weaknesses in infrastructure, workforce capacity, biosafety, biosecurity and sample referral systems. This study describes targeted interventions implemented under the Zambia Multisectoral Pandemic Preparedness and Response (ZaMPPR) Project between 2023 and 2025 to strengthen veterinary laboratory and surveillance systems in alignment with the Global Health Security Agenda.The interventions were implemented across CVRI, seven provincial and five district laboratories. Key interventions included: provision of laboratory equipment, consumables and sample packaging materials; capacity building in ISO/IEC 17025 Quality Management Systems; joint One Health biosafety and biosecurity training with the human health sector; strengthening the national sample referral system through provision of a vehicle and 30 motorbikes; and upgrading the national Laboratory Information Management System (SILAB) to enable extended real-time data access. These interventions resulted in measurable improvements in laboratory performance and surveillance efficiency. Using paired t-tests to assess changes in turnaround time (significance set at p 0.05), the mean turnaround time for sample handling decreased significantly from 13.7 days prior to the SILAB enhancement to 6.6 days following the capacity-building program, representing a mean reduction of 7.14 days (95% CI: 5.26-9.03; p 0.001). Data quality indicators also improved substantially: sample registration completeness increased from 50-90% to 80-100%, while test result entry improved from 10-80% to 80-100%. In parallel, ISO/IEC 17025 QMS implementation has been expanded to all provincial laboratories, with three laboratories targeted for accreditation and the number of accredited diagnostic tests at CVRI projected to increase to nine. Additionally, 89 field and laboratory personnel were trained in biosafety and biosecurity in 2025, supported by the development of Zambia’s first national animal health BSBS manual and standard operating procedures.Implementation of

these interventions demonstrates that coordinated, multi-component investments in laboratory systems, workforce capacity, biosafety frameworks and digital data management delivered through strong government-partner collaboration and a One Health approach can significantly strengthen veterinary services and contribute to improved pandemic preparedness. The Zambia experience offers insights for countries seeking to strengthen animal health laboratory systems as part of global health security.

918 – Advancing One Health research on pesticide-induced oxidative stress through interdisciplinary collaboration: the CAPSTONE COST Action

Luka KAZENSKY (1), Óscar HERRERO (2), Damien BAUDIFFIER (3), Katarina MATKOVIĆ (1), Marie-Agnes COUTELLEC (4), Helga STOPPER (5), Mirta MILIĆ (1), Anca Oana DOCEA (6), Rosario PLANELLÓ (2), Davide DEGLI ESPOSTI (7), Carina LADEIRA (8,9), Peter MØLLER (10), Sandrine FRELON (11), Tanima SENGUPTA (12), Olivier ARMANT (11), Dalma MARTINOVIĆ-WEIGELT (13), Hans SANDERSON (14), Denis HABAUZIT (15), Ivana ARNAUDOVA DANEVSKA (16), Tijana MILIĆEVIĆ (17), Elisa BOUTET ROBINET (18), COST Action CAPSTONE Project Members (CA24108) (19)

1: Institute for Medical Research and Occupational Health, Croatia; 2: National University of Distance Education, Madrid, Spain; 3: Evertéa Foundation, Valence, France; 4: DECOD, Ecosystem dynamics and sustainability: from source to sea, INRAE, Institut Agro, Ifremer, Rennes, France; 5: University of Wuerzburg, Wuerzburg, Germany; 6: University of Medicine and Pharmacy of Craiova, Craiova, Romania; 7: RiverLy, Ecotox team, INRAE, Villeurbanne, France; 8: Escola Superior de Saúde de Lisboa - Polytechnic University of Lisbon, Lisbon, Portugal; 9: Comprehensive Health Research Centre (CHRC), National School of Public Health, NOVA University of Lisbon, Lisbon, Portugal; 10: University of Copenhagen, Copenhagen, Denmark; 11: Laboratory of Ecology and Ecotoxicology of Radionuclides, French Nuclear Safety and Radiation; 12: NILU The Climate and Environmental Research Institute, Kjeller, Norway; 13: University of St. Thomas, Saint Paul, MN, USA; 14: Aarhus University, Roskilde, Denmark; 15: Toxicology of contaminants Unit, Fougères Laboratory, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Fougères, France; 16: PHI University Clinic for Respiratory Diseases in Children Kozle – Skopje, Ss Cyril and Methodius University, Faculty of Medicine, Skopje, North Macedonia; 17: University of Belgrade, Institute of Physics Belgrade, Belgrade, Serbia; 18: Toxalim, Université de Toulouse, INRAE, ENVT, EI-Purpan, Toulouse, France; 19: Cost Action CA24108

BackgroundPesticides are widely used in agriculture and represent an important environmental and public health concern. Increasing evidence suggests that pesticide exposure may induce oxidative stress (OxS) imbalance, a biological mechanism implicated in ecosystem disturbances and multiple human diseases. Research addressing pesticide-induced OxS is employed in disciplines such as toxicology, ecotoxicology, epidemiology, and risk assessment. The CAPSTONE COST Action (CA24108), Oxidative stress at the Crossroads of Adverse Outcome Pathways – Pesticides – One Health, aims to address this gap by creating a pan-European interdisciplinary network dedicated to advancing knowledge on the role of oxidative stress in pesticide-related adverse effects within a One Health framework.

MethodsCAPSTONE will engage scientists from academia, industry, and regulatory agencies across multiple countries, integrating expertise in toxicology, ecotoxicology, bioinformatics, epidemiology, and risk assessment. The Action promotes collaborative research coordination through working groups focusing on identifying oxidative stress biomarkers, linking pesticide exposure to adverse outcomes using the adverse outcome pathway (AOP) framework, and integrating human and ecosystem health data. Activities include systematic expert-based literature analyses, database development, interdisciplinary workshops, training schools, short-term scientific missions, and stakeholder engagement initiatives.

ResultsThe Action aims to generate a coordinated knowledge base linking pesticide-induced OxS with adverse outcomes across species and ecosystems. By integrating ecotoxicological and human health data, CAPSTONE aims to identify relevant biomarkers, support the development of new AOPs related to pesticide toxicity, and highlight mechanisms underlying long-term health and environmental impacts. The network will also strengthen interdisciplinary collaboration, foster capacity building among early-career researchers, and enhance knowledge exchange between academia, regulatory bodies, and industry.

ConclusionsCAPSTONE contributes to advancing the One Health approach by bridging human, animal, and environmental health research on pesticide exposure and OxS. Through coordinated international collaboration and knowledge dissemination, the Action aims to support improved risk assessment methodologies, inform regulatory decision-making, and promote sustainable and safer agricultural practices.*This work is based upon work from COST Action CAPSTONE CA24108, supported by COST (European Cooperation in Science and Technology).*

921 – Associations between the number of food control inspections and the compliance of FBOs

Salla AALTONEN (1), Mikko KOSOLA (1), Annukka MARKKULA (2), Janne LUNDÉN (1)

1: Department of Food Hygiene and Environmental Health, Faculty of Veterinary Medicine, University of Helsinki, Finland; 2: Food Safety Department, Finnish Food Authority, Finland

Background: Food safety is one of the fundamental issues of One Health. European Union legislation (EC 625/2017) states that food business operators (FBOs) are responsible for ensuring food safety and their compliance with legislation is overseen by official food control. Non-compliances are commonly observed at inspections, and they have also been associated with foodborne diseases. Despite the importance of inspections in ensuring food safety, we lack the understanding of how the number of inspections affects FBOs' compliance level. The objective of this study was to determine whether there is an association between the number of inspections and FBOs' compliance level. Our hypothesis was that the increase in the number of inspections results in better compliance.

Methods: The material contained all food control inspection reports regarding restaurants in Finland between 2020 and 2024 (n= 22 035). Inspection reports consisted of 17 subsections that each contained several inspection items. We included subsections that had been inspected at least 5 000 times during the study period. The restaurants were grouped into three groups based on the average number of inspections of restaurants in local food control units (Group 1 = high, Group 2 = average and Group 3 = low average number of inspections in particular food control unit). In Finland, inspections are graded on a four-level scale (A = Excellent, B= Good, C = To be corrected and D = Poor); we categorised these grades into two groups: AB = "complies with regulations or only minor non-compliances that do not impair food safety or mislead consumers" and CD = "non-compliances that impair food safety or mislead consumers and need to be corrected". Two-proportion z-test was used to compare CD-proportions between Group 1 and Group 3.

Results: Our analyses included 14 subsections with a total of 313 971 inspection entries. At least 1.4 times more non-compliances, that impair food safety or mislead consumers, were detected in six subsections in the restaurants of Group 3 than in the restaurants of Group 1 (p 0.05). The greatest differences were observed in subsections "packaging materials and food contact materials", "traceability and recalls", "food temperature management" and "hygiene of food production or handling" with 4.2, 3.2, 1.6 and 1.6 times more grades C and D, respectively.

Conclusions: These findings support our hypothesis that higher number of inspections is associated with better inspection grades. As non-compliances have in previous studies been associated with foodborne diseases this study demonstrates the importance of inspections in ensuring food safety. Previous studies show that inspections can enhance compliance for example through guidance given at inspections. Understanding the effects of inspections is essential to ensure equal and evidence-based food control. The results can be used when designing the national inspection plans.

935 – Oxidative stress at the crossroads of adverse outcome pathways -pesticides - One Health: the CAPSTONE Cost Action

Marie-Agnès COUTELLEC (1), Tanima SENGUPTA (2), Luka KAZENSKY (3), Óscar HERRERO (4), Damien BEAUDIFFIER (5), Katarina MATKOVIĆ (3), Helga STOPPER (6), Mirta MILIĆ (3), Anca Oana DOCEA (7), Rosario PLANELLÓ (4), Davide DEGLI ESPOSTI (8), Carina LADEIRA (9,10), Peter MØLLER (11), Sandrine FRELON (12), Olivier ARMANT (12), Dalma MARTINOVIĆ-WEIGELT (13), Hans SANDERSON (14), Denis HABAUZIT (15), Ivana ARNAUDOVA DANEVSKA (16), Tijana MILIĆEVIĆ (17), Elisa BOUTET-ROBINET (18), COST Action CAPSTONE WG members CA24108 (19)

1: DECOD, Ecosystem dynamics and sustainability: from source to sea, INRAE, Institut Agro, Ifremer, Rennes, France; 2: NILU The Climate and Environmental Research Institute, Kjeller, Norway; 3: Institute for Medical Research and Occupational Health, Zagreb, Croatia; 4: National University of Distance Education, Madrid, Spain; 5: Evertéa Foundation, Valence, France; 6: University of Wuerzburg, Wuerzburg, Germany; 7: University of Medicine and Pharmacy of Craiova, Craiova, Romania; 8: RiverLy, Ecotox team, INRAE, Villeurbanne, France; 9: Escola Superior de Saúde de Lisboa - Polytechnic University of Lisbon, Lisbon, Portugal; 10: Comprehensive Health Research Centre (CHRC), National School of Public Health, NOVA University of Lisbon, Lisbon, Portugal; 11: University of Copenhagen, Copenhagen, Denmark; 12: Laboratory of Ecology and Ecotoxicology of Radionuclides, French Nuclear Safety and Radiation Protection Authority, Cadarache, France; 13: University of St. Thomas, Saint Paul, MN, USA; 14: Aarhus University, Roskilde, Denmark; 15: Toxicology of contaminants Unit, Fougères Laboratory, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), Fougères, France; 16: PHI University Clinic

for Respiratory Diseases in Children Kozle – Skopje, Ss Cyril and Methodius University, Faculty of Medicine, Skopje, North Macedonia; 17: University of Belgrade, Institute of Physics Belgrade, Belgrade, Serbia; 18: Toxalim, Université de Toulouse, INRAE, ENVT, EI-Purpan, Toulouse, France; 19: COST Action CA24108

Background - Oxidative stress (OxS) plays a central role in ecosystem disturbance and human diseases. Some pesticides have already been banned partly due to their pro-oxidative properties. However, among currently athorized substances, some are suspected or known to cause OxS. OxS arises from an imbalance between reactive oxygen/nitrogen species (ROS/RNS) and cellular antioxidant defenses. Pesticides induce this stage through several distinct pathways like mitochondrial dysfunction, detoxification stress and antioxidant depletion. OxS constitutes thus a key determinant of pesticide toxicity and impairment of ecosystem functioning and human health.

There is an increasing scientific, societal, and political concern about pesticides within the One Health framework (OH). In this context, the challenge and overarching objectives of the Pan-European network CAPSTONE are to identify pesticides' adverse effects linked to OxS that are relevant for both humans and ecosystems, to describe involved molecular and cellular Key Events (KEs) and KE relationships (KERs), and integrate these into Adverse Outcome Pathways (AOPs) networks. CAPSTONE also aims to characterize gaps in existing databases and to propose new AOPs addressing OxS-based pathologies and ecological impairments.

Methods - CAPSTONE consists of nine Research Coordination Objectives addressed by six Working Groups (WGs). OxS biomarkers specifically induced by pesticides are currently analysed and ranked by relevance to both human and model species used in toxicology and/or ecotoxicology (WG1 and WG2). This work relies on manual/systematic review and text mining of the literature and databases. In parallel, a panel of existing methodologies to assess OxS is being established and their transferability between toxicology and ecotoxicology is evaluated (WG3). The analysis will be used to compare the role of OxS in AOPs in toxicology and ecotoxicology, and to assess the relevance of OxS-specific KEs to epidemiological and exposomic approaches (pesticide mixtures), and implementation of OxS protocols, using predictive tools and modelling (WG4). This work will also contribute to the sharing and dissemination of knowledge and methodological advances, through webinars, forums, workshops, conferences, and training schools, targeting industry stakeholders, policymakers, and regulatory agencies (WG5), as well as scientists, pesticide users, healthcare professionals, and the public (WG6).

Results - As analyses by WG1 and WG2 are currently underway, results will be presented according to the level of progress achieved by the time of the congress.

Conclusions - This action will contribute to 1) identifying pesticides and KE/KERs linked to OxS for pesticide adverse effects relevant to ecotoxicology and toxicology; 2) deciphering mechanistic toxicology of pesticides; 3) improving toxicity prediction (in particular for long-term and cocktail effects and multistress exposure); and 4) providing inputs to the pesticide regulatory process.

Funding - This work is based upon work from COST Action CAPSTONE CA24108, supported by COST (European Cooperation in Science and Technology).

938 – Identifying Distinct Profiles of Ontario Pet Caregivers and their Dogs to Examine Uptake of Eight Different Tick Prevention Measures: A Hierarchical Cluster Analysis

Ivana BLAGOJEVIC, Sarah MAKEPEACE, Katie M. CLOW, Jason B. COE, Lauren E. GRANT, Kelsey L. SPENCE
University of Guelph, Ontario Veterinary College, Department of Population Medicine, Canada

Background: Tick-borne diseases are a significant threat to human and animal health. While tick-borne disease prevention measures exist, it is unclear what drives caregivers to implement specific measures for their dogs. The objectives of this study were to identify distinct caregiver and dog clusters based on their demographic characteristics and tick experiences and examine whether these clusters differ in their uptake of tick prevention measures.

Methods: A cross-sectional questionnaire was conducted from November 2023 to March 2024 to collect Ontario dog caregiver demographics, pet characteristics, attitudes, and experiences with tick prevention. Hierarchal cluster analysis (HCA) was conducted using demographic, attitude. and experience variables to generate caregiver (n=412, 29 variables) and dog (n=489, 12 variables) clusters. Agglomerative HCA was conducted using Ward's linkage and Gower dissimilarity measure for mixed variables. Dendrograms were

generated to identify ideal number of clusters. Differences between cluster membership and uptake of eight tick prevention measures were investigated using a Pearson Chi-square test.

Results: Four caregiver and three dog clusters were identified as optimal. Caregivers in Cluster 1 (previous experiences and polarizing risk perception of ticks) were more likely to conduct tick checks (p 0.001) compared to Cluster 4 (large cities, no experiences with ticks, and high risk perceptions). Cluster 1 was less likely to implement pet store (p = 0.005), herbal (p = 0.007), repellent collars (p = 0.017) or avoid tick habitats (p = 0.039) compared to Cluster 3 (rural area, no travel, and neutral risk perception of ticks). Cluster 1 more often sought out tick information from veterinarians compared to Cluster 3, and Cluster 2 referred to government, doctors and news sources. Dogs in cluster 3 (adult, intact, working breed with tick bite history) were more likely to have a tick check conducted by their caregiver (p 0.001) compared to Cluster 2 (young, spayed mixed/toy breed with no tick bite history), and more likely to receive herbal (p = 0.007) or repellent collars (p = 0.036) as tick prevention. Dogs in Cluster 2 were more likely to have avoidance of tick habitats implemented (p = 0.022) as a prevention measure.

Conclusions: Caregivers' choice of tick prevention measures differed according to their demographics, tick experience, and dog lifestyle. Caregivers of dogs with previous tick bite history and polarizing risk perception of ticks tended to implement recommended tick prevention measures (i.e., tick checks) compared to other caregivers. Both caregivers and dogs in rural clusters were more likely to report using alternative products for tick prevention. Veterinarians, government, doctors, and news sources were identified as influential in caregivers' selection of tick prevention, suggesting the need for a One Health approach to generate tailored recommendations for both caregivers and their dogs.

942 – Human leptospirosis dynamics under climate change and the COVID-19 pandemic in Southern Brazil: A One Health perspective

Bruna SILVA, Cintia JUPPA, Ana SIEGLOCH

Universidade do Planalto Catarinense, Postgraduate Program in Environment and Health, Brazil

Background: Leptospirosis remains a climate-sensitive zoonosis and a persistent public health challenge in regions vulnerable to hydrological disasters. In the Alto Vale do Itajaí (Southern Brazil), recurrent floods create a complex interface for pathogen transmission. This study analyzed the temporal dynamics of human leptospirosis between 2019 and 2024 to evaluate the influence of climate variables, extreme flood events, and the epidemiological shift caused by the COVID-19 pandemic.

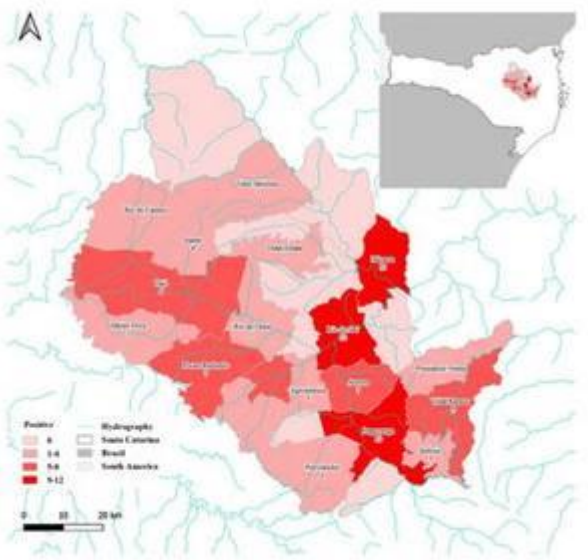
Methods: This retrospective observational study utilized data from the Notifiable Diseases Information System (SINAN), and regional hydrometeorological indicators across 28 municipalities (2019 – 2024). Statistical analysis included Pearson correlation for climate variables. The study compared pre-pandemic, pandemic (03/2020–05/2023), and post-pandemic (06/2023–12/2024) periods using Kruskal-Wallis and Dwass-Steel-Critchlow-Fligner tests (p≤0.05).

Results: The analysis confirmed 84 human cases, predominantly involving males (91.7%) of working age, with a high hospitalization rate (63.1%). Primary risk factors included rodent presence (54.8%) and contact with contaminated mud or floodwater (39.2%). A 414% increase in cases occurred in 2023 compared to 2022, coinciding with seven major flood events and extreme rainfall (e.g., 419 mm in October). Significant correlations were observed between case numbers and temperatures (mean, minimum, and maximum), rainfall volume, and the frequency of rainy days (p0.05). A temporal lag of approximately 60 days occurred between peak floods and peak confirmed cases. Furthermore, a significant shift in incidence between the pandemic and post-pandemic periods (p=0.04) highlights reduced surveillance sensitivity and underreporting during the COVID-19 health crisis.

Conclusions: Leptospirosis dynamics in this region link directly to hydrometeorological extremes and soil saturation. The post-pandemic surge reflects both environmental triggers and the recovery of surveillance sensitivity. From a One Health perspective, integrated monitoring of fluviometric and epidemiological data is essential to anticipate risks in climate-vulnerable territories. Improved urban resilience and preventive environmental management remain critical to reduce shared risk at the human-animal-environment interface in the context of global climate change.

Acknowledgments

The authors gratefully acknowledge the research financial support provided by Fundação de Amparo à Pesquisa e Inovação do Estado de Santa Catarina (FAPESC) under grant numbers TO2024TR002584 (Universal 21/2024). Cintia Cavilha Juppa acknowledges financial support from the Programa Institucional de Bolsas de Pós-Graduação – PIBPG (CNPq Nº 69/2022).



946 – Longitudinal Study of Brucellosis in Goats in Zambia: A One Health Perspective

Bertha CHITAMBO (1), Musso MUNYEME (1,2), Dinah SELIGSOHN (1,3), Erika CHENAIS (3,4), Jonas Johansson WENSMAN (3,4)

1: University of Zambia, Lusaka, Zambia; 2: Palabana University, Chongwe, Zambia; 3: Swedish Veterinary Agency, Uppsala, Sweden; 4: Swedish University of Agricultural Sciences, Uppsala, Sweden

Background: Brucellosis remains one of the most important neglected zoonotic diseases impacting global livestock productivity and human health. In Zambia, small ruminant production is important to rural livelihoods and food security. However, knowledge about the epidemiology of brucellosis in goat production systems remains limited. Understanding infection dynamics is essential for developing integrated surveillance and control strategies through a One Health approach.

Methods: A longitudinal serological study was conducted from October 2023 to July 2025 across 28 smallholder goat herds in the Central and Southern Provinces of Zambia. A total of 904 goats (aged ≥ 1 year) were sampled across four visits. Although the same herds were targeted in this study, the number of herds and individual goats fluctuated across visits due to natural turnover, creating a dynamic longitudinal cohort. Herds were defined as goats owned and managed within a single household and were classified as positive if at least one animal tested seropositive. Herds served as the epidemiological unit because individual animals could not be consistently followed across visits due to routine herd turnover and the lack of permanent animal identification. Serum samples were analysed using the ID Screen® Brucellosis Serum Indirect Multi-species ELISA (IDvet, France). Seroprevalence was calculated both at the animal and herd levels at each sampling visit. To account for the clustering of animals within herds, statistical significance was determined using clustered logistic regression in Stata® 15.0.

Results: Animal-level seroprevalence rose from 3.6% at baseline to 10.5% by the third visit before slightly dropping to 8.2% at the fourth visit. However, clustered logistic regression, accounting for herd-level clustering, showed no overall association between study visit and seropositivity (Wald x2 = 4.49, p = 0.213), although animals sampled at visit 3 had higher odds of infection compared with baseline (0R = 3.16, 95% CI: 1.06-9.48). At the herd level, the proportion of seropositive households increased from 21.4% at baseline to 52.6% at the final visit (p = 0.034). Although descriptive analysis showed minor numerical differences in animal-level seroprevalence across seasons, peaking during the hot dry season (7.4%) compared to the cold dry (6.4%) and warm wet (5.9%) periods, these differences were not statistically significant in clustered logistic regression analysis (p = 0.927).

Conclusions: The increase in herd-level prevalence and the observed rise in animal-level exposure during the study period highlights the potential for continued transmission of brucellosis within smallholder goat production systems in Zambia. Given the zoonotic nature of *Brucella* spp., it is essential to address occupational exposure risks for livestock keepers, veterinarians, and abattoir workers using a One Health approach. This can be achieved by linking veterinary services, public health authorities, and community awareness programmes for brucellosis surveillance and control, thereby reducing zoonotic transmission risks.

951 – Building Undergraduate Pathways in One Health: Interdisciplinary curriculum and experiential learning at North Carolina State University

Kristen SULLIVAN, Meredith SPENCE BEAULIEU, Michael REISKIND, Siddhartha THAKUR
North Carolina State University, United States of America

Background: Despite recognition of One Health as an essential framework for addressing complex global health challenges, structured undergraduate training pathways remain uncommon. At NC State University, an interdisciplinary approach to One Health education was developed through the Global One Health Academy (GOHA). The initiative includes a cross-college undergraduate minor that provides the curricular foundation and a complementary Global One Health Scholars program that supports experiential learning and professional development. Together, these programs prepare students to think across disciplinary boundaries and engage with health challenges linking human, animal, plant, and environmental health.

Methods: The Global One Health (GOH) minor, launched in Summer 2024, is a 15-credit program intentionally housed within the Office of University Interdisciplinary Programs to support collaboration across colleges. The minor includes two required courses, GOH 201 (Foundations of Global One Health) and GOH 302 (Global One Health Applications), plus one elective from each of three thematic areas: Integrated Human & Animal Health, Sustainable Food Systems & Plant Health, and Ecosystem Health & Climate Science. Electives are drawn from more than 65 courses across five colleges, representing biological, environmental, and social dimensions of health. GOH 201 introduces major OH issues, including infectious disease emergence, antimicrobial resistance, and climate change impacts, while developing systems-thinking skills through interdisciplinary instruction and applied learning activities. GOH 302 builds on this foundation through collaborative case studies and interdisciplinary analysis of complex health challenges. A summer offering of GOH 302 at the NC State European Center in Prague includes site visits and engagement with institutions across One Health sectors. The course is a core component of the Global One Health Scholars experience but remains open to other students. The Scholars program further supports undergraduate development through community-engaged projects, interdisciplinary team training, and workshops.

Results: Since its launch, more than 100 students from over 50 majors across eight colleges have declared the GOH minor, reflecting strong interest in interdisciplinary approaches to health. Students pursue the minor alongside majors including biological sciences, animal science, environmental sciences, engineering, and social sciences. Scholars have also engaged in applied projects with community partners, including the development of La Crosse encephalitis and Lyme disease prevention education resources in collaboration with the North Carolina Department of Health and Human Services and local health departments.

Conclusion: This integrated curricular and experiential model demonstrates how universities can build undergraduate pathways in One Health by combining interdisciplinary coursework with applied learning opportunities. Cross-college collaboration, a centralized administrative structure, and faculty leadership through GOHA have supported early implementation. This model offers a transferable framework for institutions seeking to introduce One Health concepts earlier in academic training and prepare students for interdisciplinary careers addressing complex health challenges.

967 – A regional approach to addressing AMR gaps in Animal Health Systems: improving essential veterinary medicine access in East and Southern Africa

James KITHUKA (2), Izzy HOCKING (1), Samantha OPERE (2), Laura SKIPPEN (1), Eleanor PARRAVANI (1), Shereene WILLIAMS (1), **Tewodro TESFAYE** (2)

1: Brooke Action for Working Horses and Donkeys, United Kingdom; 2: Brooke Action for Working Horses and Donkeys, East Africa

Background

Antimicrobial resistance (AMR) threatens animal health, food security, and public health globally, with complex drivers in low- and middle-income countries. In East and Southern Africa, weak regulation, uneven access to essential veterinary medicines, and limited clinical guidance for animal health practitioners (AHPs) contribute to inappropriate antimicrobial use in livestock systems.

Across five countries Kenya, Malawi, Tanzania, Uganda, and Zambia scoping visits and focus group discussions under the Fleming Fund AMR and One Health (AMROH) Regional Grant identified gaps in medicine access and prescribing practices. Limited availability of essential vaccines and non-antimicrobial treatments, alongside antimicrobial access through informal supply chains, encourages unnecessary use. The project strengthened stewardship through Essential Veterinary Medicine Lists (EVML) development, treatment guidelines, and AHP and agrovet training. It also supports countries to meet commitments in the UN Declaration on AMR and the draft Global Action Plan on AMR.

Brooke, in collaboration with World Veterinary Association, created the first global EVML, prioritizing evidence-based first- and second-line treatments, aligning medicine selection with disease burdens, and limiting use of critically important antimicrobials where alternatives exist.

Methods

Activities were implemented with the International Livestock Research Institute (ILRI) and national veterinary authorities integrating evidence generation, policy development, and practitioner capacity building. Scoping visits and focus group discussions with AHPs, veterinary prescribers, and agrovet providers identified barriers to responsible antimicrobial use and gaps in veterinary services. Findings informed collaboration with national veterinary departments to develop EVMLs and standard treatment guidelines for priority livestock species. Capacity-building workshops strengthened diagnosis, rational prescribing, record keeping, and medicines stewardship, supported by Kenya Veterinary Board accredited online training modules on veterinary pharmacy management. Colleagues from Ethiopia also shared experiences on creating their first EVML.

Results

Countries prioritised interventions most relevant to their antimicrobial stewardship needs while strengthening veterinary governance. Kenya, Malawi, and Zambia developed their first national Essential Veterinary Medicines Lists, while Tanzania and Uganda updated existing EVMLs to align medicine selection with disease priorities and responsible antimicrobial use.

Standard veterinary treatment guidelines were developed in Malawi, Uganda, and Zambia, providing clearer prescribing guidance for frontline practitioners and strengthening clinical decision-making at last-mile veterinary service delivery.

More than 60 frontline AHPs and agrovet practitioners received training on prudent antimicrobial use, diagnostic decision-making, medicine storage, and record keeping. Digital learning modules on veterinary pharmacy management attracted over 100 participants, including practitioners beyond target countries, highlighting strong demand for accessible antimicrobial stewardship training across the region.

Conclusion

Strengthening antimicrobial stewardship in animal health systems requires addressing access to appropriate veterinary medicines and prescribing practices among frontline practitioners. This regional initiative shows that combining EVMLs, treatment guidelines, practitioner training, and digital learning strengthens stewardship and supports national AMR action plans.

---

972 – “I can say with conviction that bushmeat is healthy”: How wildmeat vendors construct perceptions of health risks in the context of the ‘Bushmeat Problem’

Annalyse MOSKELAND

The London School of Economics and Political Science, United Kingdom

Growing international concern about zoonotic pandemics, particularly following high profile outbreaks like SARS (2002), Ebola (2014-2016), and more recently COVID-19, has resulted in heavy scrutiny on the practice of wildmeat consumption, particularly in cities in LMICs where demand is largely driven by taste preferences, perceived health benefits, and cultural practice rather than necessity. The persistence of this commercial trade is often assumed to be rooted in ignorance of or indifference to zoonotic risk. This paper interrogates that assumption by examining how wildmeat health beliefs are formed using qualitative interviews with urban wildmeat vendors in Kumasi, Ghana. These interviews were then thematically analyzed using three complementary frameworks for understanding risk perception construction: hazard characteristics, mental heuristics, and perceiver characteristics. Consistent with prior literature, this study found that wildmeat was almost unanimously perceived as healthy amongst vendors. This was largely informed by a natural-is-better heuristic, under which wild animals were perceived as a low-fat, organic source of protein due to their natural diets and free roaming lifestyle. Conversely, domestic animals were frequently cited as unhealthy alternatives, containing non-natural additives while being high in fat due to their poor diet and sedentary lifestyles. This mindset, along with limited direct experience with zoonoses and low trust in information sources, led most vendors to reject the threat from zoonoses but express high concern about their personal susceptibility to non-communicable diseases. This paper then uses the same three frameworks to discuss the media narratives and policy responses to the EVD epidemic and the COVID-19 pandemic. It concludes by arguing that the persistent attribution of rising zoonotic threat to the wildmeat trade is colored by subjective, culturally constructed understandings of 'meat', resulting in the stigmatization of those engaged in the trade and the misdirection of policy attention away from more significant structural drivers of zoonotic pathogen emergence.

981 – Global spatial patterns and drivers of antimicrobial resistance in livestock

Rodiat Olabisi OMOTOSO (1), **Ismail Ayoade ODETOKUN** (2), Aminu SHITTU (3), Mahmoud ELTHOTH (4), Adebowale Olusola ADEJUMO (1)

1: Department of Statistics, Faculty of Physical Sciences, University of Ilorin, Nigeria; 2: Department of Veterinary Public Health and Preventive Medicine, Faculty of Veterinary Medicine, University of Ilorin, Nigeria; 3: Quantitative Epidemiology and Animal Health (QuantEpi-AH) Group, Department of Theriogenology and Animal Production, Faculty of Veterinary Medicine, Usmanu Danfodiyo University, Sokoto, Nigeria; 4: Department of Health Studies, Royal Holloway University of London, Egham TW20 0EX, UK, Hygiene and Preventive Medicine Department, Faculty of Veterinary Medicine, Kafrelsheikh University, Kafr el-sheikh, Egypt

Background: Antimicrobial resistance (AMR) in livestock is a growing global health concern with important implications for animal health, food security, and human health. However, the spatial distribution and determinants of AMR in livestock systems remain insufficiently characterized.

Methods: This study examined global spatial patterns and drivers of AMR in livestock using data from the ResistanceBank database, encompassing multiple countries, livestock species, bacterial pathogens, and antimicrobial classes categorized according to World Health Organization (WHO) medical importance classifications. Spatial dependence was evaluated using Global and Local Moran's I statistics, while the influence of livestock species, pathogens, and antimicrobial classes was analyzed using beta regression and Extreme Gradient Boosting (XGBoost) machine learning models.

Results: Global Moran's I revealed significant positive spatial autocorrelation in AMR proportions (I = 0.1911, p = 0.0246; expected I = −0.0127), indicating geographic clustering of resistance. Hotspots were identified across South and East Asia, the Middle East, parts of Sub-Saharan Africa, and South America, whereas coldspots occurred in Southern Africa, Southeast Asia, and several European regions. Beta regression showed that cattle (β = −0.5953, p = 0.0263) and sheep (β = −0.7873, p = 0.0034) contributed less to AMR variation than buffalo, while highly important antimicrobials were associated with increased resistance proportions (β = 0.3365, p 0.0001). The XGBoost model demonstrated slightly improved predictive performance (RMSE = 0.3428) relative to beta regression (RMSE = 0.3471).

Conclusions: These findings reveal pronounced spatial clustering of AMR in livestock and underscore the need for strengthened global surveillance, improved antimicrobial stewardship, and integrated One Health strategies to mitigate the spread of AMR.

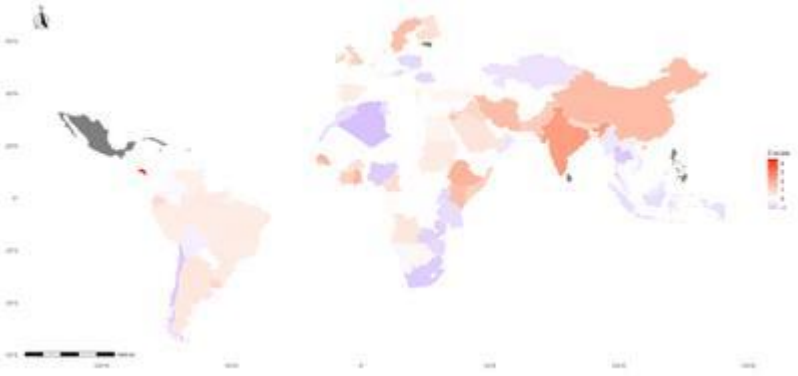


Table 1: Model Output

Variables		Beta Estimate	XGBoost (Gains)	P-value
Intercept		0.0178		0.9474
Species	Cattle	**-0.5953**	0.099	0.0263
	Chicken	-0.2401	0.137	0.3703
	Duck	-0.0429	0.019	0.8793
	Horse	-0.3180	0.005	0.3892
	Pig	-0.2422	0.070	0.3664
	Sheep	**-0.7873**	0.070	0.0034
	Buffalo	R	0.009	-
Pathogens	*E. coli*	**-0.1729**	0.054	<0.0001
	S. aureus	**-0.2416**	0.034	<0.0001
	Salmonella	**-0.5446**	0.151	<0.0001
	Campylobacter	R	0.061	-
WHO_MedImp	Highly important	**0.3365**	0.173	<0.0001
	Important	0.0899	0.016	0.0834
	Critically Important	R	0.090	-
MSE		0.1205	**0.1175**	
RMSE		0.3471	**0.3428**	
MAE		0.3057	**0.2927**	

983 – Emerging Human Streptococcus suis in the Philippines: Implications for One Health Preparedness

Apple Charm AGULTO, Razelle Ann ANG-MARCIANO, Vikki Carr DE LOS REYES, Mariz Zheila BLANCO-PAYUYO
Not Applicable, Philippines

Background

Effective zoonotic disease preparedness requires robust surveillance integration at the human–animal interface, particularly in regions where small-scale livestock production predominates. Streptococcus suis is a significant zoonotic pathogen capable of causing severe neurological disease and permanent disability, yet it remains under-monitored within many national health frameworks. Following the identification of a cluster of human infections in an agricultural province in Northern Luzon, Philippines, a One Health investigation was initiated. This study aimed to characterize the largest human S. suis case series documented in the country and to evaluate the systemic vulnerabilities that allow such emerging zoonotic threats to remain undetected.

Methods

A multi-sectoral One Health investigation was conducted following the identification of the initial cases. Hospital microbiology records (2020-2023) were reviewed to identify additional culture-confirmed human S. suis infections. Clinical charts, household visits, and semi-structured interviews with cases or proxies documented demographics, occupations, and clinical presentations. Environmental scanning assessed the presence of pig farms near case residences. Interviews with farm owners and cases employed in swine facilities and slaughterhouses evaluated biosecurity practices in their workplaces. Key informant interviews with agriculture and veterinary personnel reviewed S. suis awareness, livestock registration systems, surveillance practices, and cross-sector reporting mechanisms. Data were analyzed using descriptive statistics and spatiotemporal mapping.

Results

Nine culture-confirmed human cases were identified. Clinical severity was high: 88% presented with acute central nervous system infections upon illness onset. Two patients died (CFR=22%), while all the survivors developed permanent hearing impairment. Notably, a peak in cases in 2023 coincided with local African Swine Fever (ASF) outbreaks. Identified vulnerabilities among cases included meat handling (67%) and residential proximity to small-scale pig farms (67%). Interviews with farm owners and cases employed in swine facilities and slaughterhouses revealed inconsistent or absent implementation of biosecurity practices. A critical knowledge gap was identified in the animal sector: all interviewed agriculture and veterinary personnel were unaware of S. suis as a zoonotic threat. System review revealed outdated livestock registries, fragmented reporting between animal and human health sectors, and the absence of S. suis monitoring in swine populations.

Conclusion

This investigation represents the most comprehensive One Health assessment of human S. suis infections and related animal health system vulnerabilities in the Philippines. Recognition of the pathogen occurred only after a series of severe human cases were detected, indicating that humans are serving as “accidental sentinels” for undetected animal circulation. The findings highlight a significant blind spot in national biosecurity caused by limited surveillance integration and weak oversight of small-scale livestock production. Strengthening One Health preparedness requires transitioning from reactive human-centered detection to integrated zoonotic surveillance. Priority actions include incorporating neglected zoonoses into routine livestock monitoring and establishing formal cross-sector data-sharing mechanisms to improve early detection at the human–animal interface.

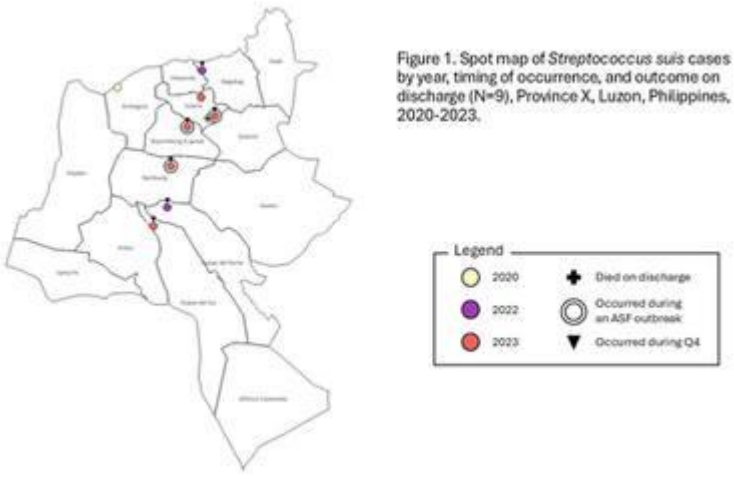


Figure 1. Spot map of *Streptococcus suis* cases by year, timing of occurrence, and outcome on discharge (N=9), Province X, Luzon, Philippines, 2020-2023.

Table 1. Epidemiologic and clinical characteristics of Streptococcus suis cases (N=9), Province X, Luzon, Philippines, 2020-2023.

995 – Unravelling Blastocystis through a One Health lens: epidemiological, genomic, and multi-omics insights from the COST Action CA21105 “Blastocystis Under One Health Action” (BUOHA)

Ana FIGUEIRO (4), Eylem AKDUR-ÖZTÜRK (7), Isabel GUADANO-PROCESI (8), C. Rune STENSVOLD (3), **Eleni GENTEKAKI** (2), Funda DOGRUMAN-AL (5), David CARMENA (6), Anastasios TSAOUSIS (1)

1: University of Kent, United Kingdom; 2: University of Nicosia, Cyprus; 3: Statens Serum Insitut, Denmark; 4: University of Aveiro, Portugal; 5: Gazi University, Turkiye; 6: Spanish National Centre for Microbiology, Spain; 7: Cukurova University, Turkiye; 8: Università di Roma Tor Vergata, Italy

Background*Blastocystis* is one of the most prevalent gut protists worldwide, colonising over one billion people, yet its clinical significance, transmission dynamics, and ecological role remain poorly understood. The fragmented nature of research across medical, veterinary, and environmental disciplines has hindered a comprehensive understanding of this enigmatic organism. COST Action CA21105 “*Blastocystis* Under One Health Action” (BUOHA) was established in 2022 to bridge these gaps by fostering transdisciplinary collaboration across 40+ countries and integrating approaches from human, animal, and environmental health.

MethodsThe Action is structured into five synergistic working groups targeting: (1) epidemiology and diagnostics harmonisation, including a pan-European survey of Blastocystis awareness and diagnostic practices; (2) subtype and microbiome databanking through the creation of standardised databases; (3) multi-omics integration encompassing genomics, proteomics, and metabolomics to elucidate host–Blastocystis–microbiome interactions; (4) in vivo and in vitro experimental models; and (5) data dissemination and public engagement. A systematic literature review was conducted to map Blastocystis prevalence and genetic diversity across Europe, while field studies employing a One Health framework collected samples from human, animal, and environmental reservoirs.

ResultsThe network has produced harmonised molecular protocols for Blastocystis subtyping, established a comprehensive epidemiological and omics database, and generated new genomic, proteomic, and metabolomic datasets (including BlastoDB) that advance our understanding of *Blastocystis* biology and its interactions within the gut ecosystem. Pan-European surveys have revealed significant heterogeneity in diagnostic approaches and awareness among clinicians and veterinarians. Epidemiological mapping has identified key transmission routes, including water and soil as primary environmental reservoirs. Multi-omics analyses have provided novel insights into the molecular underpinnings of host–*Blastocystis*–microbiome crosstalk, challenging simplistic pathogen–commensal dichotomies.

ConclusionsBUOHA demonstrates the power of a One Health approach in addressing complex questions surrounding *Blastocystis*. By integrating epidemiological, genomic, and multi-omics data across disciplines and borders, this initiative has advanced diagnostic harmonisation, identified critical transmission pathways, and deepened our understanding of *Blastocystis’s* role in health and disease. These collaborative efforts lay the groundwork for evidence-based public health policies and future targeted research.

1001 – Whole genome sequencing of non-typhoidal Salmonella isolated from human–dairy interface: A One Health Approach to Identify Antimicrobial Resistance Markers

Achenef MELAKU BEYENE (1), Mucheye GIZACHEW (1), Yismaw ALEMIE (2), Ahmed E. Yousef E. YOUSEF (3), Kornschober CHRISTIAN (4), Baye GELAW (1)

1: Department of Medical Microbiology, College of Medicine and Health Sciences, University of Gondar, Gondar, Ethiopia; 2: Department of Animal Science, Faculty of Agriculture and Medicine, Debre-Markos University, Bure, Ethiopia; 3: Department of Food Science and Technology, College of Food, Agriculture and Environmental Sciences, The Ohio State University, Columbus, Ohio, USA; 4: AGES: Agency for Health and Food Safety, National Salmonella Reference Laboratory, Institute for Medical Microbiology and Hygiene, Graz, Austria

Introduction: Non-typhoidal *Salmonella* (NTS) is a major foodborne pathogen that poses a significant threat to both human and animal health worldwide. Whole genome sequencing (WGS) is a powerful tool for the comprehensive characterization of pathogens and for the identification of antimicrobial resistance markers. Therefore, this study aimed to sequence NTS isolates and identify their antimicrobial resistance markers. The isolates were obtained from raw milk, milk container swabs, milker's hand swabs, dairy farm sewage, milker's stool, and cow feces collected from the northwestern region of Ethiopia.

Methods: Whole genome sequencing (WGS) was performed on 28 NTS isolates using a next-generation sequencing platform. Virulence-associated genes were identified using the Galaxy bioinformatics platform. Antimicrobial resistance genes were detected using the Comprehensive Antibiotic Resistance Database (CARD) and the Antibiotic Resistance Gene-Annotation (ARG-ANNOT) database.

Results: Based on these analyses, the NTS genomes had an average size of approximately 4.8 million base pairs, a GC content of 52%, and an average of 4.9 thousand protein-coding genes. Phylogenetic analysis revealed clustering of isolates according to serovar, irrespective of their origin. In total, 118 virulence genes and 46 antimicrobial resistance genes were identified.

Conclusion: The presence of virulence-and resistance-associated genes highlights the substantial public health risk posed by these isolates possible to identify antimicrobial resistance markers that can be standardized and upgraded to effective control and prevention measures to protect public health.

1004 – Mainstreaming environment and ecosystem health in the One Health approach

Alexandre CARON (1), **Salome BUKACHI** (2), Simon ANGOMBE (3), Fraser BITU (4), Rémi CARDINAEL (5), Lucinda DE ARAUJO (6), Hélène DE NYS (7), Carole GOULET (8), Yussuf HARED (9), Mirgissa KABA (10), Clovice KANKYA (11), Margaret KAREMBU (12), Theodore KNIGHT-JONES (13), Ben LUKUYU (14), Adana MAHASE-GIBSON (15), Gift MATOPE (16), Siobhan MOR (17), Chiku MTHEGA (18), Prisca MUGABE (19), Musso MUNYEME (20), Eric NARTEY (21), Joshua ONONO (22), Sean PATRICK (23), Flora PULE-MEULENBERG (24), Thato SENGWAKETSE (25), Gabriel SHIRIMA (26), Anselme SHYAKA (27), Jacques VAN ROOYEN (28), Lillian WAMBUA (29), Buke WAKO (30), Abdhalah ZIRABA (31), Nlingisisi BABAYANI (32)

1: CIRAD, UMR ASTRE - ILRI, ILRI, Nairobi, Kenya; 2: Institute of Anthropology, Gender and African Studies, University of Nairobi, Kenyabi; 3: School of Agriculture and Fisheries Sciences, University of Namibia; 4: Nelson Mandela University, South Africa; 5: AIDA, University of Montpellier, CIRAD, Montpellier, France; 6: Biotechnology Center of Eduardo Mondlane University, Maputo, Mozambique; 7: CIRAD, UMR ASTRE, Harare, Zimbabwe; 8: Colibri Consulting, Mozambique; 9: Center for Community Services, Amoud University, Borama, Somalia; 10: School of Public Health, Addis Ababa University, Addis Ababa, Ethiopia; 11: Dept of Biosecurity, Ecosystems and Veterinary Public Health, Makerere University, Makerere, Uganda; 12: International Service for the Acquisition of Agri-biotech Applications, ISAAA, Nairobi, Kenya; 13: International Livestock Research Institute, ILRI, Addis Ababa, Ethiopia; 14: International Livestock Research Institute, ILRI, Kampala, Uganda; 15: Independent Consultant, Trinidad and Tobago; 16: Department of Veterinary Pathobiology, University of Zimbabwe; 17: Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, United Kingdom; 18: Lilongwe University of Agriculture

and Natural Resources, Malawi; 19: Department of Livestock Science, University of Zimbabwe, Zimbabwe; 20: Department of Disease Control, University of Zambia, Lusaka, Zambia; 21: International Water Management Institute, Ghana; 22: Department of Public Health Pharmacology and Toxicology, University of Nairobi, Nairobi, Kenya; 23: Environmental Chemical Pollution and Health Research Unit, School of Health Systems and Public Health, University of Pretoria, South Africa; 24: Ministry of Health, Botswana; 25: Department of Crop and Soil Sciences, Botswana University of Agriculture and Natural Resources, Gaborone, Botswana; 26: Public Health-Reemerging and Emerging infectious zoonoses, Nelson Mandela African Institution of Science and Technology, Arusha, Tanzania; 27: Center for One Health, University of Global Health Equity, Kigali, Rwanda; 28: REHerd Africa Ltd, South Africa; 29: World Organisation for Animal Health, Sub-Regional Representation for Eastern Africa, Kenya; 30: International Livestock Research Institute, ILRI, Nairobi, Kenya; 31: African Population and Health Research Center, Kenya; 32: Okavango Research Institute, University of Botswana

Background: Environment and ecosystem health (EEH) has remained largely overlooked in the institutionalisation and operationalisation of the One Health (OH) approach. This omission is primarily due to EEH's delayed integration into the OH approach. Addressing this gap is critical given the interconnectedness of ongoing environmental crises with human and animal health, as well as the profound impacts of anthropogenic activities on EEH.

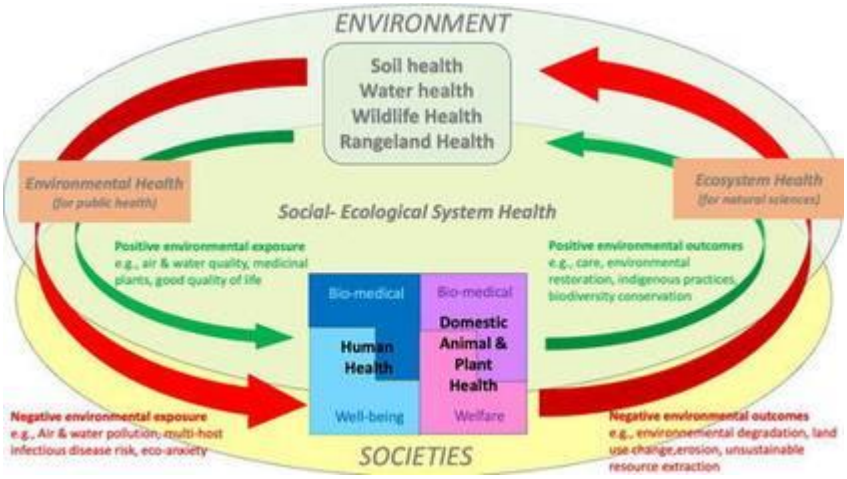
Methods: This article draws on deliberations from a conference held in Zimbabwe in February 2024, which convened over 100 academic, governmental and civil society stakeholders from 14 African countries to critically examine how EEH could be better mainstreamed in the OH approach. We identify the core elements of the EEH dimension, assess key barriers to its integration into OH, and propose practical pathways for strengthening inclusion of EEH in national OH processes in line with the JPA.

Results:

To enable more effective integration, OH stakeholders must develop a comprehensive understanding of the multifaceted nature of EEH, recognise the broad spectrum of actors involved, and address semantic discrepancies that might hinder effective collaboration and mutual understanding.

This framing of OH through the EEH perspective gives rise to four overarching observations. First, the scope, range of contributing disciplines and stakeholders encompassed by EEH is substantially broader than those traditionally engaged by OH platforms, which typically focus on human and animal health. This narrow engagement constrains the diversity of perspectives informing OH strategies and reinforces a predominantly biomedical orientation. Second, significant barriers to interdisciplinarity and intersectoral collaboration persist, including semantic ambiguities, divergent expectations regarding outcomes, mismatched temporal scales, and entrenched professional culture across disciplines. Third, effective OH operationalisation should be problem-oriented and place-based (contextual), unfolding through bottom-up frameworks that are co-produced with local stakeholders and intended beneficiaries. Fourth, the explicit integration of EEH within the revised OH definition signals a broader paradigm shift, moving OH beyond a primary focus on disease.

Conclusion: This paradigm shift positions OH as a platform capable of addressing interconnected global challenges, including climate change, biodiversity loss and environmental degradation. By situating health within SES, OH has a potential to contribute to transformative change rather than incremental risk management.



1012 – Multihazard Public Health Risk Profiling for Strategic Health Security Planning with One Health Approach in Azad Jammu & Kashmir, 2025

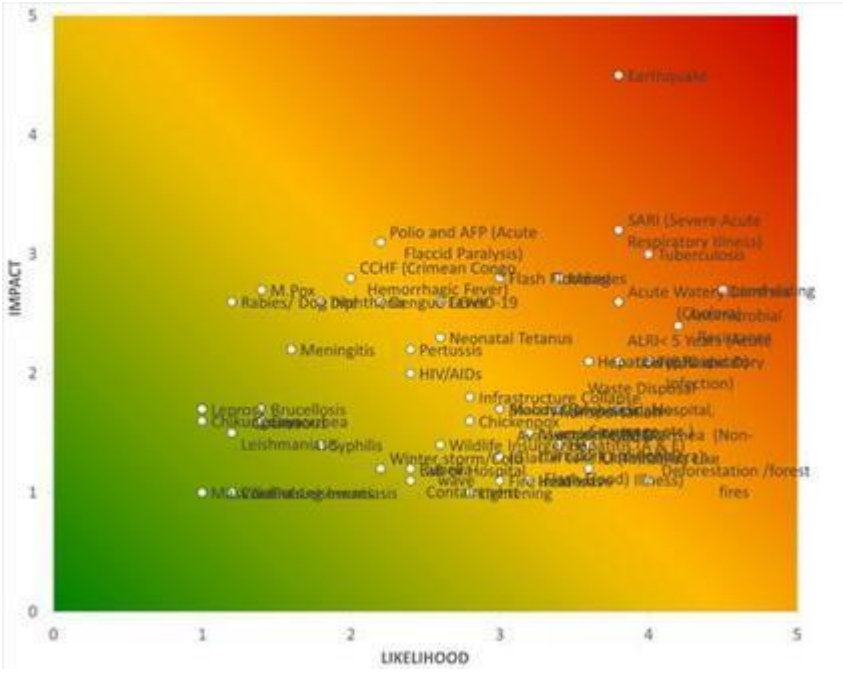
Majid Ali TAHIR, Muazzam Abbas RANJHA, Mumtaz Ali KHAN, Sidra WALI, Hafiz Suboor Ul HASSAN
National Institute of Health (NIH) Islamabad Pakistan, Pakistan

Background: Azad Jammu & Kashmir (AJK) lacked systematic multihazard public health risk assessments despite IHR (2005) recommendations. This study aimed to identify and prioritize health threats using a One Health approach. By generating evidence on natural, biological, and man-made hazards, it sought to guide strategic health security planning in a resource-limited and disaster-prone region.

Methods: A four-day multidisciplinary workshop was conducted in Muzaffarabad, engaging 51 experts nominated by 16 ministries, development partners, and One Health stakeholders across human, animal, and environmental health sectors. The US CDC/FEMA developed THIRA tool, customized with five likelihood and ten impact variables, was used to assess 51 hazards. Likelihood and impact indicators were scored 1–5 based on historical data, surveillance, vulnerability, and expert consensus. Total risk scores were calculated by summing likelihood and impact values. Hazards were ranked and a cutoff score ≥6.4 was used to identify high-priority risks. This process integrated participatory discussions, Delphi technique for consensus, and alignment with local context and resource capacity, fostering cross-sectoral collaboration for strategic planning.

Results: Six high-priority hazards were identified in this assessment. Earthquake was the highest-risk threat with a likelihood of 3.8, impact of 4.5, and total risk score of 8.3. Landslides followed with a likelihood of 4.5, impact 2.7, and total score 7.2. Severe Acute Respiratory Illness (SARI) and Tuberculosis each scored 7.0 (likelihood 3.8–4.0; impact 3.0–3.2). Antimicrobial Resistance scored 6.6 (likelihood 4.2; impact 2.4), while Acute Watery Diarrhea/Cholera reached 6.4 (likelihood 3.8; impact 2.6). Moderate-risk hazards included Measles (6.2), Typhoid (6.1), ALRI 5 years (5.9), and Flash Flooding (5.8). Common capability targets identified across these prioritized threats included strengthening Rapid Response Teams (RRTs) in high-risk districts, expanding community based surveillance and laboratory diagnostic capacities, improving emergency medical stockpiles and equipment, enhancing community awareness, WASH interventions, and conducting simulation exercises for surge preparedness.

Conclusions: Risk assessment in AJK provides evidence-based guidance for strategic health security planning, emphasizing prioritized threats and corresponding capability targets. By integrating natural, biological, and man-made hazards, the study strengthens One Health coordination across sectors. The methodology offers a replicable model for transforming fragmented data into actionable public health plans, guiding resource allocation, preparedness, and resilience in similar LMIC settings.



Sr.#	Threats/Hazards of Concern	Likelihood	Impact	Risk Score
	Very High & High			
1.	Earthquake	3.8	4.5	8.3
2.	Land sliding	4.5	2.7	7.2
3.	SARI (Severe Acute Respiratory Illness)	3.8	3.2	7
4.	Tuberculosis	4	3	7
5.	Antimicrobial Resistance	4.2	2.4	6.6
6.	Acute Watery Diarrhea (Cholera)	3.8	2.6	6.4
7.	Measles	3.4	2.8	6.2
8.	Typhoid	4	2.1	6.1
	Moderate			
9.	ALRI< 5 Years	3.8	2.1	5.9
10.	Flash Flooding	3	2.8	5.8
11.	Hepatitis (B, C and D)	3.6	2.1	5.7
12.	Scabies	3.8	1.7	5.5
13.	Polio and AFP (Acute Flaccid Paralysis)	2.2	3.1	5.3
14.	COVID-19	2.6	2.6	5.2
15.	Deforestation /forest fires	4	1.1	5.1
16.	Waste Disposal (Municipal, Hospital, Sewerage etc.)	3.4	1.7	5.1
17.	Acute Diarrhea (Non-cholera)	3.6	1.4	5
18.	Neonatal Tetanus	2.6	2.3	4.9
19.	Dengue Fever	2.2	2.6	4.8
20.	CCHF (Crimean Congo Hemorrhagic Fever)	2	2.8	4.8
21.	Hepatitis (A & E)	3.4	1.4	4.8
22.	ILI (Influenza Like Illness)	3.6	1.2	4.8
23.	Bloody Diarrhea	3	1.7	4.7
24.	Malaria	3	1.7	4.7
25.	Mumps	3.2	1.5	4.7
26.	Transportation accident (Mass transport accidents)	3.2	1.5	4.7
27.	Pertussis	2.4	2.2	4.6
28.	Infrastructure Collapse	2.8	1.8	4.6
29.	Chickenpox	2.8	1.6	4.4
30.	Diphtheria	1.8	2.6	4.4
31.	HIV/AIDs	2.4	2	4.4
32.	Heat wave	3.2	1.1	4.3
33.	Avalanches / Glacial Lake Outburst	3	1.3	4.3
34.	M.Pox	1.4	2.7	4.1
35.	Fire incidents	3	1.1	4.1
	Low			
36.	Wildlife Insurgence	2.6	1.4	4
37.	Meningitis	1.6	2.2	3.8
38.	Rabies/ Dog bite	1.2	2.6	3.8
39.	Lightening	2.8	1	3.8
40.	Rubella	2.4	1.2	3.6
41.	Lab or Hospital Containment	2.4	1.1	3.5
42.	Winter storm/Cold wave	2.2	1.2	3.4
43.	Syphilis	1.8	1.4	3.2
44.	Brucellosis	1.4	1.7	3.1
45.	Gonorrhea	1.4	1.6	3
46.	Cutaneous Leishmaniasis	1.2	1.5	2.7
47.	Leprosy	1	1.7	2.7
48.	Chikungunya	1	1.6	2.6
49.	Visceral Leishmaniasis	1.2	1	2.2
50.	Conflicts	1.2	1	2.2

1017 – Hospital Wastewater as an Environmental Interface for Carbapenem Resistance Dissemination: Integrated Genomic and Metagenomic Evidence

Yaovi Mahuton Gildas HOUNMANOU, Anders DALSGAARD
University of Copenhagen, Denmark

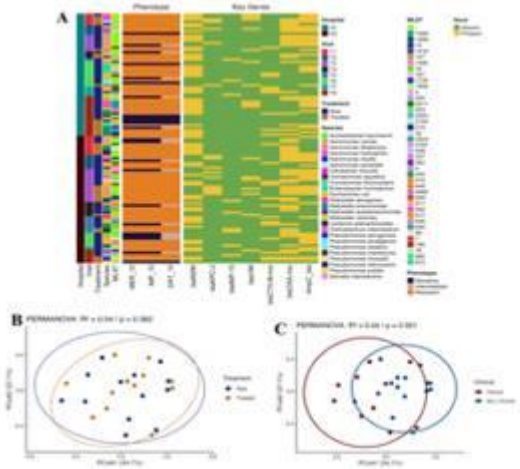
Background: Hospital wastewater systems represent critical interfaces where antimicrobial resistance (AMR) determinants may enter environmental microbial ecosystems. Carbapenem-resistant Enterobacterales (CRE) are of particular concern due to their clinical importance and the mobility of carbapenemase genes. However, the effectiveness of hospital wastewater treatment in removing CRE and preventing dissemination of mobile resistance elements remains insufficiently characterized.

Methods: Within the JPI-AMR I-CRECT project, longitudinal sampling was conducted quarterly across eight time points from raw influent and treated effluent (using chlorination) at two hospitals in Vietnam. Culture-based enumeration using selective chromogenic media was performed to quantify CRE populations. A total of 152 isolates were sequenced using Illumina short reads, with hybrid Nanopore assemblies generated for 32 carbapenemase-carrying isolates to resolve plasmid structures. In parallel, metagenomic analyses combining Nanopore long-read sequencing (21 samples) and Illumina short-read

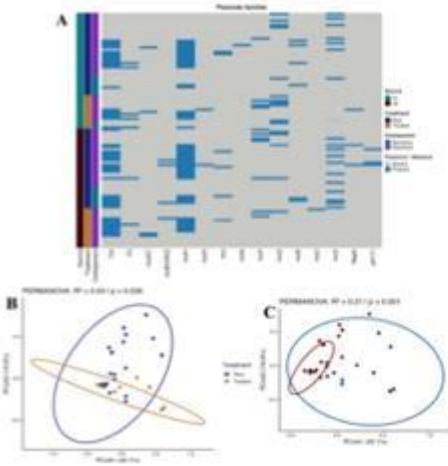
sequencing (52 samples) were conducted to characterize microbial community composition, resistome structure, and mobile genetic elements.

Results: Wastewater treatment resulted in partial but inconsistent reductions in CRE loads, typically ranging from 1–2 log10 CFU/mL. Despite reductions in overall bacterial counts, carbapenem-resistant populations frequently persisted in treated effluent across multiple sampling events. CRE isolates were dominated by *Escherichia coli* and *Klebsiella pneumoniae*. Genomic analyses revealed widespread distribution of carbapenemase genes on conjugative plasmids across diverse bacterial species. Metagenomic profiling showed restructuring of microbial communities following treatment, with increased Shannon diversity consistent with aerobic enrichment. Beta-lactamases dominated the resistome, and clinically relevant carbapenemases, including blaNDM, were associated with mobile plasmids detected across multiple bacterial hosts. Mobile resistance elements were also detected in environmental bacterial taxa, indicating potential horizontal gene transfer beyond clinically relevant species. Multivariate analyses of resistome and plasmid profiles demonstrated distinct clustering between influent and treated effluent communities.

Conclusions: Hospital wastewater treatment reduced bacterial loads but did not eliminate carbapenem-resistant populations or mobile resistance genes. Instead, treatment systems may act as ecological interfaces that enable persistence and exchange of resistance determinants among diverse environmental bacteria. These findings identify hospital wastewater as a potential environmental reservoir and dissemination pathway for clinically relevant AMR, with possible human exposure where treated wastewater is reused for downstream irrigation. Integrated culture-based monitoring combined with rapid nanopore-based genomic surveillance could provide a scalable strategy for early detection and environmental tracking of carbapenem resistance within a One Health framework.



A. Heatmap showing the distribution and relative abundance of antimicrobial resistance genes (ARGs) across hospital wastewater influent and treated effluent samples, grouped by antibiotic class;
B. Principal coordinates analysis (PCoA) of ARG composition illustrating clustering patterns between influent and effluent communities;
C. Distribution of clinically relevant resistance determinants, including carbapenemase genes, across bacterial taxa and sample types



Mobile genetic elements associated with carbapenem resistance.
A. Distribution of plasmids and mobile genetic elements carrying carbapenemase genes detected in wastewater isolates and metagenomic assemblies;
B. Comparison of plasmid-associated resistance determinants across bacterial hosts identified in wastewater samples;
C. Presence of carbapenemase genes, including blaNDM, across bacterial species and environmental compartments, indicating potential horizontal gene transfer

1024 – Reframing antimicrobial stewardship by empowering stakeholders through the One Health lens

Conor MULROONEY, Zachary RAMSAMAROO, Jennifer BRITTON, Hind AWAD, Grace ROTHWELL-KELLY, Maeve DOYLE, Grace CHAN

University Hospital Waterford, Ireland

Background

The WHO Global Action Plan on Antimicrobial Resistance (AMR) objective of improving understanding of AMR through effective communication, education and training is achieved by the novel Annual Regional Antimicrobial Stewardship (AMS) Campaign, designed to promote One Health and behavioural change in AMS. Since 2022, this local initiative has evolved into a regional campaign, being awarded a National Patient Safety Office AMR Award and national educational grant.

Methods

This multi-faceted programme runs in conjunction with World Antimicrobial Awareness Week, comprising an AMS case competition with oral presentations delivered by non-infection clinicians across the 1200-bed Regional Acute Hospitals Network and the community, with focused mentoring of clinicians as AMS champions and a tailored educational self-assessment tool with feedback. Engagement is measured by participation in the campaign and self-assessment tool.

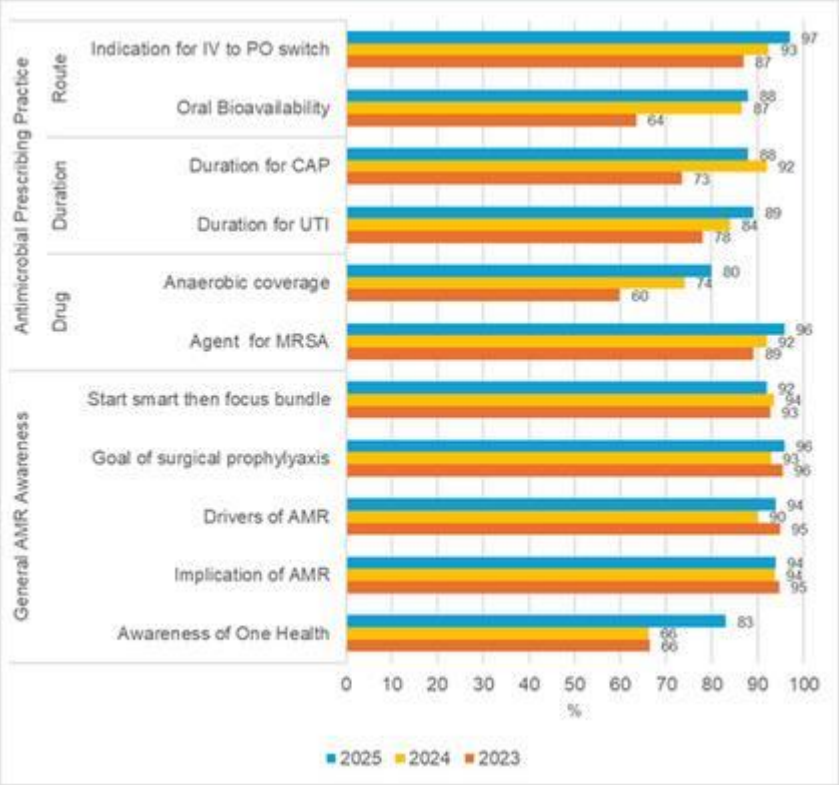
Results

Since 2022, participation has expanded from medical, surgical and multidisciplinary teams from a single hospital site to now include participants from five hospital sites, public health and the community. In 2025 the campaign was developed further to include advanced nurse practitioners as AMS champions. 23 case presentations showcased predominantly One Health themes including Verotoxigenic *Escherichia coli* bacteraemia, *Clostridioides difficile*, listeriosis, AMR, and associated community and hospital outbreaks. Participants' feedback demonstrated that 95% of respondents rated the campaign as informative/very informative for their clinical practice with an overall score of 4.8/5.

453 individuals have participated in the self-assessment tool increasing from 68 participants in 2022 to 141 in 2025. Sustained year-on year improvements were observed in the awareness of best practice in IV to PO switch (87% to 97%), oral bioavailability (64% to 88%), treatment duration for community acquired pneumonia (74% to 88%) and urinary tract infection (78% to 89%), anaerobic coverage (60% to 80%), MRSA coverage (89% to 96%) and awareness of One Health (66% to 83%).

Conclusions

This novel AMS campaign fosters interprofessional engagement and clinicians' behavioural change. Through focused mentoring, non-infection specialists are empowered to be peer mentors and AMS champions through reflective clinical practice. The campaign has demonstrated high stakeholder engagement and an improved awareness in AMR, AMS and One Health.



1034 – An analysis of the livestock trade network in The Gambia and implications for disease control

Santiago RAYMENT GOMEZ (1), Jose Gabriel NINO BARREAT (2), **Saidal Ali BAH** (1), Hellena DEBELTS (3), David REDDING (2), Kris MURRAY (1)

1: London School of Hygiene and Tropical Medicine, United Kingdom; 2: Natural History Museum London, United Kingdom; 3: Robert Koch Institute, Berlin, Germany

BackgroundLivestock mobility is central to production systems in West Africa, with animal trade through markets being a major pathway shaped by economic and cultural factors. In The Gambia, many rural households rely on traditionally reared livestock, but these systems are burdened by high disease incidence, including Rift Valley fever. Markets can therefore amplify transmission among infectious animals, while trade can spread pathogens to new areas.

MethodsGovernment-issued movement permits were used to capture livestock movements between locations. Directed networks were built from edge lists, where each edge represented at least one livestock movement to or from a market, and nodes represented markets or origin/destination localities. Edges were weighted by total animals moved (flow volume) and the number of times a route occurred (flow frequency). Separate networks were created for small ruminants, cattle, and combined livestock. Topology was analysed using node-level metrics: in- and out-degree (transmission pathways), closeness centrality (potential speed of transmission), and betweenness centrality (bridging transmission pathways), and network-level metrics: density (overall connectedness), giant components (extent of network reach), and clustering (local transmission potential). Temporal variation was assessed by classifying trade routes by the number of months active annually. To explain drivers of livestock trade flow, negative binomial gravity models will be fit using origin livestock population, destination human population, and origin-destination travel time.

ResultsThere was substantial temporal variation in livestock movement, with spikes in trade frequency and volume before a major religious event and after the cash-crop harvest season. Small ruminant trade occurred in a more highly connected network than cattle, with a larger giant strongly connected component (74/104 [72%] vs 33/104 [32%]), greater density (0.0603 vs 0.0265), and more clustering (0.172 vs 0.0866). At the node level, Farafenni and Fass ranked highest in the small ruminant and cattle

networks, respectively, according to their centrality metrics (Farafenni: in-degree = 51, out-degree = 75; Fass: in-degree = 32, out-degree = 63), identifying them as important market hubs. Gravity model analyses are ongoing and will quantify how origin, destination, and travel-time covariates shape trade flows and identify important pathways for disease spread.

ConclusionThese findings suggest that small ruminant movements pose a greater risk for rapid, widespread disease dissemination. Their higher density, clustering, and larger giant connected components indicate more frequent and interconnected trade pathways, increasing opportunities for pathogens to spread and persist. In contrast, the cattle network appears more fragmented and less clustered, which could slow transmission and limit outbreak reach. Highly connected market hubs such as Farafenni and Fass are likely key propagators of disease and potential control points. Targeted, market-based interventions at these central nodes could substantially reduce epidemic spread.

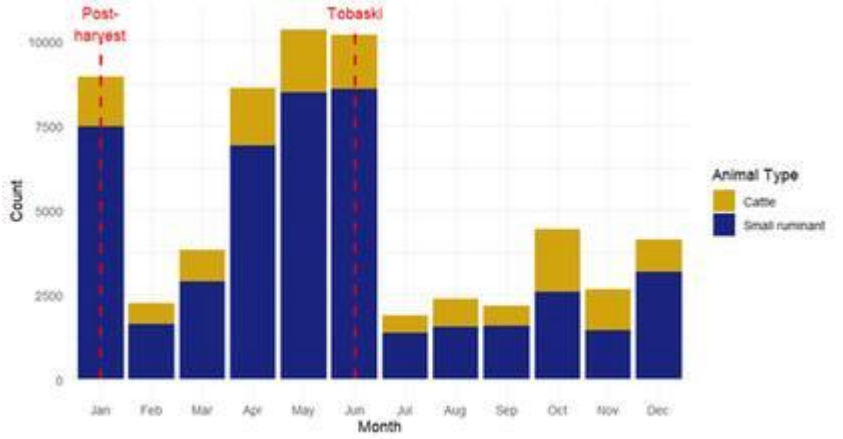


Figure 1. Number of livestock traded per month. Red lines indicate post-harvest season and major religious event.

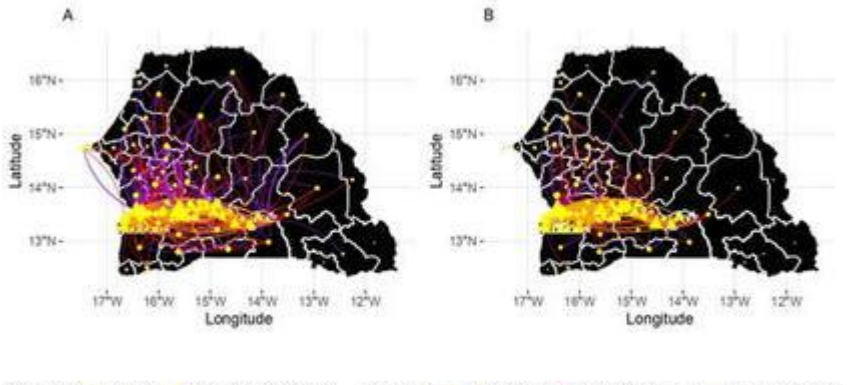


Figure 2. A) Small ruminant trade network and B) cattle trade network. Edges are weighted by the volume of flow.

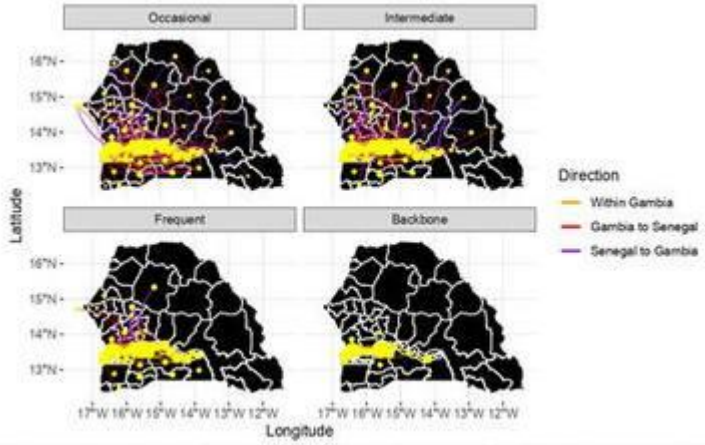


Figure 3. Occasional: 1 month/year, intermediate: 2–3 months/year, frequent: 4–9 months per/year, backbone: 10–12 months per/year.

1041 – Deciphering the Serological Responses of the European bat species Miniopterus schreibersii Against Potential Zoonotic Viruses Using a Multiplexed Immunoassay

Lucie CAPPUCCIO (1), Victoire PERRAUD (1), Angela BRISEBARRE (1), Marine WASNIEWSKI (2), Maxime LEUCHTMANN (3), Olivier REYNARD (4), Pierre LAFAYE (5), Gaelle CHAUVEAU-LE FRIEC (5), Jordan DIMITROV (6), Laurent DACHEUX (1)

1: Institut Pasteur, Université Paris-Cité, Environment & Infectious Risks Unit (ERI), 28 rue du Docteur Roux, 75724 Paris Cedex 15, France; 2: INTERFAS Unit, Nancy Laboratory for Rabies and Wildlife, ANSES - Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail, Bâtiment H, Technopôle Agricole et Vétérinaire, CS 40 009, 54220 Malzéville Cedex, France; 3: Nature Environnement 17, Surgères, France / France Nature Environnement Nouvelle-Aquitaine, Angoulême, France; 4: Horvat B-IbIV Unit, CIRI – Centre International de Recherche en Infectiologie, 46 Allée d'Italie 69364 Lyon Cedex 07, France; 5: Institut Pasteur, Université Paris-Cité, Antibody Engineering CNRS-UMR3528, 25 rue du Docteur Roux, 75724 Paris Cedex 15, France; 6: French Institute of Health and Medical Research, Sorbonne Université, U872- Inserm, 15 rue de l'Ecole de Médecine, 75006 Paris, France

Background

In recent years, several RNA virus families found in bats have been associated with the emergence of human diseases. Surveillance in this large diverse group of mammals has revealed that bats are significant reservoir hosts for many viruses, however traits that trigger emergence of potential zoonotic viruses are still poorly understood, partly due to a lack of tools. This is the case in Europe with the bat species *Miniopterus schreibersii*, which has been shown to harbor viruses with zoonotic potential, including *lyssaviruses*, *filoviruses*, and *coronaviruses*.

As part of the EU's OneBAT project, which aims to elucidate the interactions between this bat species and these viral families that could lead to emergence mechanisms, this study was to develop a dedicated multiplex immunoassay (MIA) to assess the exposure and degree of circulation of viruses of interest in colonies.

Methods

To assess the viral exposure of *Miniopterus schreibersii* species we selected *in silico* bat-related *coronaviruses*, *lyssaviruses* and *filoviruses* to obtain various target in different system of expression. In parallel, none bat-related recombinant proteins were sourced from different compagnies.

The coupling of protein to magnetic bead for the MIA (Luminex ® technology) was performed using the Bio-Plex Amine Coupling Kit (Bio-Rad) as manufacturers' instructions. Then, the coupled beads with recombinant proteins were tested using reference serums from NIBSC and in-house recombinant pseudovirus inactivated serum. Finally, we dedicated reagents to detect the IgG of the M*iniopterus schreibersii* serum by comparing commercial reagents (protein A, G and goat anti-Bat (H+L) secondary antibody) and in-house anti-bat IgG nanobodies.

Results

The final multiplex bead-based assay comprising 38 antigens. We validated all the recombinant proteins of bat-associated *coronavirus* (Msch1, *Sarbecoviruses*, etc.), *lyssavirus* (West Caucasian bat virus, Lleida bat virus, etc.) and the European *filovirus* Lloviu (LLOV) using the specific reference sera from NIBSC and in-house LLOV inactivated-hamster serum. Finally, we demonstrated the low level of cross-reactivity between viral families.

We confirmed that protein A allow the recognition of M*iniopterus schreibersii* IgG whereas protein G does not. Furthermore, the use of the goat anti-Bat has shown strong reactivity against most antigenic targets. Finally, we obtained 12 different nanobodies that can recognize bat-IgG from three species (*Rhinolophus*, *Miniopterus* and *Myotis*) differently.

Conclusions

Our study provides a comprehensive assessment of IgG recognition of a panel of viral antigens in the species *Miniopterus schreibersii* for studying seroprevalence and, consequently, the circulation of zoonotic viruses.

This MIA offers a promising option, addressing many of the limitations of conventional techniques as for instance a single and small-volume sample, scalability and cross-reactivity consideration.

This tool could be exploited and compared to complementary available tools, to decipher viral transmission, seroprevalence and probable routes for exposures including spillover interfaces.

1044 – Development of methodological tools dedicated to viral surveillance in bat colonies

Victoire PERRAUD (1), Lucie CAPPUCCIO (1), Angela BRISEBARRE (1), Stefania LEOPARDI (2), Gábor KEMENESI (3), Simon SCOTT (4), Marine WASNIEWSKI (5), Jordi SERRA COBO (6), Vasiliki CHRISTODOULOU (7), Elke MÜHLBERGER (8), Silvia BOFILL MAS (6), Edward WRIGHT (9), Anton VLASCHENKO (10), Nigel TEMPERTON (4), Sandra MARTINEZ PUCHOL (6), Petra DRZEWNIOKOVA (2), Maria Francesca PRIORE (2), Adam HUME (8), Gorfol TAMAS (3), Zsófia LANSZKI (3), Valentina PANZARIN (2), Dominique PONTIER (11), Maxime LEUCHTMANN (12,13), Evelyne PICARD-MEYER (5), Paola DE BENEDICTIS (2), Laurent DACHEUX (1)

1: Institut Pasteur, Université Paris-Cité, Environment & Infectious Risks Unit (ERI), 28 rue du Docteur Roux, 75724 Paris Cedex 15, France; 2: Istituto Zooprofilattico Sperimentale delle Venezie; 3: University of Pecs; 4: University of Kent; 5: INTERFAS Unit, Nancy Laboratory for Rabies and Wildlife, ANSES - Agence nationale de sécurité sanitaire de l'alimentation, de l'environnement et du travail, Bâtiment H, Technopôle Agricole et Vétérinaire, CS 40 009, 54220 Malzéville Cedex, France.; 6: Universitat de Barcelona; 7: Ministry of Agriculture, rural development and environment of Cyprus; 8: The trustee of Boston University; 9: University of Sussex; 10: H.S. Skovoroda Kharkiv National Pedagogical University; 11: Biometry and Evolutionary Biology Laboratory, CNRS UMR 5558 (LBBE), Université Claude Bernard Lyon 1, 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France; 12: Nature Environnement 17, Surgères, France; 13: France Nature Environnement Nouvelle-Aquitaine, Angoulême, France

Background

Because of their impact on humans, the emergence of zoonotic diseases has become a global health concern. Among animal reservoirs, bats represent a major source of zoonotic viruses, as demonstrated by recent epidemics associated with henipaviruses, filoviruses and coronaviruses. Similarly, lyssaviruses were detected very early in bats, which are now recognized as one their main reservoir worldwide. Consequently, monitoring and studying viral circulation in these animals are essential elements in any attempt to anticipate future zoonotic emergences.

In Europe, several viruses with zoonotic potential have been identified in bats. These include mainly lyssaviruses (such as West Caucasian bat virus, WCBV, and Lleida bat lyssavirus, LLEBV), alpha and beta coronaviruses, and Lloviu virus (LLOV), the single European filovirus identified to date. Intriguingly, the Schreibers' bat (*Miniopterus schreibersii*) is the only European bat species known to harbour all these different viruses, making it a valuable sentinel animal.

Our objective, within the framework of the European HORIZON OneBAT program, is therefore to develop and apply complementary methodological approaches, to study the presence and the circulation of these viruses in selected colonies of *Miniopterusschreibersii* bats in Europe (e.g. Figure 1).

Methods

These approaches include: 1/ dedicated multiplexed serological analysis tools based on Luminex technology or seroneutralization tools (using viruses or viral pseudotypes); 2/ targeted or broad-spectrum molecular detection systems, including both nucleic acid detection (RT-qPCR) and/or metagenomics approaches; 3/ cell-culture models for viral isolation and for assessing the spectrum of infectivity; and 4/ environmental analysis tools applied to colony sites (such as air virome analysis).

Results

These methodological approaches have enabled us: 1/ to develop a 38-antigen multiplex panel of bat-associated viral proteins, which showed that only protein A reliably detects *Miniopterus schreibersii* IgG, and to also develop a representative pseudotypes of target viral species (LLEBV, WCBV, LLOV, and three α-coronaviruses); 2/ to review the various PCR-based molecular diagnostic protocols (real-time or conventional) and test them on multiple field-collected samples (saliva, blood and faeces); 3/ to generate multiple primary bat cell lines (e.g. Figure 2) and succesfully infect them with field-collected samples ; 4/ to test and implement air sampling in the european bat colonies monitored for our project (e.g. Figure 3).

Conclusion

Combined with the epidemiological data collected, the results obtained will provide a better understanding of viral circulation in these animals. Moreover, these methodological approaches could also be extended to other reservoir animal species.

Figure 1: Example of counting and sampling campaign in a bat colony.
(The pictures were taken in the south-west of France thanks to France Nature Environment Nouvelle-Aquitaine, and the CCPNA program)

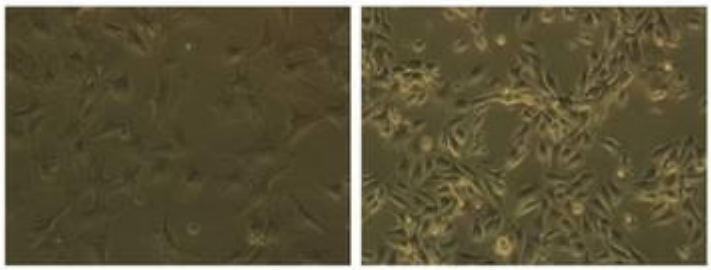


Figure 2: Primary bat cell lines obtained from diverse organs (patagium, kidney or lung) from two different individual of the *Miniopterus schreibersii* species.

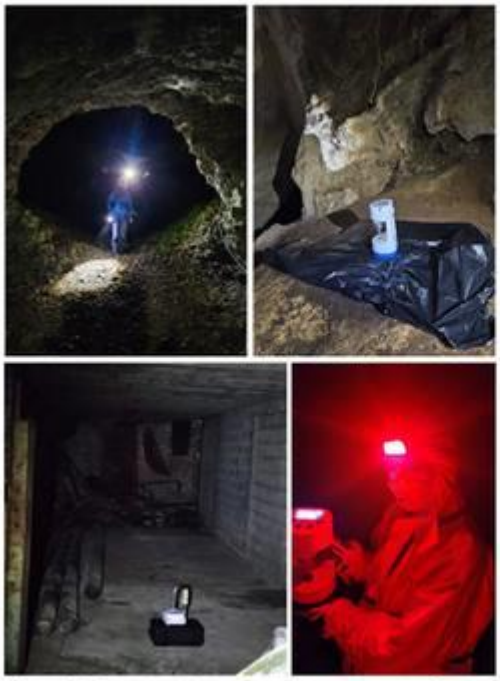


Figure 3: Exemples of air sampling in caves using Coriolis Micro and Compact in France.

1057 – An Integrated One Health Approach for Characterizing Zoonotic Arbovirus Transmission Dynamics Across Florida Landscape Gradients

Caleb J STICA (1), Athena CHLAPOWSKI (1), Nathan BURKETT-CADENA (1), Carla MAVIAN (1,2), Katheryn HANLEY (3), Michaela BUENEMANN (3), Gabriella STEELE (4), Shannen LEAHY (4), Keira J LUCAS (4), Suzanne LI (4), David F HOEL (5), Aaron M LLOYD (5), James C DUNFORD (5), Milton P STERLING (5), Joy BARKER (5), Jackson MOSLEY (6), Hugo ORTIZ (6), Amanda BOCANEGRA (6), Marisa FONESCA (6), Amy VITTOR (1,7)

1: University of Florida, United States of America; 2: Stellenbosch University, South Africa; 3: New Mexico State University, United States of America; 4: Collier Mosquito Control District, United States of America; 5: Lee County Mosquito Control District, United States of America; 6: Polk County Mosquito Control District, United States of America; 7: Emerging Pathogens Institute, United States of America

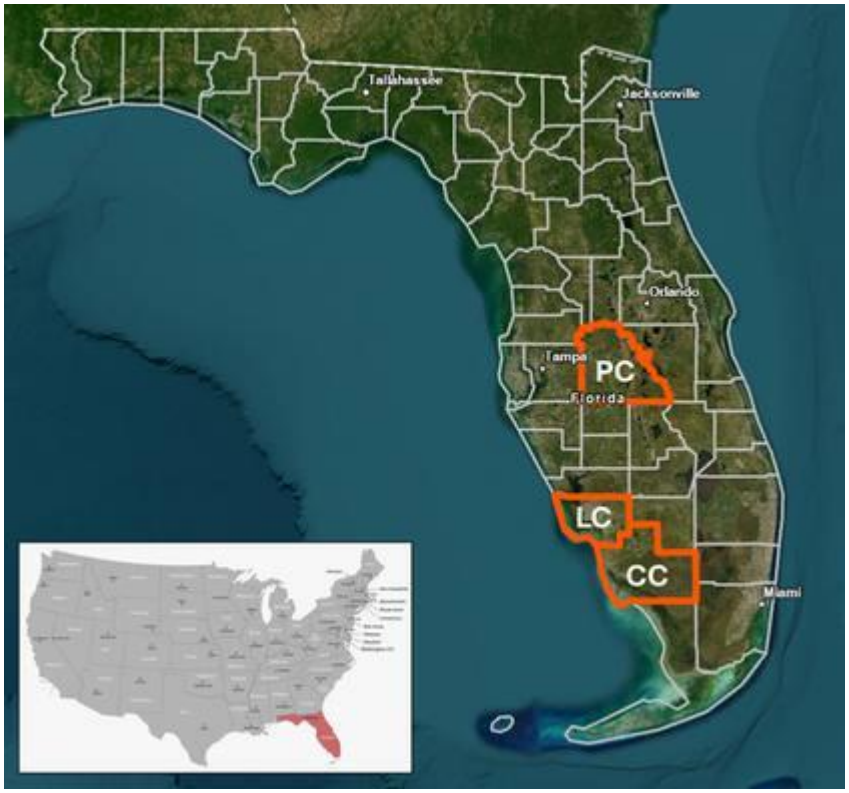
Background: Anthropogenic land-use change and biodiversity loss are important drivers of zoonotic viral emergence. Routine surveillance primarily focuses on well-known pathogens, resulting in a knowledge gap for lesser-known arboviruses. In Florida, land-use change and urban sprawl into wetland ecosystems have restructured host-vector dynamics, potentially increasing the risk of spillover zones for these and other neglected arboviruses. This research evaluates the transmission network of arboviruses across the Florida landscape gradient (forest/marsh, forest edges, cropland, pastureland, and urban edge), investigating the viral transmission dynamics of neglected arboviruses, such as Everglades virus, Keystone virus, and Tensaw virus, for which little is known regarding the ecological drivers of their transmission.

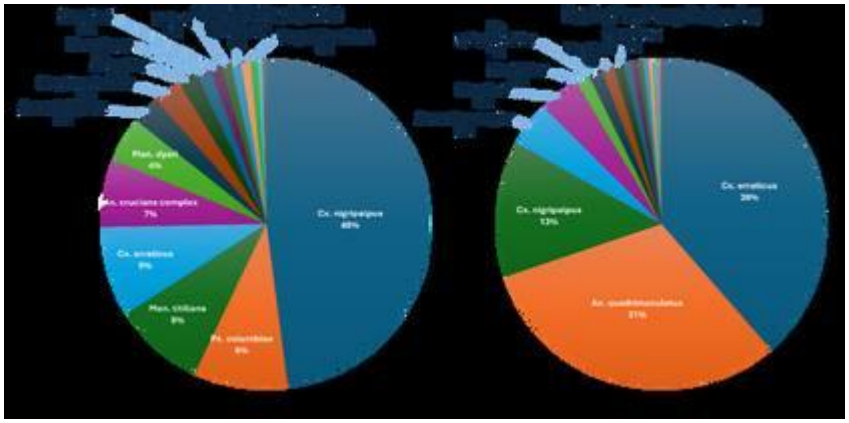
Methods: We employed an integrated One Health framework across Southwest Florida's forest-urban gradients. Resting traps were used to capture key mosquito species, using CDC light traps as a diversity baseline at the same locations. Microclimate data loggers were deployed to discriminate microclimatic changes influencing mosquito resting behaviors. To identify ecological drivers, the impact of land-cover variables on vector abundance was modeled using negative binomial generalized linear mixed models. Host blood meal analysis was coupled with host-antibody detection via microPRNT to map vector host interactions and previous arboviral exposure across diverse landscapes.

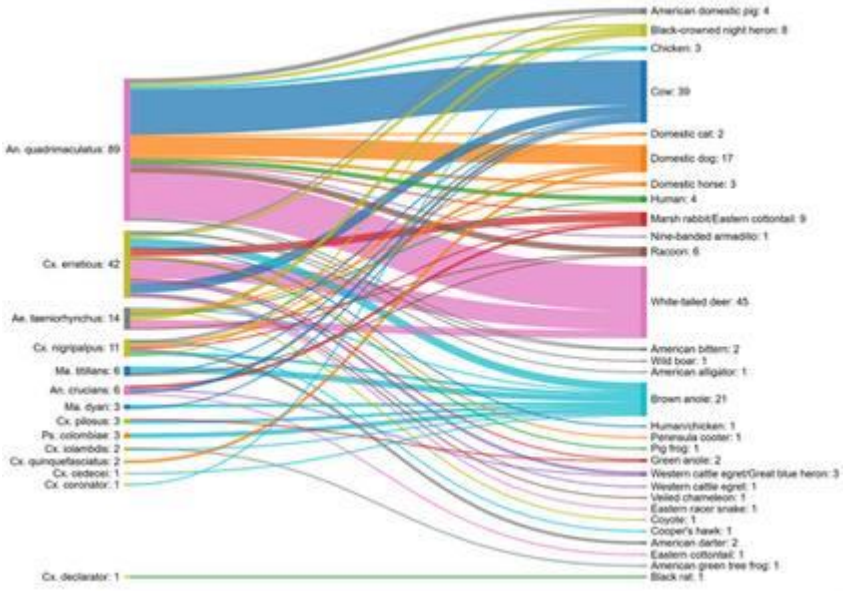
Results: Analysis from collections in 2025 in Collier County, FL (Figure 1) showed that CDC light traps captured a larger volume and diversity of mosquitoes. However, resting trap collections preferentially selected for bloodfed tree hole breeding species, many of which have been implicated in arboviral transmission cycles (Figure 2). *Cx (Mel.) cedecei,* the primary vector for Everglades virus was found primarily in intact wetlands (p 0.001) but showed a positive association with agriculture-forest edges (p =

0.032). Blood meal analysis revealed a high degree of heterogeneity in host preference across the forest-urban landscape gradient (Figure 3). *An. quadrimaculatus*, a historic vector of malaria in the Southeastern United States, *Cx. erraticus*, a potential bridge vector for Eastern equine encephalitis virus, and *Ae. taeniorhynchus*, a vector for Keystone virus, were the three most predominant bloodfed species collected. Mosquito species fed predominantly on mammalian hosts (74%), cows, deer, and domestic dogs; and least on amphibian hosts (1%). Host antibody analysis by microPRNT has been optimized with the same mosquito blood meals and will further discriminate prior arboviral exposures of these vertebrate hosts.

Conclusions: These findings demonstrate that current surveillance systems, which are optimized for specific outbreak pathogens, are blind to the broader zoonotic emergence landscape. This study emphasized the importance of moving toward integrated surveillance that monitors the entire ecological network. By characterizing the complex network of understudied vectors and hosts across land-use gradients, we can move from reactive disease management to a proactive understanding of zoonotic risk.







1060 – Hidden Threats on the Plate: Antimicrobial Resistance in Poultry Meat from India

Muhammad ASADUZZAMAN

University of Oslo, Norway

Background: In line with global trends, poultry in India has emerged as the leading source of meat, now representing 65 percent of total meat consumption, a significant increase from 23 percent two decades ago. Additionally, poultry consumption is projected to increase by 577% between 2000 and 2030. Currently, India is world's third largest egg producer falling behind China and USA, and the world's fifth largest poultry producer, following the USA, Brazil, China and the European Union. However, increasing reports of bacterial contamination and antimicrobial resistance (AMR) in chicken meat raise significant public health concerns. This systematic review aims to assess the prevalence of key bacterial pathogens in chicken meat across India and their resistance profiles.

Methods: A comprehensive literature search was carried out across PubMed, Web of Science, and Scopus databases for studies published up to August 2024. Additionally, gray literature was retrieved using Google Scholar. Studies that identified bacterial isolates from chicken meat samples in India and reported antimicrobial susceptibility results were selected for inclusion. Data were extracted on bacterial species, sample location, antibiotics tested, and resistance rates using Microsoft Excel. A heatmap and summary tables were generated to visualize resistance trends.

Results: A total of 32 studies were included in this review, with *Escherichia coli* and *Salmonella* spp. emerging as the most frequently detected pathogens. High resistance rates were observed to ampicillin, tetracycline, ciprofloxacin, and streptomycin. The overall multidrug resistance (MDR) rate exceeded 60% for several species. Resistance genes such as *bla*, *tet*, and *sul* families were frequently reported, along with virulence genes like *invA* and *icaA*. The included studies spanned several Indian states and union territories, with South India being the most represented region. Tamil Nadu contributed the highest number of studies (6 out of 32, 18.75%), followed by Assam and Maharashtra (4 each), and Andhra Pradesh, Karnataka, and Punjab (3 each). States such as Bihar, Meghalaya, Mizoram, Telangana, West Bengal, and Delhi each had one study. Notably, several regions, including Goa, Gujarat, Kerala, Odisha, and parts of the northeastern and Himalayan zones, had no studies.

Conclusion:

This review highlight a critical public health concern of AMR in India, where chicken meat is widely contaminated with MDR bacteria, including *E.coli, Salmonella, Klebsiella,* and *S. aureus*. The widespread nature of AMR in poultry pathogens underscores the urgent need for a coordinated One Health response that integrates surveillance, stewardship, and regulatory interventions across human, animal, and environmental sectors. In this context, aligning national antimicrobial usage policies with the WHO AwaRe

classification is essential to ensure rational use of antibiotics, thereby preserving their efficacy. Continued research, improved data standardization, and expanded regional representation are necessary to fully address this growing threat and to safeguard both animal and human health.

Figure 1: PRISMA flow chart*

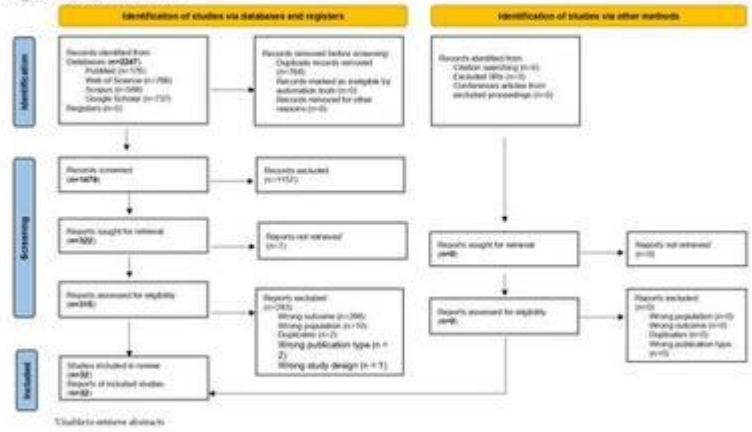


Figure 2: Geographical distribution of studies reporting bacterial pathogens in chicken meat across India

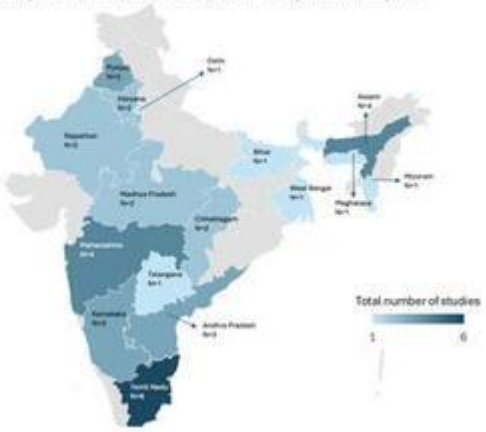
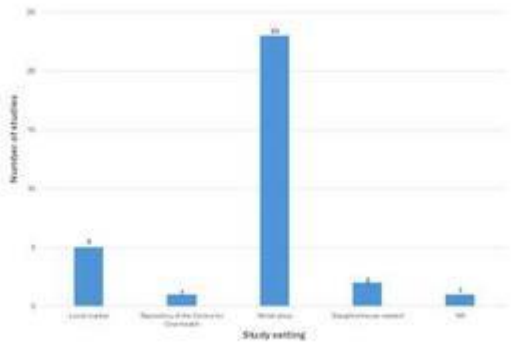


Figure 3: Distribution of study settings in included studies on bacterial pathogens in Indian chicken meat.



1063 – Strengthening Policy Frameworks for Primary Pandemic Prevention at Wildlife Trade Interfaces in Guatemala

Luis Fernando GUERRA (1), Kurt DUCHEZ (1), Ana Cecilia ESCOBAR (2), Lucy KEATTS (3), **Sofia Valeria CORTES CALDERON** (4)

1: Wildlife Conservation Society, Mesoamerica & Western Caribbean; 2: Wildlife Conservation Society, Guatemala; 3: Wildlife Conservation Society, Health Program; 4: World Organisation for Animal Health, France

Background: In Guatemala, wildlife trade was recognized by multisectoral stakeholders as a health governance issue requiring stronger institutional coordination, clearer procedures, and regulatory measures to reduce zoonotic risk. A national consultative process was undertaken to identify policy and operational gaps affecting primary pandemic prevention at wildlife trade interfaces.

Methods:A descriptive policy and governance case study was developed using the Guatemala component of a wider technical consultation. A co-developed government consultation questionnaire explored trade characterization, health perceptions, and gaps and opportunities for risk reduction. Data were gathered through interviews and workshops with stakeholders from justice, environment, agriculture, public health, academia, civil society, rescue centers, and protected area institutions. The process also informed short- and long-term needs identification and guided two expert consultancies focused on biosecurity and inter-agency legal and procedural integration.

Results: In Guatemala, 29 people were interviewed and 79 participated in workshops. Participating institutions included the Public Ministry, Nature Protection Division, Center for Conservation Studies, Ministry of Agriculture, Livestock, and Food, Ministry of Public Health and the National Health Laboratory, National Council of Protected Areas, Criminal Investigations Directorate, National Avian Health Program, National Forestry Institute, ARCAS, FUNDAECO, Defenders of Nature, Tikal National Park, Yaxhá National Park, and other civil society actors. Priority short-term needs included identifying zoonotic risks at wildlife use and rescue-center interfaces, strengthening knowledge of zoonoses and biosecurity protocols, improving wildlife import and export health requirements, and developing regulatory proposals for prevention, mitigation, and control of zoonotic diseases associated with illegal wildlife trafficking. Long-term needs included strengthening wildlife health management, improving intersectoral coordination and communication, implementing active and passive zoonoses surveillance and regulating standards for prevention, mitigation, and control. Concrete outputs included biosecurity guidelines for safe handling of wildlife specimens in trade, communication flowcharts and collaboration procedures among institutions in the wildlife trafficking subcommittee, roadmaps for disease notification and wildlife trafficking data management, and a gap analysis with recommendations for operational integration of laws. The process also strengthened coordination across health, environment, agriculture, and justice sectors; supported the One Health Technical Commission and a national zoonotic prevention strategy.

Conclusions: The Guatemala case shows that structured multisectoral consultation can generate actionable governance tools for One Health policy implementation at wildlife trade interfaces. Linking legal analysis, biosecurity guidance, inter-agency procedures, and surveillance-oriented roadmaps may strengthen primary pandemic prevention and improve institutional readiness to address zoonotic risks associated with wildlife trafficking.

1069 – Strengthening Early Warning in low-resource settings: Lessons from a fictional country

Marta MENDES, Fernanda DÓREA, Crawford REVIE, Madhur DHINGRA

Food and Agriculture Organization of the United Nations (FAO), Rome, Italy

BackgroundThe FAO Framework for Early Warning (EW) of Animal Health Threats was recently published as a high-level, goal-setting document to guide countries in strengthening early warning systems for infectious animal diseases using a systems approach. Rather than creating new systems, it supports countries in reviewing and reinforcing capacities already in place, while recognizing that operationalization pathways are context-specific. However, countries often struggle to know where to start, how to navigate the framework, and how to translate its concepts into practical action, particularly in low-resource settings where capacities are uneven and strengthening must be progressive. To address this gap, a scenario-based course was built around “Sentara”, a fictional country with limited early warning capacity. The course is available in the FAO Virtual Learning Centre and aims to support operationalization of the framework.

MethodsWe designed a four-module online course based on two core tools used side by side: the EW Framework, which explains what to look for in an early warning system, and the Self-Assessment Checklist, which provides a structured way to record findings, scores, notes, gaps and priorities. Module 1 introduces early warning foundations, the framework's scope and structure, and the distinct functions of the framework and checklist as complementary tools. Module 2 uses Sentara to guide self-assessment through disease prioritization, framework annotation and checklist scoring. Module 3 expands this into a peacetime national tabletop exercise in which learners map how the early warning system functions through stakeholder dialogue and identify priority gaps. Module 4 moves from assessment to improvement, using those gaps to build a strengthening pathway and a vision for "Sentara of the future".

ResultsThe resulting VLC course provides a pathway for turning a high-level framework into a working tool. Across the modules, learners are trained to understand and navigate the framework, use it for structured assessment, and apply it to improvement planning. Through Sentara, they work through a realistic low-resource scenario in which weaknesses span surveillance, risk assessment, communication, decision-support, intervention pathways and the enabling environment. The course helps learners identify strengths, gaps and bottlenecks, discuss priorities across stakeholders, select feasible actions, and visualize how a stronger early warning system could function in practice. In this way, the framework serves not only as guidance, but also as a practical tool for review, prioritization and strengthening.

ConclusionsPublishing a framework is an essential step, but publication alone does not ensure uptake. Practice-oriented learning products are also needed to help countries translate guidance into action. The Sentara VLC course offers one such model: a fictional-country learning journey that helps users understand, assess and strengthen early warning systems in a progressive and context-sensitive way, with lessons relevant to other One Health capacity-strengthening efforts.

1071 – Epidemiological Profile of Animal Bite Cases Attended at Doane Health Center, Govuro District, Mozambique, January–June 2024

Percília BILA (1), **Jose JEMUSSE** (2)

1: Serviço Distrital de Saúde Mulher e Acção Social de Govuro; 2: Serviço Provincial de Saúde-Inhambane, Mozambique

Introduction

Rabies is a neglected zoonotic viral disease responsible for tens of thousands of human deaths each year, with approximately 40% occurring in children under 15 years of age. Most infections occur following dog bites, which account for approximately 99% of human rabies cases. In Mozambique, approximately 18,000 animal bite cases and about 20 suspected human rabies deaths are reported annually. The objective of this study was to describe the epidemiological characteristics of animal bite cases reported at the Doane Health Center.

Methods: A retrospective descriptive cross-sectional study with a quantitative approach was conducted using data from the Doane Health Center, located in Govuro District, Inhambane Province, Mozambique, between January and June 2024. All recorded animal bite cases during the study period were included.Data were extracted from adult consultation registers, sick child consultation registers, and emergency service records, and were complemented with information from animal bite notification forms. Descriptive statistical analysis was performed using Microsoft Excel, including the calculation of absolute and relative frequencies as well as measures of central tendency. The results were presented in tables and figures.

Results: During the study period, a total of 49 animal bite cases were recorded at the Doane Health Center. Of these, 51.0% (25/49) of the cases occurred in males, and 32.7% (16/49) were observed in the 15–24-year age group **(Figure 1).** Most bite incidents were caused by dogs, accounting for 85.7% (42/49) of cases, followed by cats at 12.2% (6/49) and monkeys at 2.0% (1/49) **(Figure 2).** Additionally, 80.8% (21/26) of the attacks occurred without apparent provocation. Regarding temporal distribution, cases were recorded between epidemiological weeks 1 and 26 of 2024, showing variation throughout the period, with the highest number of cases observed in epidemiological week 23. In terms of geographic origin, notifications were reported from 13 villages within the Doane health area. The village of Doane recorded the highest number of cases, accounting for 24.5% (12/49) of all notifications **(Table 1).** Information on the aggressor animal was available for 26 cases in which the animal responsible for the attack was identified.

Among these, 65.4% (17/26) involved domestic animals, and only 29.4% (5/17) had an up-to-date rabies vaccination status **(Table 2)**.

Conclusion: Although no confirmed human rabies cases were reported during the study period, the occurrence of bites from animals potentially capable of transmitting rabies, combined with low animal vaccination coverage and limited access to post-exposure prophylaxis, suggests the continued risk of rabies transmission in the Doane health area. These findings highlight the need to strengthen preventive strategies, including regular animal rabies vaccination campaigns.

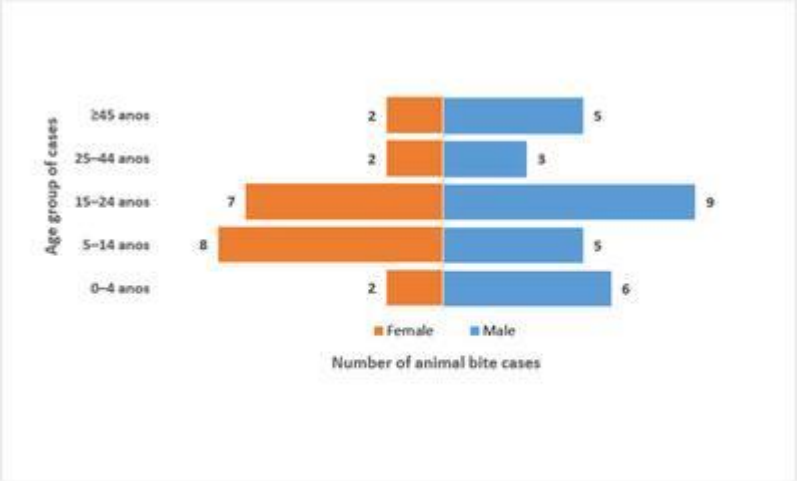


Figure 1. Distribution of animal bite cases by sex and age group in the Doane health area, January–June 2024.

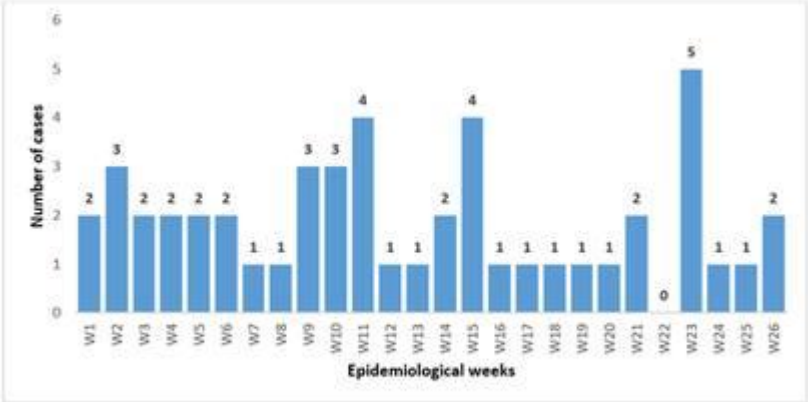


Figure 2. Temporal distribution of animal bite cases by epidemiological week in the Doane health area, January–June 2024

Table 1. Epidemiological profile of animal bite cases in the Doane health area, January–June 2024.

Age group	Dog bite (N=42) n/N (%)	Cat bite (N=6) n/N (%)	Monkey bite (N=1) n/N (%)
0–4 years	8 (19.0)	0 (0.0)	0 (0.0)
5–14 years	11 (26.2)	1 (16.7)	1 (100)
15–24 years	14 (33.3)	2 (33.3)	0 (0.0)
25–44 years	3 (7.1)	2 (33.3)	0 (0.0)
≥45 years	6 (14.3)	1 (16.7)	0 (0.0)
Sex			
Male	23 (54.7)	2 (33.3)	0 (0.0)
Female	19 (45.2)	4 (66.6)	1 (100)
Village of origin of cases			
Batata	1 (2.3)	0 (0.0)	0 (0.0)
Chimunda	1 (2.3)	0 (0.0)	0 (0.0)
Colonato	1 (2.3)	0 (0.0)	0 (0.0)
Doane	12 (28.3)	1 (16.6)	1 (100)
Genga	5 (11.9)	1 (16.6)	0 (0.0)
J. Machel	1 (2.3)	0 (0.0)	0 (0.0)
Macomba	3 (7.1)	0 (0.0)	0 (0.0)
Matasse	1 (2.3)	0 (0.0)	0 (0.0)
Mataula	7 (16.6)	1 (16.6)	0 (0.0)
Matique	1 (2.3)	0 (0.0)	0 (0.0)
Mucumbugdje	4 (9.5)	0 (0.0)	0 (0.0)
Mussassa	3 (7.1)	3 (50.0)	0 (0.0)
Nasso	2 (4.7)	0 (0.0)	0 (0.0)

1080 – Extreme Climate Events in Minas Gerais: Impacts on Urban Sustainability and Health under a One Health Perspective

Halisson GONÇALVES, Érica REIS, Flávia VIEIRA, Clarice ABREU, Ana Cristina PINTO, Raysa TORRES, Mônica PINTO, Amanda LOPES, **Carla CAMPOS**

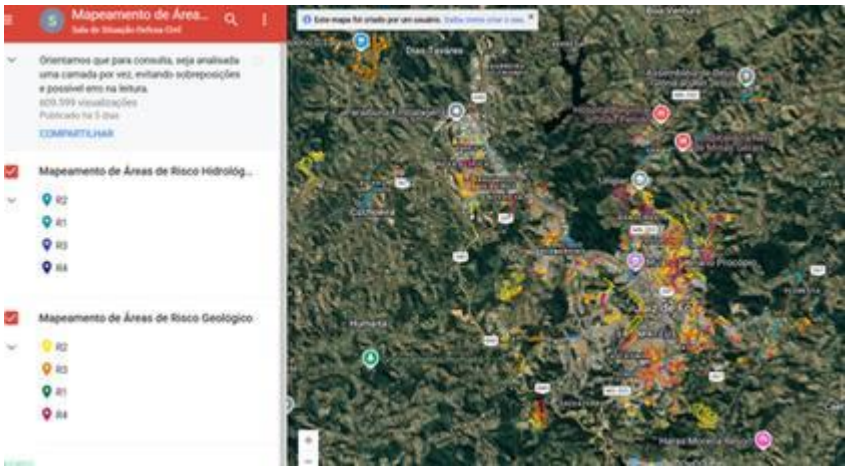
FUNDAÇÃO OSWALDO CRUZ - FIOCRUZ, Brazil

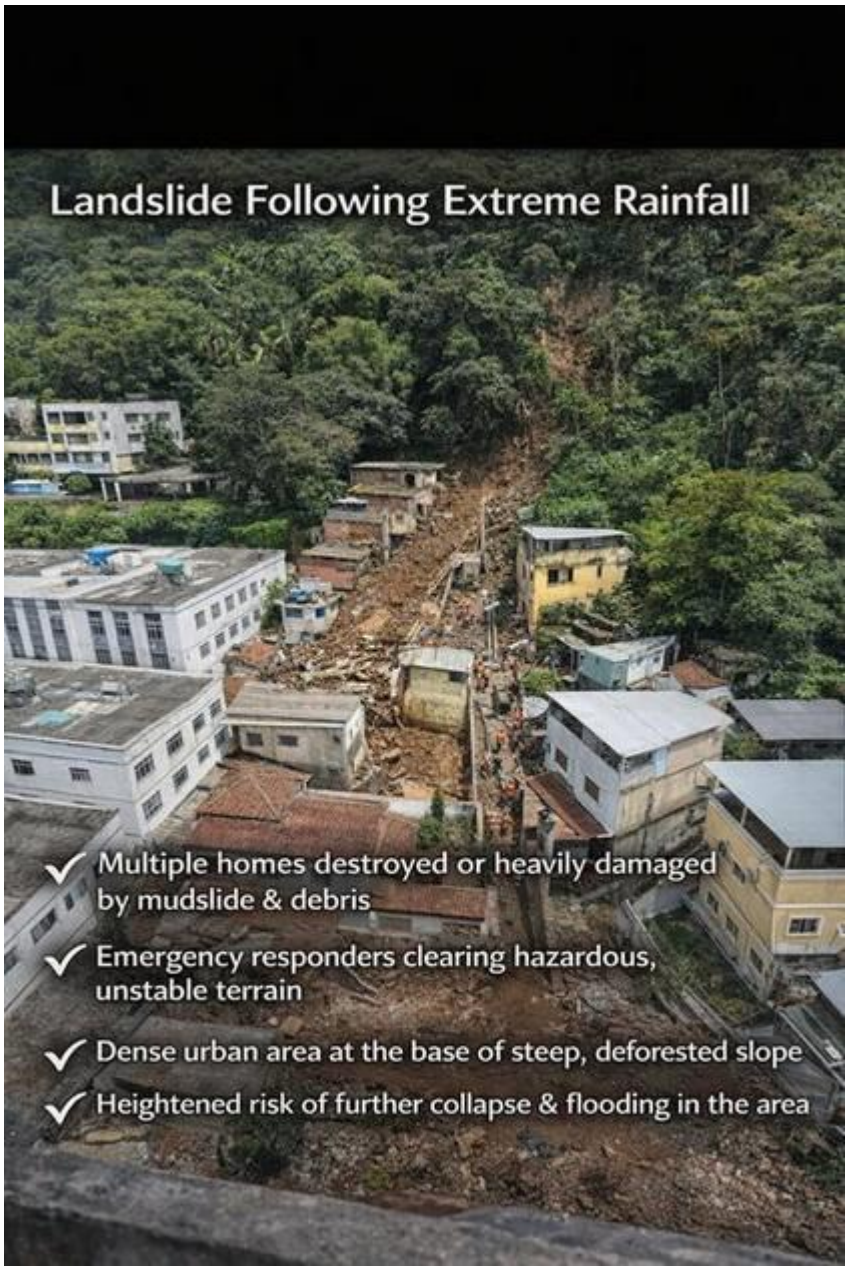
Background: The flooding event that occurred in February 2026 in the municipalities of Juiz de Fora and Ubá, located in the Zona da Mata region of Minas Gerais, was characterized by intense precipitation. A total of 138.7 mm of rainfall was recorded within 24 hours in Juiz de Fora, approaching the historical monthly average of 170.3 mm. The heavy rains caused flooding, landslides, and significant damage to urban infrastructure. Structural factors, including unplanned land occupation, weaknesses in urban planning, and limitations in risk management, likely amplified the effects of this extreme hydrometeorological event. The analysis examines how climate change, socio-environmental vulnerability, and institutional response capacity interact across human, animal, and environmental dimensions, situating extreme flooding events within a systemic One Health context.

Methods: This exploratory and descriptive study combined qualitative and quantitative approaches to examine the February 2026 flooding events in Juiz de Fora and Ubá. Data sources included institutional civil defense reports, official meteorological records, and publicly available municipal documents. Field observations were documented during post-event site visits. Data were analyzed through descriptive statistical synthesis of reported impacts and qualitative thematic analysis of institutional and environmental response patterns.

Results: A total of 72 deaths were reported, 65 in Juiz de Fora and 7 in Ubá. More than 8,500 individuals were displaced, requiring emergency shelter in public facilities. The most affected locations were concentrated in territories with higher socio-environmental vulnerability, characterized by irregular land occupation, hillside settlements, and floodplain housing. In the Paraibuna River basin (Juiz de Fora), rainfall exceeded historical averages, leading to river overflow, soil saturation, and landslides. In the Pomba River basin (Ubá), limitations in urban drainage systems contributed to increased material losses and family displacement. Erosion processes, alterations in watercourses, and potential water contamination were documented. Institutional review identified gaps in early warning systems and limited operational capacity for coordinated human and animal emergency response. The displacement of domestic and wild animals into urban and shelter areas altered human–animal interfaces under compromised sanitation conditions, increasing the potential for zoonotic transmission and environmental contamination.

Conclusion: The events analyzed illustrate that climate vulnerability encompasses exposure, infrastructural fragility, and urban sustainability constraints. The findings indicate that environmental degradation, animal displacement, and human health impacts operated as interconnected components of a single territorial process. These results support the relevance of integrated climate adaptation strategies, improved urban planning, and coordinated human–animal–environment surveillance to strengthen territorial resilience.





1094 – Monkeypox Virus in Rattus norvegicus: One Health evidence from mpox Case Household Surveillance in Nigeria

Adeyinka ADEDEJI (1), Clement MESEKO (1), , Ismaila SHITTU (1), Nicodemus MKPUMA (1), Mpox TEAM (1,2,3,4,5), Maryam MUHAMMED (1), Shelley LEE (6), Chioma ACHI (6), Hilary BOWER (6), Gwenda HUGHES (6)

1: National Veterinary Research Institute Vom Nigeria, Nigeria; 2: Rivers State Ministry of Agriculture, Port Harcourt, Nigeria; 3: Ogun State Ministry of Agriculture, Abeokuta, Nigeria; 4: Nigeria Centre for Disease Control and Prevention, Abuja, Nigeria; 5: Niger Delta University, Wilberforce Island, Amassoma, Bayelsa State, Nigeria; 6: London School of Hygiene & Tropical Medicine, United Kingdom

Background: After a 40-year hiatus, mpox, a zoonotic disease caused by monkeypox virus (MPXV) reemerged in 2017 in Nigeria. Although human mpox cases are frequently reported in Nigeria, MPXV transmission pathways, including the animal reservoir status remain unknown. To better understand transmission dynamics, we conducted a survey in Ogun and Rivers States, which are considered mpox high-burden States, from April 2024 to October 2025.

Methods: The study focused on households with confirmed human mpox cases. Rodents were trapped and hard surfaces swabbed within 14 days of mpox case confirmation in these households. We enrolled 56 consenting households, sampled 1362 rodents/small mammals, and collected 1001 environmental hard-surface swabs.

Results: Analysis by real-time polymerase chain reaction of the rodent samples revealed detection of MPXV in 0.44% (6/1362). MPXV positive samples were detected in skin/visceral organs of Rattus norvegicus, linked to four case households. Also, MPXV was detected in 27.87% (279/1001) of environmental samples from 34 of 56 case households sampled. Furthermore, 19 MPXV whole genome sequences were generated from positive samples. Phylogenetic analysis confirmed all sequences belonged to MPXV Clade IIb and clustered with other strains sequenced in Nigeria since 2022.

Conclusions: Our findings offer new critical insights into mpox infection and transmission, highlighting rodents and the environment as potential source of MPXV at the human-animal-environment interface in households. Strengthening one Health risk-communication is key to reducing community transmission

1099 – Developing a One Health Career Toolkit: Supporting Veterinarians to Pave the Education-to-Employment Pipeline

Alice MATOS (1), Jennifer PUNT (2), Benjamin ANDERSON (3), Claire TUCKER (4), Amanda M. BERRIAN (1), Hayley BENSON (1)

1: Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, Columbus, Ohio, United States; 2: School of Veterinary Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, United States; 3: University of Florida, Gainesville, Florida, United States; 4: One Health Institute, Colorado State University, Fort Collins, Colorado, United States

Background: As the One Health (OH) approach gains global recognition and veterinarians are identified as key stakeholders, there is a growing need to integrate OH competencies into veterinary education and OH training programs. Despite the well-defined need for a robust OH workforce, OH is still seen as a “non-traditional” career path, where terminology, competencies and expected qualifications have yet to be matched between employers and job seekers. To help address these barriers, this project aims to develop a One Health Career Toolkit designed to support veterinary students and recent graduates entering or considering the OH workforce.

Methods: Our approach included three stages:

1) Employer Identification: Initial screening of OH employers was conducted from available directories (e.g., One Health Commission, North America One Health University Network) and guided by a large language model using predefined inclusion criteria (e.g., U.S.-based, cross-sectoral collaboration, employ veterinarians). This was followed by a manual review of results and brainstorming of additional organizations by the research team to build a comprehensive directory.

2) Job Advertisement Analysis: OH-related job postings were identified from stakeholders mapped in stage 1. Postings were analyzed using computer-assisted text mining and manual coding (NVivo 15) with codes informed by well-established OH frameworks to generate a preliminary set of keywords, competencies, and qualifications from the active job descriptions.

3) Employer Survey: Developed to assess employer expectations regarding veterinarians’ qualifications and skills in OH roles, expanding the results from stage 2. The survey was administered electronically to respondents drawn from the directory.

Findings will inform the development of a One Health Career Toolkit, which will include a searchable employer directory, frequently cited skills and competencies, as well as job titles and keywords to aid job seekers.

Results: To date, 268 employer organizations have been identified; 116 were classified as potential OH employers, with hiring pathways for veterinarians. Employers include non-profit (n=46), government (n=28), educational (n=27), for-profit (n=12), and intergovernmental organizations (n=3). Organizations working at the human-animal-environment interface without an explicit OH scope (e.g., museums) or clear hiring pathways (e.g., professional associations) were included in subsequent stages to explore untapped opportunities and highlight the potential value of the OH approach and veterinarians’ role to

unengaged stakeholders. Stages 2 and 3 are in progress with expected completion by August 2026, with the final Toolkit expected to be developed by December 2026.

Conclusions: Insights gathered through this U.S.-based OH market analysis will shape our continued understanding of OH careers and competencies and aid the development of valuable tools and strategies for the emerging workforce, paving the education-to-employment pipeline. The Toolkit may help attract veterinary graduates to this expanding field, support employers in reaching suitable candidates, and aid training institutions in their curriculum development, ultimately strengthening the OH workforce.

1106 – Interpreting human brucellosis trends in pastoral Kenya: health system influences and implications for One Health surveillance and livestock disease control

Buke Yussuf WAKO (1,2), Shauna RICHARDS (1), Henriette VAN HEERDEN (2)

1: International Livestock Research Institute (ILRI), Kenya; 2: University of Pretoria, South Africa

Background

Brucellosis remains endemic in pastoral livestock systems in Kenya and continues to pose a significant zoonotic threat at the human–animal interface. In many endemic settings, human health facility data are frequently used to infer disease trends and inform livestock disease control strategies. However, variations in reported human cases may reflect changes in diagnostic practices, testing availability, and healthcare access rather than true epidemiological changes. This study examined retrospective human brucellosis trends in Isiolo County, Kenya, and explored healthcare professionals' perspectives to assess the reliability of hospital-based data for informing One Health disease control strategies.

Methods

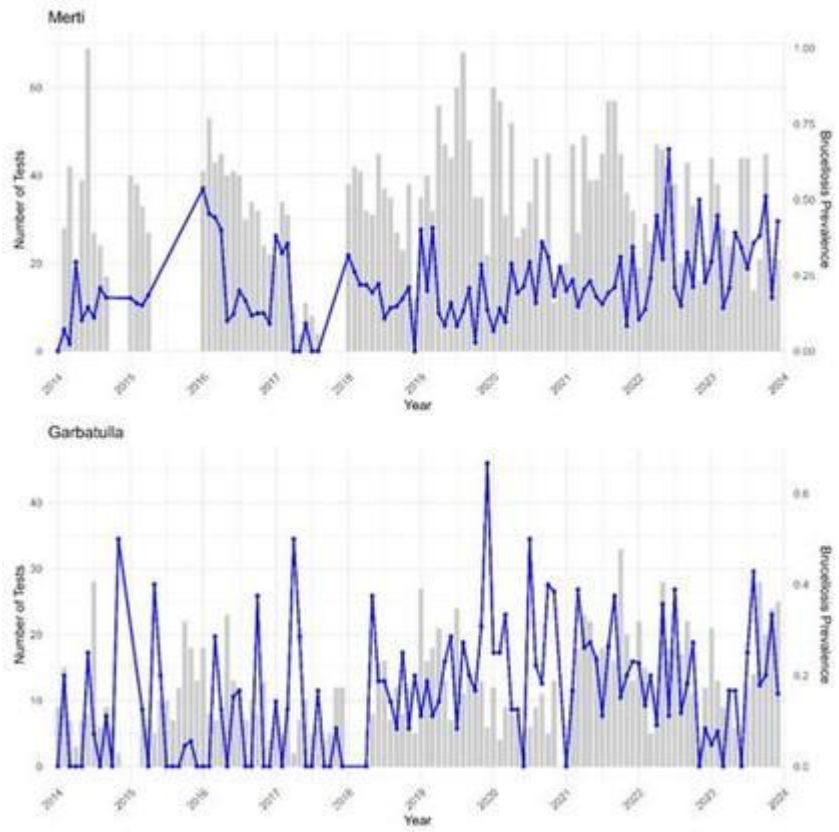
A mixed-methods retrospective study was conducted using hospital laboratory records from three public hospitals in Isiolo County, Isiolo County Teaching and Referral Hospital, Garbatulla District Hospital, and Merti District Hospital covering the period 2014–2023. Quantitative analysis examined testing frequency, number of positive cases, positivity proportions, and cases relative to total hospital admissions to assess trends over time. Qualitative data were collected through key informant interviews with healthcare professionals, including clinicians (n=6), laboratory personnel (n=13), and community health promoters (n=39), to explore diagnostic practices, testing criteria, and perceptions of brucellosis trends.

Results

Between 2014 and 2023, a total of 6,817 patients were tested for brucellosis, of whom 1,254 tested positive using the febrile Brucella agglutination test. While some healthcare professionals perceived increasing case numbers, quantitative analysis indicated that apparent increases often coincided with expanded testing rather than consistent changes in positivity proportions. Positivity rates and cases relative to total hospital admissions remained relatively low and stable across the decade. Differences between hospitals reflected variation in diagnostic availability, clinician-driven testing practices, and healthcare access. Interviews further showed reliance on a single screening test, limited access to confirmatory diagnostics, and structural barriers affecting timely diagnosis and treatment.

Conclusions

Human brucellosis trends derived from routine hospital data in Isiolo County appear to be strongly influenced by diagnostic practices and health system factors rather than clear changes in transmission dynamics. These findings highlight important limitations in using human surveillance data alone to infer livestock infection pressure or evaluate zoonotic disease control efforts. Strengthening confirmatory diagnostic capacity, harmonizing case definitions across sectors, and integrating human and animal health surveillance systems are critical steps toward more effective OH brucellosis control in pastoral production systems.



1118 – Addressing Wicked Problems through Veterinary Education: Rethinking Day-1 Competencies for Pastoralist Service Delivery in Ethiopia

Maria P. COUTO (1), Alice MATOS (1), Ashenafi SYOUM (2), Fikadu ALLEMU (3), Dereje ABERA (4), Latera S. KARO (5), Seleshe N. WOLDEGEBREAL (6), Armando E. HOET (1), Amanda M. BERRIAN (1)

1: Department of Veterinary Preventive Medicine, College of Veterinary Medicine, The Ohio State University, United States of America; 2: College of Veterinary Medicine and Animal Science, Samara University, Ethiopia; 3: College of Veterinary Medicine, Jigjiga University, Ethiopia; 4: School of Veterinary Medicine, Wollega University, Ethiopia; 5: School of Veterinary Medicine, Borana University, Ethiopia; 6: College of Veterinary Medicine and Animal Sciences, University of Gondar, Ethiopia

Background: Ethiopia's Veterinary Education National Action Plan (VEd-NAP, 2025–2028) was established to harmonize the national veterinary curriculum with WOAH Day-1 Competency (D1C) standards. While WOAH D1Cs provide a framework for National Veterinary Services, they do not address the specific demands of pastoralist and small-scale producer (SSP) contexts - Ethiopia's dominant livestock production systems, where human livelihoods, animal health, and ecosystem sustainability are deeply interconnected. The UN International Year of Rangelands and Pastoralists (2026) has recognized these livestock-dependent livelihoods as key to ecosystem and natural resources sustainability, advocating for greater investment in animal health services, pastoral mobility protection, and recognition of indigenous knowledge. Internationally harmonized veterinary curricula systematically fail to reflect these realities: while veterinary and ethnoveterinary services operate across pastoralist regions, no formal Day-1 curriculum reference or learning outcomes currently address them, leaving graduates formally untrained and unassessed for such veterinary delivery practices. In response, VEd-NAP established its Grassroots Needs Task Force (GRTF) - a community advisory body - to generate Ethiopia's first evidence base for contextually grounded D1C learning outcomes to enable veterinarians to provide high quality services to pastoralists and SSP.

Methods: Conducted across Ethiopia, with focus on pastoralist regions, this mixed-methods study integrates three components.

1) Stakeholder Mapping: identifies actors in animal health service delivery across regions, levels of operation (e.g., research, education & community service; policy & advocacy; implementation & capacity

building; restoration of livestock services) and sectors (e.g., inter-/governmental organizations, NGO, academia, community-based, private sector), characterizing motivations, scope of action, and resources at each level.

2) PRISMA-guided Scoping Review: synthesizes published and grey literature on veterinary interventions and service demands in pastoralist and SSP contexts, documenting service delivery status and knowledge gaps.

3) Stakeholder Outreach: assesses stakeholder perception of veterinary service delivery barriers and unmet needs, through structured questionnaires, semi-structured interviews, and multistakeholder focus group discussions.

Results: To date, 44 stakeholders have been mapped nationwide, spanning government veterinary services, NGOs, intergovernmental and academic organizations, community-based animal health networks, veterinary associations, and private sector actors. The three activities are expected to yield results by August 2026. Together, these evidence streams will (1) reveal where critical veterinary service gaps persist; (2) identify where established competency frameworks diverge from field realities and stakeholders' explicit knowledge and decision-making; and (3) show where veterinary practice already exceeds formal education.

Conclusions: This study will inform the development of formal learning outcomes for pastoralist and SSP veterinary service delivery, providing the framework for a contextually relevant D1C-harmonized veterinary curriculum in Ethiopia. Anchored in national and international regulatory priorities for pastoralist animal health and ethnoveterinary knowledge preservation, and built with the communities it aims to serve, this framework will equip veterinary graduates to navigate the wicked problems converging at Ethiopia's human-livestock-ecosystem interface.

1123 – PREVALENCE, ANTIBIOTIC RESISTANCE AND BIOFILM-FORMING ABILITIES OF Salmonella enterica FROM ADULT BIRDS AT SELECTED LIVE BIRD MARKETS AT OLUYOLE IBADAN, NIGERIA

Moturayo A. MAKANJUOLA, Olayemi K. BOLATITO, **Victoria O. ADETUNJI**
University of Ibadan Ibadan Nigeria, Nigeria

ABSTRACT

Background: Live bird markets (LBMs) integral to poultry commerce, are marked by widespread misuse of antibiotics and a consequent rise in antibiotic resistance. There are limited data that identified the factors that contributes to antibiotic usage and the development of antibiotic resistance in *Salmonella enterica* (*S. enterica*) from live birds (LBs) in Ibadan, Nigeria. This study therefore, evaluated antibiotic usage and stewardship, and determined the prevalence, antibiotic resistance and biofilm forming abilities of *S. enterica* from adult birds at selected live bird markets at Oluyole in Ibadan Nigeria.

Methods: This cross-sectional survey administered a semi-structured questionnaire to all consenting Live Bird Retailers (LBRs) in two LBMs, Oluyole Ibadan, Oyo State from March to August 2025. Data on LBMs characteristics, LBRs demographics, biosecurity, antibiotic usage, antimicrobial resistance (AMR), and preferred channels of information on antimicrobial stewardship (AMS) were gathered. Furthermore, fresh fecal samples were collected for detection of *S. enterica* from LBs of consenting LBRs using standard bacteriological assay. Isolates were tested for susceptibility to seven antibiotics (meropenem 10µg, tigecycline 15µg, tetracycline 30µg, cefotaxime 30µg, ceftazidime 30µg, ampicillin 10µg, gentamicin 10µg) belonging to 6 different classes using disc diffusion method. Also, biofilm forming abilities of *S.enterica*was determined using Crystal Violet Binding Assay. Biofilm formation was evaluated at incubation periods of 0, 12, and 24 hours.

Results:A total of 13 LBRs comprising of female (76.9%) and male (23.1%) participants were reported in the study. The ABs were mainly used for therapeutic and prophylactic (100.0%) purposes, and frequently used ones were tetracycline and metronidazole. Biosecurity practices were generally low among LBRs. The prevalence of *S.enterica*and multidrug resistant (MDR) *S.enterica*isolates at LBMs level were 6.15% and 81.3% respectively. Multidrug resistance to at least three different classes of ABs occurred in all of the two LBMs investigated. The multiple antibiotic resistance (MARI) of the *Salmonellaenterica*isolates (range; 0.6-to 1.0) and extremely high resistance rates were observed for cefotaxime and ampicillin (100.0%) and ceftazidime (93.8), while lowest rates for gentamicin (37.5%). A consistent increase of biofilm formation

from 0h to 12h and a reduction at 24h was observed. Likewise, both high and low biofilm forming isolates exhibited similar levels of antibiotic resistance.

Conclusion: This study detected multidrug-resistant *Salmonella enterica* among birds sold in these markets, indicating a potential hazard to both public health and food safety. These findings highlight the importance of strengthening hygiene practices and promoting more responsible antibiotic use among live bird retailers.

Word count :411

Table 1: Antibiotic Susceptibility Patterns of *Salmonella enterica* isolates from selected live bird markets at Oluyole in Ibadan

Antibiotic discConcentration	Total number Susceptible	Total number intermediate	Total number resistant	Percentage resistant (%
Meropenem(10µg)	-	2	14	87.5
Tigecycline (15µg)	3	5	8	50
Tetracycline(30µg)	3	-	13	81.3
Cefotaxime (30µg)	-	-	16	100
Ceftazidime(30µg)	-	1	15	93.8
Ampicillin (10µg)	-	-	16	100
Gentamicin(10µg)	10	-	6	37.5

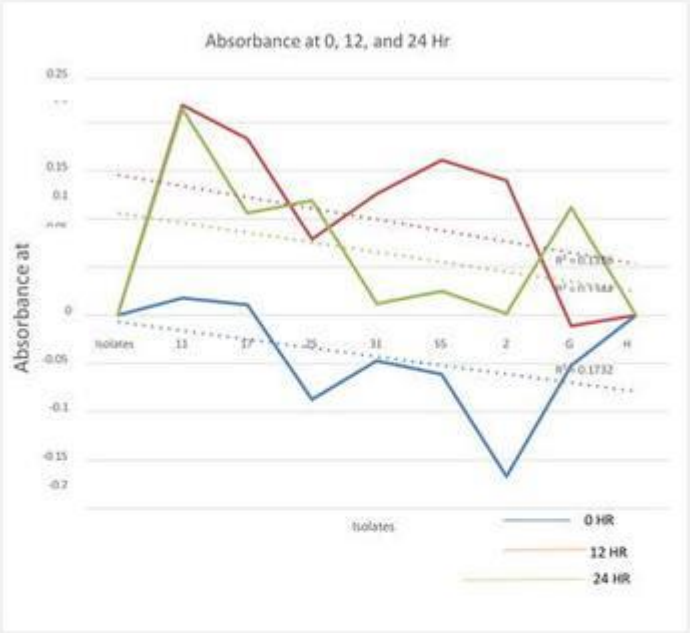


Figure 1: Biofilm formation in *Salmonella enterica* isolates at 0, 12,24 hours

1127 – A One Health Approach to Pandemic Risk Mapping: Landscape Heterogeneity, Biodiversity, and Human-Wildlife Contact in Washington State

Poojita GARG (1), Jared PALAZZA (2,3), Girish NARAYANSWAMY (1,4), Peter RABINOWITZ (2,3), John CHOE (5), Shwetak PATEL (1,4), **Julianne MEISNER** (2,6)

1: Paul G. Allen School of Computer Science and Engineering, University of Washington, Seattle, WA, United States; 2: Center for One Health Research, University of Washington, Seattle, WA, United States; 3: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA, United States; 4: Department of Electrical and Computer Engineering, University of Washington, Seattle, WA, United States; 5: Department of Industrial and Systems Engineering, University of Washington, Seattle, WA, United States; 6: Department of Global Health, University of Washington, Seattle, WA, United States

BackgroundNovel pathogen emergence accelerates at human-wildlife interfaces where ecological change, host communities, and human activity converge. This project develops high-resolution datasets for Washington State using remote sensing, citizen science, and AI to characterize three key risk factors: agricultural landscape heterogeneity, vertebrate biodiversity, and human-wildlife contact intensity.

MethodsWe conceptualize agricultural heterogeneity as the inverse of monoculture cropping and quantify it using crop-type diversity metrics including standard diversity indices, crop richness, edge density, patch size, texture-based metrics, and 3-year and 10-year crop rotation indicators. We then

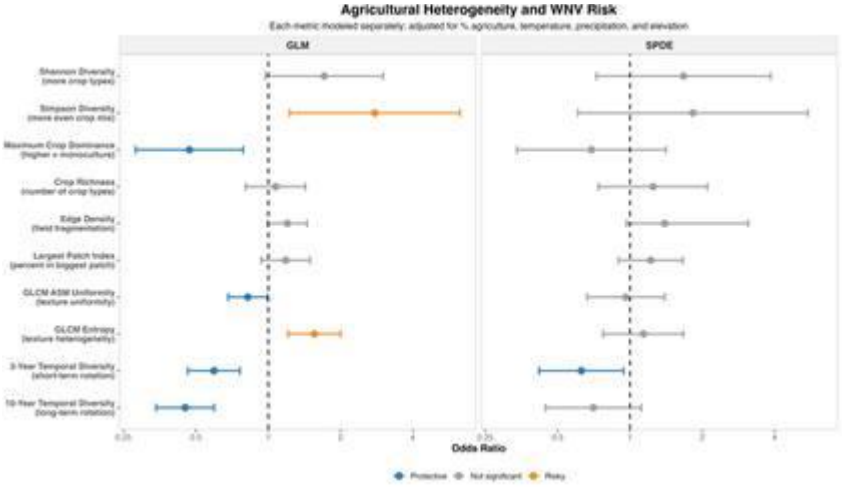
validated these metrics using vector surveillance data for West Nile virus (WNV). We applied separate logistic regression models (non-spatial GLM and spatial SPDE) for each heterogeneity metric, adjusting for percent agriculture, temperature, precipitation, and elevation.

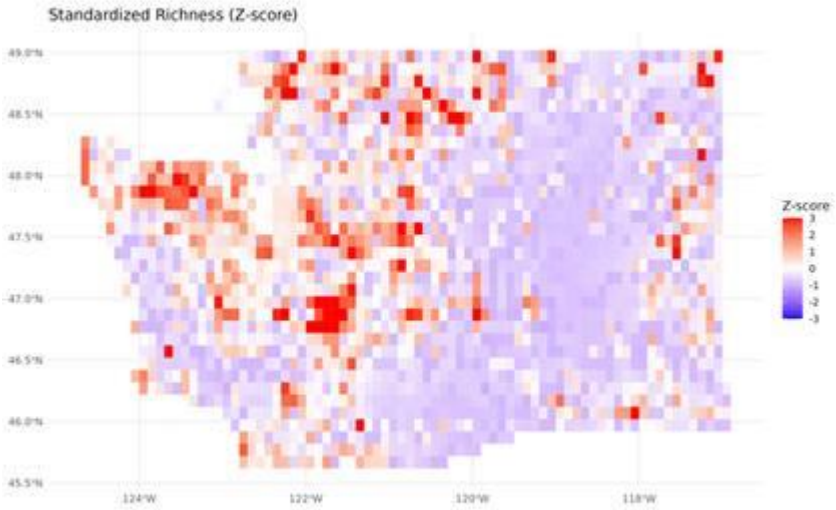
Human-wildlife contact intensity was approximated using VIIRS nighttime lights and Washington Trails Association trip reports as spatially and temporally explicit proxies for human activity in remote areas. Avian and mammalian biodiversity metrics were derived by integrating iNaturalist observations with IUCN range-based richness rasters. A detectability-correction framework was developed that classifies geographic areas by landscape accessibility and fits a generalized additive model to isolate ecological signal from citizen science sampling artifacts. Kriging was used to interpolate richness across unobserved areas.

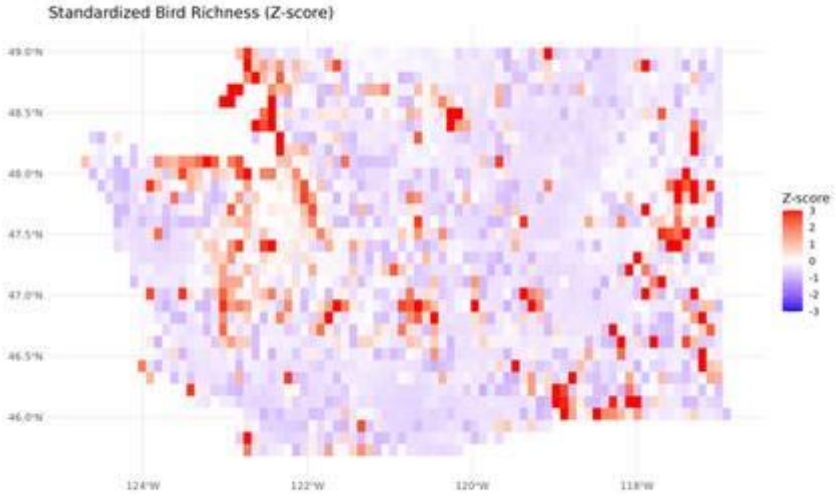
ResultsLand use classification using unsupervised machine learning and multimodal large language models applied to satellite imagery produced inconsistent results. We therefore used the USDA Cropland Data Layer to construct the agricultural heterogeneity metrics. Agricultural heterogeneity analyses did not reveal a consistent protective effect on WNV trap positivity: associations varied in direction and magnitude across metrics and model specifications (Figure 1). GLM models showed mixed effects including maximum crop dominance as protective: OR: 0.47 (95% CI: 0.28, 0.79) and Simpson diversity as risky: OR: 2.78 (95% CI: 1.23, 6.28), while SPDE models showed 3-year rotation diversity protective (OR: 0.59, 95% CI: (0.46, 0.76) (all other effects non-significant). Potential explanations include mismatch between cropland classifications and mosquito-relevant habitats, scale misalignment between landscape metrics and surveillance data, and unmeasured effects of specific crop types.

Preliminary dataset outputs include detectability-corrected avian and mammalian richness surfaces and human activity layers derived from nighttime lights and trail use density, together revealing spatial heterogeneity in biodiversity and human-wildlife contact that administrative-level data would obscure.

ConclusionThis project highlights the potential and limitations of using machine learning and large-language tools to build datasets for pandemic risk assessment. Pathogen emergence arises from interactions between land use, host communities, and human behavior that coarse regional data cannot capture, necessitating high-resolution proxies. Current language models are unreliable for consistent land use classification, and citizen science biodiversity data needs explicit correction for sampling artefacts to reliably reflect ecological reality. Nonetheless, combining innovative ecological proxies with advancing AI offers a promising frontier for disease emergence prediction.







1142 – Evaluation of the impact of the ALERT serious game on knowledge acquisition and stakeholder engagement in zoonotic disease surveillance

Mathias TALLA MBA (1,2), Sylvain DERNAT (3), Flaubert MBA DJONDZO (4), Marisa PEYRE (1,2), Ahidjo AYOUBA (5), Charles KOUANFACK (6,7), Marie-Marie OLIVE (1,2)

1: CIRAD, UMR ASTRE, Montpellier, France; 2: ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France; 3: INRAE, UMR Territoires, GAMAE, Aubière, France 4 : IRD, Yaoundé, Cameroun; 4: IRD, Yaoundé, Cameroun; 5: TransVIHMI, Univ. Montpellier, INSERM, IRD, Montpellier, France; 6: Centre de Recherche sur les Maladies Emergentes et Réémergentes (CREMER), Yaoundé, Cameroon; 7: Univ Dschang, Yaoundé Cameroun

Background. Local stakeholders are at the forefront of zoonotic disease emergence. Their involvement in zoonotic pathogens surveillance is therefore essential for early detection, particularly in Cameroon where outbreaks repeatedly emerge (1). Innovative tools, such as serious games, are developed to strengthen stakeholders' engagement in many fields, including health. The ALERT board game was developed with

the aim of improving the knowledge and engagement of actors working at the human-animal-environment interface for zoonotic diseases surveillance by strengthening good practices through a One Health approach. Players collaborate to prevent emergence by enhancing health information flows from citizens to central authorities through event-based surveillance (2). The present study aims to assess the short and middle terms effects of the game.

Methods. The study was conducted in Campo district in the southern region of Cameroon. It mobilised local and decentralized actors from animal, human and environmental sectors and members of civil society. The evaluation protocol used is based on Kirkpatrick's model (3)(4). The evaluation framework covers the first three levels of the model: Reaction (Criteria 1), Learning (Criteria 2) and Willingness to commit (Criteria 3) (Figure 1). Reactions during and after the game, knowledge acquisition, new attitudes to adopt, and actions to be implemented to strengthen existing surveillance systems were assessed during an initial phase. Five months later, a follow-up study was conducted to identify the actions implemented after the game, the main constraints encountered by participants, the factors likely to influence the game's effects, and the key requirements for the practical implementation of these actions. A multisectoral process was adopted to identify the areas of support requested by participants and to determine the most appropriate strategies to implement. Data were collected using observation, Likert scale, participatory methods, semi-structured interviews and focus groups. Descriptive statistics analyses were performed to the observational and participatory data and thematic analysis from interviews.

Results. A total of 28 participants were involved in the process. Results of the criterion 1 show satisfactory reactions from participants, criterion 2 reveals acquisition of multiple knowledge, and in criterion 3, potential for diverse post-game actions (Figure 2 and Table 1). Logistical and communication constraints were identified during the implementation of post-game actions. Supporting areas were grouped into three categories: those addressed within this research project, those supported by the participants themselves, and those relating to public institutions, each linked to implementation strategies proposed by the participants.

Conclusion. Our study highlights the game's potential to convey knowledge tailored to different participant profiles, while promoting engagement of zoonotic diseases surveillance and encouraging concrete action in the field. The evaluation process will be pursued to assess the long-term effects of the game on the changes of surveillance practices.

Figure 1 : General framework for assessing the effects of the ALERTE game

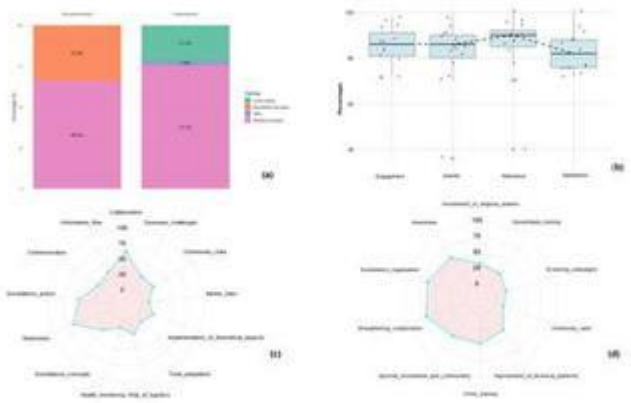


Figure 2: Aggregated figures from descriptive analyses (a) distribution of scores by type of elements observed (criterion 1), (b) distribution of scores for each attribute resulting from participants' assessments (criterion 1), (c) radar chart showing the distribution each knowledge category (criterion 2), (d) radar chart showing the distribution each category of action to be implemented (criterion 3).

Table 1: an overview of the main results of criteria 2 and 3

Criterion	attributes	Results obtained
Criterion 2	Knowledge	Knowledge of surveillance, Cross-sector collaboration, stakeholders of surveillance
Criterion 3	potential of actions	Involvement and awareness-raising, strengthening collaboration at local level
	Actions implemented	Promotion of cross-sector collaboration, raising awareness among new stakeholders.
	Constraints	Logistical and communication, mentalities and the reluctance of communities.
	Influencing factors	Impact of projects in study site, other research work
	Requirements	material, logistical and financial needs, training and capacity-building needs.

1145 – Environment and Health program manager

Oxana KRAVTSOVA
Regional Environmental Centre for Central Asia (CAREC), Kazakhstan, iNGO

Central Asia: A "One Health Frontier" – Building Resilience at the Crossroads of Continents

Background: Central Asia stands at a critical ecological and geopolitical crossroads, connecting Europe and Asia along major migratory flyways, expanding livestock trade routes, and zones of rapid environmental transformation. Glacier melt, desertification, and land degradation combined with increasing cross-border movement of people and goods create conditions where zoonotic diseases and antimicrobial resistance can emerge and spread. Yet the region's health security infrastructure remains a legacy of fragmented, post- Soviet systems, with limited cross- sectoral collaboration between human, animal, and environmental health services.

In response, Central Asian governments have made significant progress. In November 2023, the five countries endorsed the Central Asia One Health Framework for Action - a regional strategy laying the groundwork for cooperation. A $130 million regional program, supported by the World Bank, the Pandemic Fund, and the Health Emergency Preparedness and Response Trust Fund, was launched in 2025 to implement this framework through coordinated action across health, agriculture, and environment sectors. A key outcome is the establishment of Central Asia's first regional One Health coordinating entity, hosted by the Regional Environmental Centre for Central Asia (CAREC). This Secretariat provides a neutral platform for ministries to align priorities, develop joint risk assessments, and build multi- sectoral capacity creating a concrete mechanism for channeling investments into prioritized activities.

This session addresses a practical question: how does a region move from political commitment to funded, coordinated implementation? It will explore the processes that enabled Central Asia to develop compelling regional narratives linking health, environment, and economic resilience that mobilized significant financing. Presenters will share lessons from building cross-sectoral and cross-border cooperation, establishing new coordination structures, and translating regional strategies into investable programs.

The session connects to multiple congress themes: climate change and ecosystems (Theme 1), governance and policy frameworks (Theme 8), One Health implementation and financing (Theme 9), preparedness and resilience (Theme 10), and private sector engagement (Theme 12). Speakers include Central Asian government representatives, the World Bank, and the Regional One Health Secretariat, ensuring diverse perspectives from those driving this work.

Participants will gain insight into Central Asia's distinct challenges and opportunities, understand how the Regional Secretariat functions as an entry point for partners, and learn about specific investment areas ready for support, including surveillance systems, laboratory networks, and cross-border response capacity. They will also explore financing pathways beyond traditional aid, including links to climate adaptation funds, blended finance, and private sector engagement.

The takeaway is practical: a clearer understanding of where Central Asia fits in the global One Health picture, what the region needs, and how interested partners can engage through an established regional mechanism

WORLD BANK GROUP

ONE HEALTH Central Asia
Humans·Animals·Ecosystems

carec

1152 – Slaughterhouse wastewater shows potential for AMR surveillance by reflecting pig-associated AmpC-producing Escherichia coli

Olga TYNI (1), Kirsi-Maarit LEHTO (2), Johanna HAAVISTO (3), Seija PIHLAJAVIITA (3), Ahmad Ibrahim AL-MUSTAPHA (1), Annamari HEIKINHEIMO (1,4)

1: Department of Food Hygiene and Environmental Health, Faculty of Veterinary Medicine, University of Helsinki, Finland; 2: Faculty of Medicine and Health Technology, Tampere University, Finland; 3: Atria Plc, Seinäjoki, Finland; 4: Finnish Food Authority, Seinäjoki, Finland

Background

Wastewater-based surveillance has shown potential for monitoring antimicrobial resistance (AMR) in humans, but its feasibility to animal AMR surveillance is poorly investigated. Slaughterhouse wastewater could serve as a pooled microbial sample of processed animals, thus cost-effectively complementing existing surveillance programs.

Slaughterhouse wastewater surveillance contributes to cross-sector One Health AMR monitoring, as the wastewater is directed into municipal wastewater treatment and ultimately reaches the environment.

The objective of this research was to evaluate whether slaughterhouse wastewater contains AmpC/ESBL-producing *Escherichia coli* (AE-EC) similar to those in slaughter pigs and could therefore serve as a surveillance tool.

Methods

Animal sampling was conducted on two visits to a Finnish pig slaughterhouse. Cecal content from 121 slaughter pigs was pooled by slaughter batch, resulting in 12 pooled samples from 9 batches. On the same visits, slaughter-line wastewater from five sampling points (n=10) and food-factory wastewater (n=1) were collected.

Monthly influent (n=9) and effluent (n=8) wastewater were collected from the on-site wastewater pretreatment plant between February and November 2025. Influent originating from the slaughter line was pretreated, and the resulting effluent was discharged to the municipal treatment plant. All samples were grab samples except the effluent was a 24-h composite.

AE-EC were isolated and characterized phenotypically and genotypically. A subset underwent whole-genome sequencing (WGS). Core-genome Multilocus Sequence Typing (cgMLST) was used to determine genetic relatedness between the animal and wastewater isolates.

Results

AE-EC was detected in 26/28 wastewater samples (93%) and 9/12 cecal pools (75%), representing 6/9 slaughter batches (67%).

The sequences (n=42) formed three cgMLST clusters. The largest cluster (n=31) comprised ST88:H9 with AmpC-promoter mutation C-42T, found in 9/9 influent (100%), 7/8 effluent (88%), and 7/10 slaughter-line wastewater samples (70%), and in 2/6 AE-EC-positive slaughter batches (33%).

The second cluster (n=4) comprised ST88:H12:C-42T isolates from 1/10 slaughter-line (10%), 1/1 food-factory wastewater samples (100%), and 2/6 AE-EC positive batches (33%).

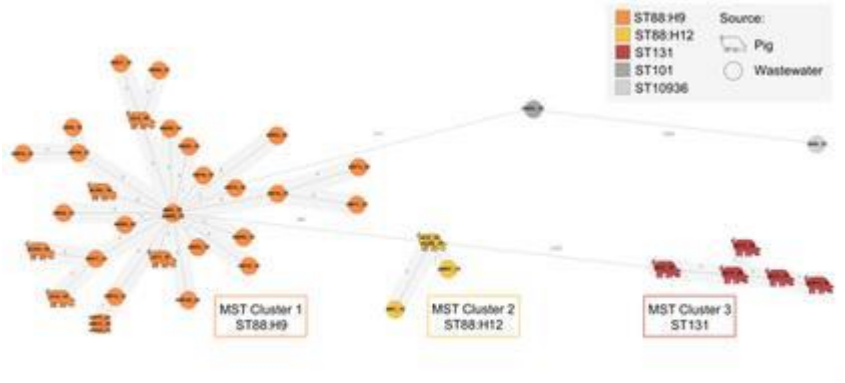
The third cluster (n=5) contained ST131 with AmpC-promoter mutation T-32A, from 3/6 AE-EC-positive slaughter batches (50%). Notably, ST131 was not detected in wastewater.

Conclusions

ST88:H9:C-42T was consistently detected in wastewater throughout the study, with the same strain also detected in pigs. This suggests either wastewater persistence or repeated introduction to wastewater. In national surveillance, C-42T is the most prevalent AmpC/ESBL determinant in pigs. In our study, C-42T was associated with ST88, which supports its spread in the pig population.

The most widespread strain among pigs, ST131:T-32A, was not detected in wastewater. It is possible that wastewater sampling and methodology favor other ST-types, or the number of isolates is insufficient.

Pig-associated AmpC-*E. coli* was detected in wastewater, supporting the potential of slaughterhouse wastewater for AMR surveillance. However, ensuring detection of all major strains will require further investigations, increased sampling, and systematic comparison with animal surveillance data.



Minimum spanning tree based on cgMLST showing genetic relatedness among 42 AmpC/ESBL-producing *E. coli* isolates from pigs and slaughterhouse wastewater. Clusters defined as ≤10 allele differences.

1158 – Using a multi-stakeholder One Health approach to improve rural livestock health care: A case study for community-based livestock health surveillance and community empowerment

Tedson NKOANA (1), Wanda MARKOTTER (1,2)

1: Future Africa Platform, University of Pretoria, South Africa; 2: Centre for Viral Zoonoses, Medical Virology, Faculty of Health Sciences, University of Pretoria, South Africa

Background

Livestock farming plays a critical role in the economic stability of many rural communities in Africa. In rural communities, farming is often categorized as communal and smallholder owing to the practice of keeping livestock for sustenance and economic benefit in shared pastural lands. Although this type of farming curbs food insecurity and economic instability, it is susceptible to the effects of common livestock diseases, some of which are zoonotic. This study explored a multi-stakeholder One Health approach to livestock health care improvement in a rural, under-resourced community by (1) improving

community-level animal health care practice through multi-stakeholder disease training and awareness education, and (2) tracking temporal cattle health through a livestock health surveillance system.

Methods

The site was the rural community of Ga Mampa, Limpopo Province, South Africa. The animal health care awareness targeted livestock owners and made use of knowledge from private, government and research actors as well as the community. Disseminated knowledge included general care, disease control and links to One Health. The training targeted three individuals from the community who were trained on disease identification, prevention and treatment, and animal production and management. The livestock health surveillance had a target of 720 cattle observations for 12 months, which tracked tick load per cattle, udder condition, body condition score and skin condition. Data was collected using the KoboToolBox (v2024.2.4), which can function offline via a cellphone application.

Results

The tracked health parameters all showed an upward trajectory of improvement in the cattle (Figure 1). Observations of ticks and swelling on the udder, which affect production and nursing ability in cows, gradually decreased as the year progressed. Likewise, observations of wounds and abscesses on the skin of cattle also decreased. The tick load remained variable throughout the year. A spike in tick load was linked to dip resistance. Acceptable cattle body condition scores (2 and 3) were not progressively observed, which could be attributed to poor nutrition, climate- linked stress, and tick-borne disease.

Knowledge dissemination workshops were attended by most of the farmers in the community. This positive response was reciprocated through regular dialogue check-ups during cattle dipping days to ensure knowledge translates to practice.

Conclusion

Data collection showed trackable evidence of cattle health improvement in the sampled herd. Tracking temporal health trends further functioned as an early detection tool, which in this instance was used to improve dip effectiveness. The effects of zoonotic risk in the wildlife-livestock-human interface are also an important yet unstudied factor in this community. The animal health care training empowered trainees with skills that can potentially open economically viable opportunities in future. Overall, this study has shown the impact of a community-driven multistakeholder intervention to improve livestock health in a low-resource, rural setting.

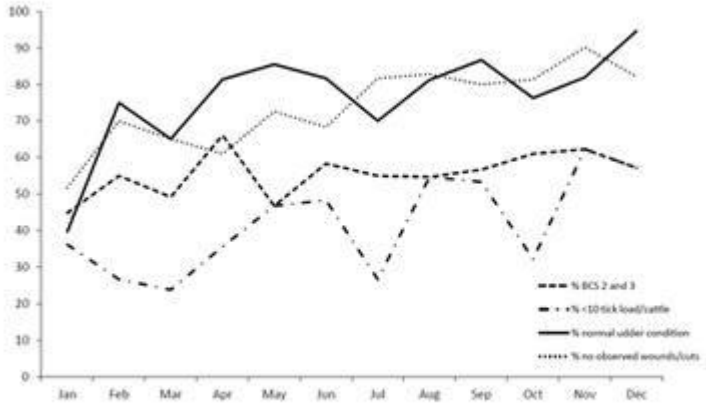


Figure 1: A depiction of the proportion of cattle with positive health indicator rankings including: body condition scores (BCS) of two (obvious frame) and three (well-balanced frame and covering), tick load of <10/animal, normal udder condition (no ticks and swelling), and normal skin condition (no observed wounds, cuts and abscess).

1161 – Bacterial resistance of Salmonella spp. in foals in Mexico: a one-health perspective

Valeria Jazmín RODRIGUEZ VILLAVICENCIO, **Linda Guiliana BAUTISTA GÓMEZ**
Universidad Autónoma del Estado de México, Mexico

Introduction. Salmonellosis is a zoonotic disease found worldwide and considered one of the most significant infections in both public and animal health, as it is linked to diarrhoea in humans and various animal species, including horses. In a global context in terms of human health, the WHO estimates that 11

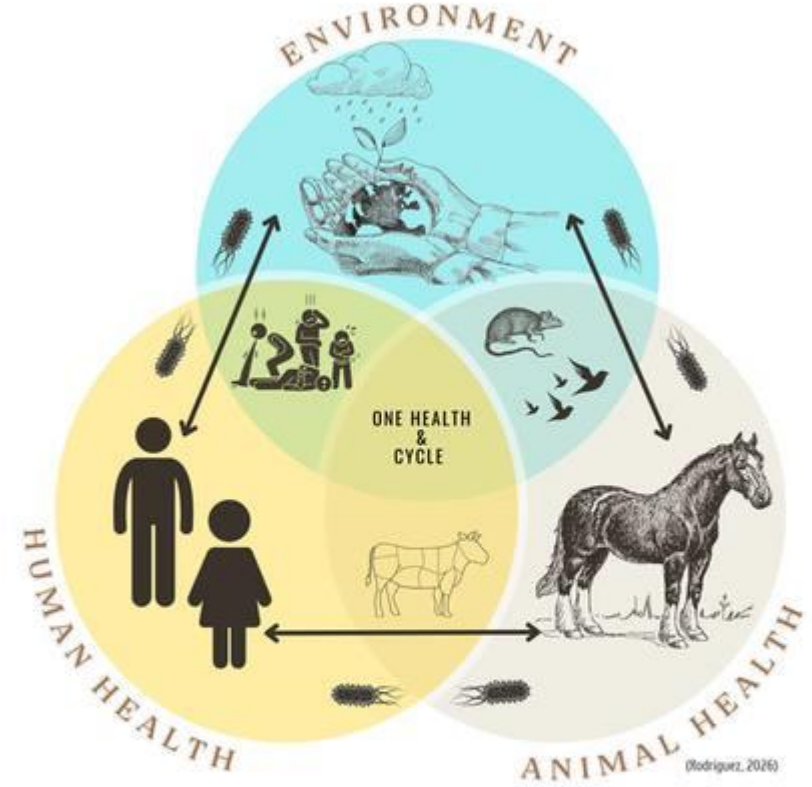
to 20 million people worldwide fall ill each year, of whom between 128,000 and 161,000 die. In terms of animal health, specifically in horses, the prevalence of salmonellosis is also global, and in countries with a large horse industry, such as the United States, Europe, and Australia, it is considered a notifiable disease because outbreaks can affect multiple horses and because of the high zoonotic potential it represents for humans and other animal species. In addition, since 2017, the WHO has compiled, for the first time, a list of antibiotic-resistant 'priority pathogens,' which includes the 12 families of bacteria most dangerous to human health, among which is *Salmonella* spp. Therefore, the objective of this study was to identify Salmonella spp. in samples from foals with diarrhoea from central Mexico and to evaluate their antimicrobial resistance profile.

Method. In this study, biological samples were collected from foals with enteric signs from the centre of the country. The samples were rectal swabs and were processed using conventional bacteriological culture techniques. Once the isolates were obtained, antimicrobial susceptibility tests were performed using an antibiogram in Mueller-Hilton Agar medium. Antimicrobial susceptibility testing and interpretation of results were based on values established by the Clinical and Laboratory Standards Institute for Enterobacteriaceae.

Thirteen antimicrobials commonly used in gastrointestinal diseases in humans and horses, belonging to seven classes, were tested. The ATCC reference strain E. coli 25922 and ATCC Salmonella Typhimurium 14028 were used to control the antimicrobial susceptibility tests.

Results. Seven out of 29 strains of Salmonella spp. were found to be resistant to 50% of antibiotics commonly used in humans and animals to treat salmonellosis, suggesting a danger to 'one health' considering its mode of transmission and reproduction cycle, as according to global studies, this bacterium does not respect species or locations.

Conclusion. The isolates showed resistance to antimicrobials frequently used in veterinary practice, which not only limits therapeutic options for horses, but also increases the risk of persistence and spread of resistant bacteria in equines, stables, veterinary hospitals and the environment. Therefore, from an epidemiological perspective, the detection of multidrug-resistant profiles in horses is a critical indicator of the role these animals can play as key points in the AMR transmission chain, since horses often travel between different regions, facilitating the geographical spread of resistant bacteria and increasing the possibility of outbreaks associated with zoonoses.



1173 – Strengthening One Health Capacity and Coordination for AMR in West Africa

Athina PAPADOPOULOU (1,4), Jazmin CONWAY (2,4), Andrew JOSEPH (1,4), Elizabeth MARIER (3,4), Alpha Ahmadou DIALLO (5), Solomon OLORUNLEKE (6), Kofi AFAKYE (7), Esther DSANI (8), Rene BESSIN (9), Kululeko DUBE (9), Jacqueline LICHOTI (9), Craig BAKER-AUSTIN (1,4), Ahmadou Tidiane NIANG (5), **Roderick M. CARD** (2,4)

1: Centre for Environment Fisheries and Aquaculture Science, Weymouth, United Kingdom; 2: Animal and Plant Health Agency, Addlestone, United Kingdom; 3: Veterinary Medicines Directorate, Addlestone, United Kingdom; 4: UK FAO Reference Centre for Antimicrobial Resistance, United Kingdom; 5: Food and Agriculture Organisation of the United Nations, Dakar, Senegal; 6: Food and Agriculture Organization of the United Nations, Abuja, Nigeria; 7: Food and Agriculture Organization of the United Nations, Accra, Ghana; 8: Food and Agriculture Organization of the United Nations, Regional Office for Africa, Accra, Ghana; 9: Food and Agriculture Organisation of the United Nations, Freetown, Sierra Leone

Background

Antimicrobial resistance (AMR) threatens human, animal, plant, and environmental health. An effective response requires a One Health approach that extends into non-human sectors, where data can be sparser, capacity for surveillance lower, and policies less well developed. We report on a grant that supported Ghana, Nigeria, Senegal, and Sierra Leone to strengthen AMR surveillance systems in animal, aquaculture, plant, and environmental domains by: (1) strengthening regional coordination; (2) providing technical assistance for capacity strengthening; (3) promoting practitioner engagement to mobilise action on AMR and antimicrobial use (AMU).

Methods

Following country needs assessments and an inception planning process that ensured alignment with existing programmes, we implemented a multi-theme package with significant emphasis on animal, aquaculture, plant, and environmental domains. **Regional collaboration**: established a cross-country Expert Network Group; conducted reviews of AMR strategies, active surveillance sampling plans, and laboratory protocols, focusing specifically on animal, aquaculture, and environmental systems. **Capacity strengthening:** e-learning, webinars, and tailored in-country and regional laboratory training for antimicrobial susceptibility testing, aquaculture and environmental microbiology, antimicrobial consumption (AMC), and antibiotic residues in food-of-animal-origin. **Practitioner engagement**: piloting Aquaculture Farmer Field Schools in Ghana; design and deployment of questionnaires for AMU assessments in crop and aquaculture sectors across all four countries.

Results

Regional collaboration: A standing Expert Network Group convened a cross-sector community (veterinary, policy, diagnostics, food safety), improving comparability and expertise sharing. Coordinated surveillance strategy reviews delivered consolidated insights and practical recommendations to align national strategies and sampling plans with One Health priorities, within animal, aquaculture, and environmental domains.

Capacity strengthening: Over 90 professionals were trained on residue and AMC surveillance and residue testing. Two national and one regional hands-on laboratory training events reached >50 professionals from human, animal, aquaculture, and environmental sectors. These activities improved Quality Assurance practices and readiness for active surveillance.

Practitioner engagement: The region's first Aquaculture Farmer Field Schools (FFS) were piloted in Ghana, engaging >80 participants (facilitators, farmers, and fisheries staff) to support disease recognition, AMU data generation, and rational use. A framework for future Aquaculture and Poultry FFS was developed for Nigeria. Poultry FFS were initiated in Senegal through workshops and training 18 facilitators. Crop and aquaculture AMU surveys were deployed across the four countries with over 1,000 and 300 farmer responses respectively, addressing major evidence gaps at the agriculture–environment interface.

Conclusions

A regional, theme-based One Health model can accelerate country progress by coupling technical strategy review with workforce development and front-line practitioner engagement. We created durable platforms, strengthened laboratory competence for credible AMR/AMU/residues data generation, and produced actionable recommendations to align national strategies with implementation realities. This integrative approach was well aligned to national priorities, directly filling operational AMR delivery gaps essential for One Health, and offers a transferable model for broader application.

1177 – Human Leptospirosis in a Peri-Urban Landscape: Insights from Odisha, India through a One Health lens

Debaprasad PARAI, **Rachita PRADHAN**, Debdutta BHATTACHARYA, Sanghamitra PATI
ICMR Regional Medical Research Centre, Bhubaneswar, India

Introduction:

Leptospirosis, caused by *Leptospira* spp., is an emerging zoonotic disease of increasing public health concern in India. In Odisha, recurrent outbreaks are frequently reported following monsoon rains and flooding events, highlighting the role of environmental conditions in disease transmission. Despite evidence suggesting endemic circulation of the pathogen, there remains a paucity of literature on the community-level seroprevalence of leptospirosis in the state. Peri-urban regions are particularly vulnerable, as they often experience frequent human-animal interactions, inadequate sanitation, and seasonal waterlogging that facilitate pathogen persistence and transmission. Therefore, this study aimed to assess the seroprevalence of leptospirosis, identify associated risk factors, and delineate its transmission dynamics in a peri-urban cohort in Odisha, India.

Materials and Methods:

A community-based cohort study was conducted in the two administrative blocks (Balianta and Balipatana) of Khordha district, Odisha, including 1252 individuals from six villages. Sociodemographic and exposure-related data were collected through a standardized questionnaire covering household environment, livestock ownership, presence of rodents, and community knowledge, attitudes, and practices (KAP) toward leptospirosis. Blood samples were collected both from human and livestock to detect antibodies against *Leptospira spp.* using ELISA and MAT, respectively. Geospatial mapping was carried out to corelate the distribution pattern of positive cases with nearby water bodies.

Results:

Among 1,252 participants, the median age was 42 years (IQR: 32-54), with 66.6% females. IgG seroprevalence, indicating past exposure, was 28.3% (n=354), while IgM seroprevalence was 12.7% (n=159). Households with livestock had higher IgG seropositivity compared to those without. Livestock samples tested using MAT also showed evidence of *Leptospira* exposure, and the distribution of MAT-positive livestock corresponded with higher human seropositivity in the same households. Leptospirosis risk was higher among individuals with livestock ownership (AOR: 2.25, 95% CI: 1.70-2.97) and those reporting rodents in their households (AOR: 3.89, 95% CI: 2.42-6.24), whereas living in pucca houses significantly reduced the risk (AOR: 0.32, 95% CI: 0.20-0.50). Geospatial analysis identified seropositive clusters closer to water bodies commonly used for both human and animal activities. Awareness about leptospirosis was low, with only 10.15% of participants having heard of the disease.

Conclusion:

The high seroprevalence of leptospirosis, coupled with poor community awareness, underscores the urgent need for integrated One Health-based interventions, including community education, enhanced diagnostic and surveillance systems, and targeted preventive strategies to mitigate transmission in endemic peri-urban regions of Odisha.

1189 – A One Health and Social-Ecological Systems framework for pastoralism: the case of northern Kenya

Sirimon THOMAS (1,2), Rowan JACKSON (1)
1: University of Edinburgh, United Kingdom; 2: International Livestock Research Institute (ILRI), Kenya

Background: Pastoralism is a well adapted but threatened livelihood in Arid and Semi-Arid Lands (ASALs), which cover roughly 80% of Kenya. However, pastoral systems face persistent challenges including malnutrition, water insecurity, zoonotic diseases, and environmental degradation, exacerbated by climate change and population growth. Addressing these challenges requires moving beyond siloed interventions towards integrated frameworks that consider the complex interdependencies within pastoral systems.

This work explores the combined application of Social-Ecological Systems (SES) theory and the One Health approach to pastoralism in northern Kenya, through the challenges of food security, water security and health.

We propose an integrated SES and One Health framework and demonstrate its utility through a case study of pastoralism in Marsabit County, Kenya. By recognising cross-scale interactions, interdisciplinary dynamics, and system-level outcomes, this approach offers practical pathways to advance Sustainable Development Goals (SDGs) in pastoral regions. The insights presented serve as a call for systems thinking and interdisciplinary collaboration to design interventions that are adaptive, inclusive, and resilient.

Methods: To examine the efficacy of a combined One Health and SES framework, the nature of water security, food security and health in pastoral communities in Marsabit County, northern Kenya, is selected as a complex, multi-dimensional case study that spans human, animal and ecosystem health.

Results: We find that the One Health approach is fundamental to understanding interactions between components of the broader SES due to the pillars of One Health overlapping with the basic components of pastoral systems. This includes equal consideration of people, livestock, wildlife and pathogens as users in the system, recognition of the role of zoonotic disease in human and animal health, and a focus on the basic resources such as grazing and water, which sustain pastoral livelihoods.

We also find that the SES framing is powerful for organising pastoral system components, and understanding how wicked problems arise and can be tackled in these complex adaptive systems. This approach promotes interdisciplinarity in development interventions, in turn promoting sustainability and cost efficiency.

The integration of the two frameworks highlights the One Health dynamics in the system and provides an organising structure for prioritising, designing and implementing programs to create sustainable change and move towards the SDGs.

Conclusions: We present an integrated One Health and SES framework for pastoral systems in northern Kenya. Through this case study, we show how a One Health approach is critical in pastoral systems, how a systems framing is important for understanding and organising complex adaptive systems such as pastoral systems, and how an integrated One Health and SES framework can improve sustainability, collaboration and cost effectiveness, ultimately gaining progress towards the SDGs.

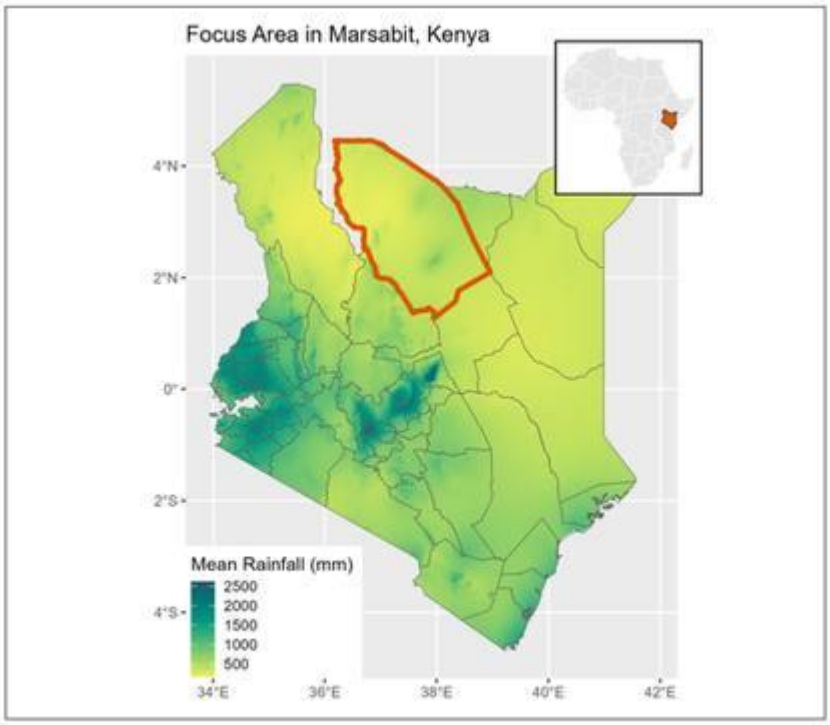


Figure 1 Marsabit County (highlighted in red), over mean annual rainfall for Kenya

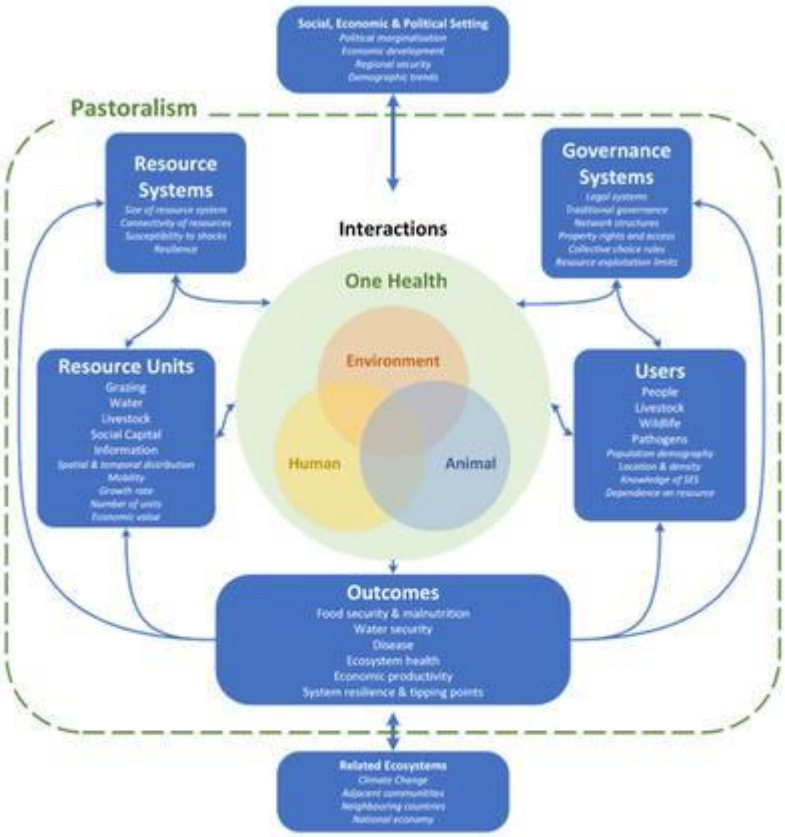


Figure 2 Integration of an expanded One Health conceptualisation (Laing et al., 2023) embedded as the Interactions component of the Socio-Ecological System (Ostrom, 2009; McGinnis and Ostrom, 2014) for pastoralism in northern Kenya. Italicised details are lower-tier variables that define the first-tier sub-components of the system and are specific to the Kenyan pastoralism SES

1200 – Sentinel cats: How companion animal veterinary diagnostics revealed high-consequence public health threats in Bangladesh

Eric BRUM (1), Shukes Chandra BADHY (2), Mir Nishat Tasnim TANIA (3), M Taifur RAHMAN (4), Shiyong WANG (1), Shruti GOGIA (4)

1: World Bank Group; 2: Department of Livestock Services, Government of Bangladesh; 3: Bangladesh Animal Care Center; 4: Food and Agriculture Organization of the United Nations (FAO)

Background

Companion animals live in close proximity to humans and share the same environmental exposures, positioning them as potential sentinels for emerging environmental and zoonotic threats. Despite this, the role of small animal veterinary clinical diagnostics in identifying hazards of public health significance is often under-recognized within surveillance systems. Clinical pattern recognition in veterinary practice may provide early signals of environmental contamination or emerging infectious diseases before they are recognized or spillover in human populations. This paper highlights the importance of small animal veterinary diagnostic capacity for the detection of high-consequence public health threats through two illustrative case investigations involving pet cats in Bangladesh.

Methods

Two case-based investigations were retrospectively analyzed to illustrate how atypical clinical presentations in companion animals led to the identification of broader public health risks. The first case involved a 7-year-old domestic cat presenting with acute-on-chronic renal failure in a geographically localized area in Dhaka. Veterinary clinical evaluation, laboratory diagnostics, and exposure history

prompted investigation of potential environmental toxicants. The second case involved two imported serval cats from South Africa presenting with atypical acute respiratory illness in Narayanganj district. Clinical examination and further molecular testing were used to investigate potential infectious etiologies.

Results

In the first case, a 7-year-old cat presented with atypical acute on chronic renal failure. After common causes were ruled out, the veterinarian initiated an assessment of the patient's water supply, including testing a municipal water sample from the patient's home for known nephro-toxins. Testing identified significantly elevated uranium concentrations in patient's drinking water, suggesting environmental contamination with potential serious public health implications. The second case involved two serval cats presenting with acute respiratory disease characterized by rapid progression and death with a history of being fed poultry meat. Diagnostic testing identified infection with a previously unknown variant of highly pathogenic avian influenza (HPAI) H5N1.

Conclusion

These cases demonstrate how routine veterinary clinical diagnostics can generate critical early signals for environmental and infectious public health threats. Companion animal veterinarians may detect unusual disease patterns that reflect shared environmental exposures or emerging zoonoses. Integrating clinical observations from small animal practice into broader One Health surveillance systems could strengthen early detection capacities. Improved veterinary clinical diagnostic skills, laboratory capacity for testing companion animal samples, mechanisms for cross-sectoral reporting, and communication between veterinary, environmental, and public health sectors are essential to leverage the sentinel value of companion animals. Recognizing the diagnostic contributions of small animal veterinarians represents an important opportunity to enhance operationalization of the One Health approach in surveillance and early warning systems.

Poster zone 2

Olive Tree

1207 – KNOWLEDGE, ATTITUDE, AND PERCEPTION OF MPOX AMONG AT-RISK AND INFECTED POPULATION AT THE HUMAN-ANIMAL-ENVIRONMENT INTERFACE IN EBONYI STATE, NIGERIA

Emmanuel OKPARA (1), Paul IZIOMO (2), **Samuel AYANWALE** (2), Funmilayo OLALEYE (2), Simeon CADMUS (1,2,3,4)

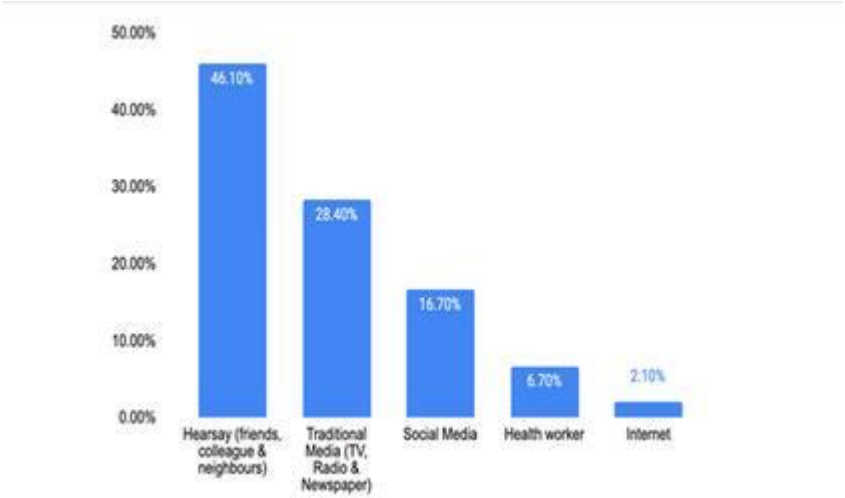
1: Department of Veterinary Public Health and Preventive Medicine, University of Ibadan, Ibadan, Nigeria; 2: Damien Foundation Centre for Genomics and Global Health, University of Ibadan, Nigeria., Nigeria; 3: Centre for Control and Prevention of Zoonoses, Faculty of Veterinary Medicine, University of Ibadan, Ibadan, Nigeria; 4: Nigerian Institute of Medical Research, Yaba, Lagos, Nigeria

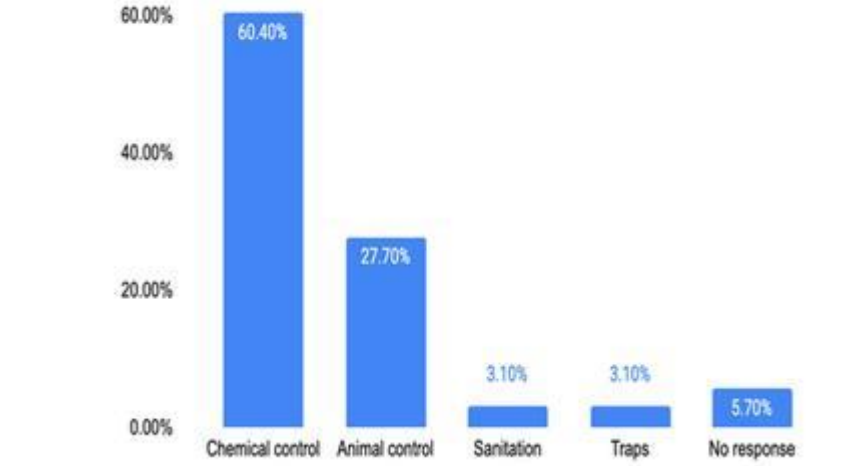
Background: Mpox is an emerging zoonotic viral disease of significant public health concern, particularly among populations in settings with high human-animal-wildlife interaction. Despite the increased spread and transmission of the disease, the knowledge, attitude, and perception (KAP) of mpox remain very poorly understood in at-risk communities. This study, therefore, examines the KAP of mpox among at-risk and infected populations in Ebonyi State, Nigeria.

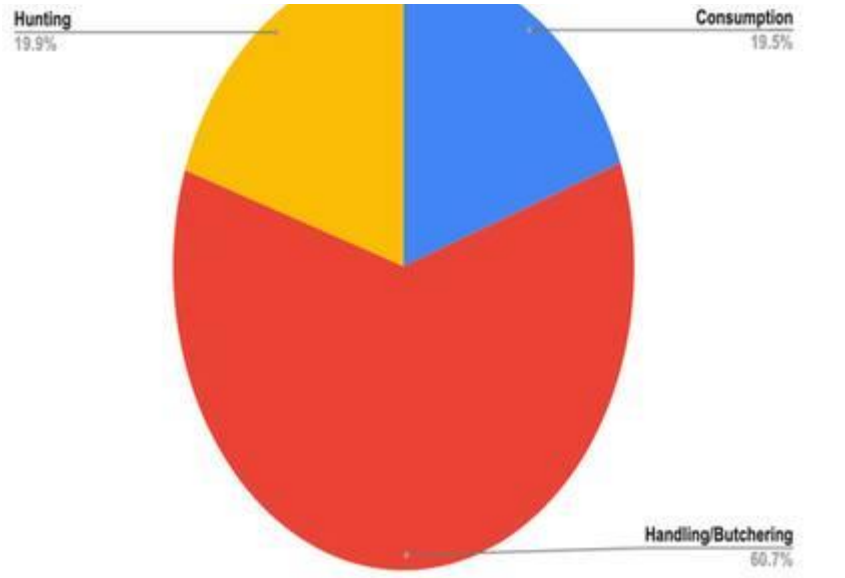
Methods: A cross-sectional study design was adopted, and an interviewer-administered structured questionnaire was used to collect data from 763 participants across the 13 LGAs in Ebonyi State. Descriptive statistics were performed to assess knowledge, attitude, and perception about mpox. Independent t-tests were conducted to compare KAP levels between at-risk and infected populations at the 5% significance level.

Results: The mean age of the respondents was 40.70 ± 14.4, with 431 males and 332 females. Of the 763 respondents, 80.1% had poor knowledge. The mean knowledge score was 13.99 (SD = 4.064). Infected individuals demonstrated significantly higher knowledge scores (p0.001) compared to at-risk individuals, suggesting that the acquisition of knowledge is often reactive rather than proactive. Specific knowledge gaps in mpox aetiology, transmission, symptoms, and methods of prevention were found, as only 43.6% identified mpox as a viral disease, while 18.4% mentioned vaccination as a preventive measure. Attitudinal assessment revealed negative perceptions towards preventive measures, with 51.4% of respondents deeming personal protective equipment (PPE) as unnecessary, and 52.1% not seeing the need to avoid contact with infected individuals. Risk perception was low, despite high exposures to risk factors. A high proportion (62.6%) reported direct contact with wild animals, primarily through handling and butchering (60.7%), while 78.6% often consumed bush meat. As many as 89.2% slaughtered and consumed sick animals, instead of taking them to veterinary service providers. Additionally, 79.2% did not implement any rodent control measures, although rodents are reportedly natural reservoirs of the mpox virus.

Conclusion: This study emphasised critical gaps in mpox knowledge, negative attitude toward prevention, and low perceived risk, which together contribute to increased vulnerability within the State. The substantial knowledge gap between infected and at-risk populations calls for urgent, proactive public health education and community-based interventions to address misinformation, reduce stigma, and promote behavioural change to mitigate mpox outbreaks in Ebonyi State, Nigeria, and other endemic settings.







1212 – Robust Metagenomic Workflows are Critical to Effective Monitoring of Wildlife Health – A Tale of Phages

Bethan MASON (1), Vladislav ILIK (2), Elif KAPLAN (2), Frédéric Stéphane SINGA NIATOU (3), Solange Patricia MAKATIA WANGO (4), Lucie ABA-TOUMNOU (4), Klara Judita PETRZELKOVA (1,5,6), Dagmar CIZKOVA (1), Jakub KREISINGER (1,2)

1: Institute of Vertebrate Biology, Czech Academy of Sciences, Czech Republic; 2: Department of Zoology, Faculty of Science, Charles University, Czech Republic; 3: WWF Central African Republic Programme, Central African Republic; 4: Faculty of Science, University of Bangui, Central African Republic; 5: Institute of Parasitology, Biology Centre, Czech Academy of Sciences, Czech Republic; 6: Liberec Zoo, Czech Republic

The metagenome incorporates genetic material from all organisms present in an environmental sample. Metagenomic research has expanded rapidly in recent years, from gut microbiome studies to environmental DNA-based biodiversity assessments, largely driven by advances in sequencing technologies which reduced costs and amplified data output. The rapid growth of this field has outpaced the development of standardized analytical workflows, while variability in experimental design further complicates cross-study comparisons. This poses challenges for the cross-disciplinary data integration required for effective One Health monitoring.

This gap is especially pronounced in bacteriophage metagenomics. Despite their central role in regulating bacterial populations, phage communities remain understudied, particularly in wildlife systems, compared to bacterial components of the gut microbiome. Existing wildlife phage studies frequently rely on shallow shotgun metagenomics originally designed for bacterial profiling and often lack phage enrichment, host identity verification, or systematic benchmarking of analytical workflows.

Using western lowland gorillas as a model, we developed an integrative workflow for gut phage metagenomics in wild mammals. Faecal samples were collected from free-ranging gorillas in the Dzanga-Sangha Protected Areas (Central African Republic) and captive gorillas in Prague Zoo (Czech Republic). We compared methodological approaches across the workflow, including sample preservation, filtration-based VLP (virus-like particles) enrichment, and bioinformatic phage prediction. Using paired VLP-enriched filtrates and unfiltered total metagenomes, we evaluated the performance of multiple phage prediction tools and assessed the effectiveness of filtration-based VLP enrichment under field conditions. We also tested how post-defecation sampling intervals affect phage community stability. Total genomic DNA was extracted and sequenced on the DNBSEQ platform, targeting short read and deep sequencing for VLP-enriched and total metagenome samples. Bioinformatic analyses compared multiple computational pipelines for genome assembly and phage prediction.

Our results show that filtration and preservation strategies strongly influence phage sequence recovery and diversity, although overall taxonomic composition remains consistent across sampling approaches. VLP enrichment efficiently characterizes core extracellular phage communities, whereas unfiltered faecal samples preserved in ethanol or RNA-stabilizing buffers capture substantially broader phage sequence diversity, while simultaneously enabling reconstruction of host mitochondrial genomes for host identity verification from the same dataset. We further demonstrate that combining multiple bioinformatic prediction tools maximizes phage detection without altering underlying biological patterns. Together, these results provide a validated and scalable framework for wildlife phage metagenomics. While optimal workflows represent a balance between discovery depth, logistical feasibility, and computational resources, partial standardization of analytical pipelines will be essential for accurately integrating phage ecology into One Health monitoring systems.

1222 – Environmental DNA-Based Biosurveillance to Support One Health Biosecurity at Borders

Edward HAYNES (1), Marco BENUCCI (1), Sarah CARROLL (1), Chris CONYERS (1), Bryden FIELDS (1), Angelika KIEPAS (1), Roy MACARTHUR (1), Charlotte PAIN (1), John WALSHAW (1), Sarah EUSTACE (2), Kong-Wah SING (2), Damien HICKS (3)

1: Fera Science Limited, York, United Kingdom; 2: Animal and Plant Health Agency, Manchester, United Kingdom; 3: Defra, Penrith, United Kingdom

Background The global movement of goods poses a risk of cross-border transmission of plant, animal and human pathogens. One Health-aligned biosurveillance approaches that detect biological threats across environmental matrices are increasingly of interest as a means of sharing sampling costs, reducing duplication of effort, and detecting unexpected risks. This study evaluated the feasibility of applying environmental DNA (eDNA) sampling at Border Control Posts (BCPs) and subsequent high-throughput

sequencing to identify potential biological risks, generating data relevant across the One Health spectrum.

Methods A six-week environmental sampling campaign at two UK BCPs (Port of Liverpool; Manchester Airport), was conducted in collaboration with APHA border inspectors. Daily air filters, weekly sticky traps and ad hoc dust wipes were collected (n = 194), followed by DNA extraction and sequencing using 16S, ITS and COI metabarcoding, complemented by shotgun metagenomics on a subset of samples. ASVs were taxonomically classified using in house pipelines, and taxonomic and diversity patterns were analysed to assess temporal resolution, site-level differences, and detection of taxa of plant health relevance. Metagenome data was interrogated to determine the presence of AMR genes.

Additionally, a workshop was held with UK stakeholders across One Health domains, including experts with human, animal, plant, environment, food, invasive species and AMR focus. The aim of the workshop and subsequent detailed follow up was to identify applications, benefits and limitations of combined One Health environmental surveillance at borders.

Results All three sample types yielded detectable environmental DNA, with clear and statistically significant differences in community composition between air, dust, and sticky traps across bacterial, fungal, and invertebrate barcodes. Air and sticky trap samples could provide time-resolved detection, with significantly lower dissimilarity among samples collected at overlapping times for several metabarcoding loci. eDNA detections included multiple taxa of plant health relevance. Metagenomic datasets additionally contained evidence of antimicrobial resistance genes, and along with feedback from subject matter experts, demonstrated added One Health value beyond plant health surveillance.

Conclusions Environmental DNA surveillance at borders is a feasible and potentially informative, complementary approach to traditional inspection. The method detected diverse taxa across kingdoms and provided evidence of time-resolved detections in border environments. After further development and validation, the outputs from eDNA surveillance could be used to guide the focus of conventional inspection regimes or inform policy decisions to maintain biosecurity. This pilot demonstrates strong potential for integrated One Health biosurveillance, including detection of taxa of plant health relevance and AMR signatures, and generated interest among stakeholders. Further work is ongoing to optimise sampling intensities, develop interpretation frameworks with stakeholders, and expand deployment across BCP types.

1233 – Building the next generation of One Health leaders: a multidisciplinary mentorship program in Cameroon

Elisabeth BETSI DIBONGUE (1), **Cha-ah Crystella NGONG** (1), Serge NZIETCHUENG (2), Conrad NKUO (1)
1: National One Health Platform, Cameroon; 2: Faculty of Veterinary Medicine, University of Liège, Belgique

Background: Strengthening an interdisciplinary and multisectoral workforce is essential for countries to meet core capacities required to prevent, detect, and respond to public health threats through a One Health approach. However, opportunities for early-career professionals to gain practical experience in multisectoral collaboration remain limited in many settings. To address this gap and complement limited human resource capacity, the Cameroon National One Health Platform established a mentorship and internship program aimed at preparing young pre-service professionals for future leadership in One Health.

Methods: Since 2022, the One Health Platform has hosted mentees through periodic calls for applications. Candidates are selected based on academic background, motivation, and potential contribution to One Health activities. Selected participants include young professionals from diverse disciplines such as veterinary medicine, human medicine, epidemiology, project management, psychology, and field epidemiology. Upon onboarding, mentees receive orientation on the platform's functioning and training in administrative and technical writing, reporting, and activity planning and implementation. They are integrated into routine platform activities such as trainings, multisectoral coordination meetings, development of policies and strategies, simulation exercises, joint risk assessments, epidemiological surveillance and investigations, communication activities, and research tasks. Mentees are assigned activities and encouraged to lead their implementation under structured mentorship and periodic evaluation.

Results: Since its inception, the program has supported 23 mentees, strengthening multidisciplinary workforce capacity through practical exposure to One Health coordination and implementation. Mentees developed One Health core competencies including leadership (activity coordination, technical communication, problem solving), multisectoral collaboration and system's thinking. Each mentee is given an opportunity to lead at least an activity from inception to implementation while benefiting from direct mentorship from senior experts. 04 out of 23 mentees have transitioned into public health positions, while 5 resumed roles in their respective ministries (ministries in charge of public health and livestock), including Cameroon Field Epidemiology Training Program fellows. 11 continue to support platform activities while awaiting career opportunity. The initiative has fostered professional networks between early-career professionals and senior practitioners, contributing to a growing pool of young pre-service professionals equipped to advance One Health implementation in Cameroon.

Conclusion: This mentorship model effectively strengthens multidisciplinary workforce capacity by integrating early-career professionals into high-level One Health coordination. Success is driven by practical immersion in routine activities and structured guidance from senior experts. However, the primary challenge remains the transition of all mentees into public health roles. Sustainability depends on clear career pathways for mentees. This scalable approach is a vital strategy for countries facing similar workforce gaps in global health security.

1243 – SCALARE: Building a One Health platform for advanced training and interdisciplinary research to strengthen resilience in post-earthquake Central Italy

Silvia D'ALBENZIO (1), Chiara ALBANELLO (1), Barbara BARBONI (2)

1: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Italy; 2: Università degli Studi di Teramo, Italy

Background

Natural disasters can profoundly disrupt socio-economic systems and expose vulnerabilities at the human–animal–environment interface. Within the Disaster Management Cycle adopted by WOAH, Veterinary Services contribute to the recovery phase by protecting animal health and welfare, safeguarding human and environmental health, and supporting countries in restoring economic and societal conditions.

Following the 2016–2017 earthquakes in Central Italy, the Abruzzo region faced major challenges in rebuilding infrastructure and restoring social confidence.

In this context, the University of Teramo (UNITE) and the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (IZSAM), the main veterinary academic and research institutions located in the affected area, launched **"SCALARE – Regional School for Advanced Training and Research in One Health"**, an unique initiative designed to overcome disciplinary silos and promote multidisciplinary collaboration through a shared governance model integrating doctoral education within the One Health paradigm.

Methods

Established in 2025 with financial support from the Italian Presidency of the Council of Ministers, SCALARE develops a regional hub for advanced education and research aligned with global One Health priorities.

Core activities foresee **competitive doctoral fellowships and postdoctoral positions**,jointly supervised by both institutions.

The model combines **personalised research pathways, interdisciplinary mentoring, and structured mobility at international research centres and companies**.

Key innovation of the initiative is a **shared governance model** to ensure cross-institutional integration and intersectoral collaboration, including a **School Management Team**, responsible for strategic coordination and administrative oversight, and a **Scientific Committee** involving representatives from academia, research institutions and industry, tasked with evaluating projects and guiding scientific priorities.

Dedicated **technical committees** support training activities, Open Science dissemination, data-sharing practices, ethical oversight and technology transfer.

Results

SCALARE has established a **scalable platform for interdisciplinary One Health advanced training and research**.

The programme launched its first cohort of **12 PhD fellowships in 2025**, followed by **17 additional fellowships in 2026**, alongside **11 postdoctoral positions**.

Current projects address several strategic areas, including **cryo-electron microscopy applied to host–pathogen interactions, advanced proteomics for food fraud investigations, environmental monitoring of antibiotic residues, and stem-cell applications for cultivated meat and regenerative medicine**.

Postdoctoral research further expands into fields such as **comparative oncology and regenerative medicine**, while supporting early-career researchers in becoming competitive candidates for **Marie Skłodowska-Curie Actions (MSCA)**.

Conclusions

SCALARE provides an innovative model linking **post-disaster recovery with long-term capacity building and regional scientific resilience in One Health**.

By integrating interdisciplinary research, cross-institutional supervision, industry collaboration and international mobility, the initiative strengthens regional research ecosystems and supports the development of a new generation of scientists addressing challenges at the human–animal–environment interface.

The programme also enhances the scientific visibility and resilience of the Abruzzo region, contributing to the **“Six Tracks” of the Quadripartite One Health Joint Plan of Action**.

1250 – Umbre Virus Detection and Dissemination in Birds of Prey: Implications for One Health Surveillance of Emerging Viruses

Shreya G GURUNG, Emmanuelle MÜNGER, Marjan BOTER, Anne van der LINDEN, Suchada KHEMTONG, Lonneke LEIJTEN, Lineke BEGEMAN, Reina SIKKEMA, Bas Oude MUNNINK, Marion KOOPMANS
Erasmus MC, Netherlands, The

Background:

Many emerging infectious diseases originate from wildlife, highlighting the importance of surveillance at the animal-human interface. The Netherlands is identified as a potential hotspot for emerging zoonoses due to its large populations of migratory and resident wild birds. Birds of prey are apex predators and can accumulate pathogens circulating within ecosystems, making them valuable sentinel species for monitoring zoonotic infections. They have previously been shown to be susceptible for several arboviruses including West Nile virus, and can provide early signals of pathogen circulation in the environment. Metagenomic sequencing enables unbiased detection of known and novel viruses without prior assumptions regarding the causative agent, thus making it ideal for virus discovery. Here, we applied viral metagenomic sequencing on archived owl brain samples to identify potential viruses circulating in wildlife.

Methods:

Metagenomic sequencing was performed on brain tissue from 23 deceased owls with undetermined causes of death collected across the Netherlands between 2006 and 2020. Viral nucleic acids were enriched using a capture-based approach and sequenced using the Illumina platform. Following identification of Umbre virus, a quantitative PCR (qPCR) assay was developed based on the detected sequence and publicly available reference genomes. This assay was used to screen additional archived samples stored in the Erasmus MC biobank, including specimens originating from Blijdorp Zoo and birds of prey from other locations. Nanopore metagenomic sequencing was used to attempt recovery complete viral genomes, and in situ hybridization (ISH) was performed to assess viral distribution in tissues.

Results:

Metagenomic analysis identified Umbre virus in brain tissue of a Northern Hawk Owl that died in 2006 at Blijdorp Zoo, Rotterdam. Umbre virus is an Orthobunyavirus first isolated from *Culex* mosquitoes in 1955 and has been associated with encephalitis in three immunocompromised human patients reported in

2016, 2018 and 2019. Histopathological findings in the infected owl were consistent with encephalitis. Subsequent qPCR screening increased the total number of Umbre virus positive cases to four, all Northern Hawk Owls originating from the same cage at Blijdorp Zoo, while other samples tested negative. Initial genome reconstruction showed 97-98% nucleotide similarity across the three Umbre genome segments compared with previously reported human derived sequences. Preliminary ISH results demonstrated viral RNA localization primarily around blood vessels and immune cells in owl brain tissue, contrasting with the neuronal tropism reported in human infections.

Conclusions:

This study expands the known geographical and host range of Umbre virus and provides evidence of infection in captive owls in the Netherlands, highlighting previously unrecognized interactions with birds and its zoonotic potential. These findings demonstrate how integrating wildlife pathogen discovery and metagenomics can strengthen One Health surveillance and improve detection of emerging arboviruses in Europe, particularly as climate and ecological changes increasingly influence vector-borne disease dynamics.

1253 – Bangladesh's One Health Pathway to Financing Pandemic Prevention, Preparedness and Response

Motahara TASNEEM (1), **Mohammad Rafiqul ISLAM** (1), Eric BRUM (3), Filip CLAES (1), Scott NEWMAN (1), Antonio MELE (1), Katrin TAYLOR (1), Shiyong WANG (3), Shruti GOGIA (1), Tahmina SHIRIN (2), Md Abu SUFIAN (2), Jahidul KABIR (2), Md Bozlur RAHMAN (2), YinMyo AYE (1)

1: Food and Agriculture Organization; 2: Government of Bangladesh; 3: World Bank

Background

Bangladesh lies at the centre of several drivers of emerging infectious diseases, including high population density, rapid urbanization, environmental pressures, and close human–animal interactions. Although the country has achieved major progress in infectious disease control and primary health care over the past two decades, outbreaks such as avian influenza exposed persistent coordination gaps between the human, animal, and environmental health sectors. Surveillance, laboratory systems, and response mechanisms have often evolved within sectoral silos, limiting effective management of zoonotic threats.

Bangladesh has progressively institutionalized the One Health approach by establishing a One Health Secretariat and developing 2 national One Health Strategic Frameworks. Despite these advances, financing for pandemic prevention and preparedness remained limited and largely focused on emergency response rather than prevention. This study examines how Bangladesh translated long-standing One Health collaboration into large-scale financing for pandemic prevention, preparedness and response (PPR).

Methods

A qualitative case study approach examined Bangladesh's transition from conceptual adoption of One Health to investment planning through three phases: diagnosis, planning, and investment case development.

The diagnostic phase synthesized findings from major assessments including the Joint External Evaluation (JEE), Performance of Veterinary Services (PVS), and Self-Assessment Annual Reporting (SPAR), leading to the development of a national One Health country profile and identification of system gaps.

The planning phase involved participatory engagement of stakeholders from government ministries, technical agencies, academia, and development partners. Problem tree analyses, thematic workshops, and consultations informed the development of Bangladesh's third One Health Strategic Framework. Budgeted priorities were translated into investment cases through participatory return-on-investment analyses through the piloting of a new One Health Conceptual Framework.

Results

The participatory process strengthened cross-sectoral ownership and enabled the emergence of political, technical, and institutional champions. Early engagement with economic and planning authorities ensured alignment with national financing processes.

Bangladesh leveraged this coordinated approach to mobilize new resources for One Health implementation. The country secured approval for a US$25 million Pandemic Fund grant to strengthen One Health surveillance and early warning systems. In parallel, the Government of Bangladesh developed a US$225 million World Bank–financed One Health Project, currently under review by the planning commission.

Conclusion

Bangladesh's experience shows how sustained institutionalization, participatory governance, and evidence-informed planning can translate the One Health concept into large-scale financed action. Aligning multisectoral leadership with global financing mechanisms enabled the country to transform a long-standing technical agenda into a major development investment and provides practical lessons for countries seeking to operationalize One Health for pandemic preparedness.

1260 – Interactive Simulation for One Health Workforce Development: A Card-Based Game to Strengthen Cross-Sector Collaboration in Zoonotic Disease Outbreak Response

Jill JOHNS, Jessica SCHWIND, Michelle TREMBLAY

Institute for Health Logistics & Analytics at Georgia Southern University, United States of America

Background

Zoonotic disease outbreaks are increasing in frequency and complexity due to climate change, land-use change, globalization, and fragile health systems. Effective response requires coordinated action across human, animal, plant, and environmental sectors; however, most professionals are trained within disciplinary silos and rarely have opportunities to practice collaborative decision-making in real-time scenarios. Differences in terminology, training frameworks, and sector priorities can hinder communication and the integration of diverse expertise during emergencies. To address these gaps in One Health education and workforce development, the Institute for Health Logistics & Analytics (IHLA) developed an interactive, card-based simulation game designed to build transdisciplinary collaboration skills through experiential learning. This study examines the design and pilot implementation of the simulation and evaluates its potential as a scalable educational tool supporting the Knowledge, Education, and Communities agenda in One Health practice.

Methods

The simulation places participants in defined One Health roles—including Epidemiologist, Veterinarian, Environmental Health Specialist, Water Management Specialist, Agricultural Extension Officer, and Community Leader—to respond to a dynamic zoonotic outbreak scenario. Gameplay utilizes three primary card types: Event Cards introducing evolving outbreak conditions, Action Cards presenting potential response strategies, and Resource Cards representing available assets and constraints. Players collaborate to contain the outbreak while balancing resource limitations, competing sector priorities, and long-term community resilience goals.

The game was piloted in facilitated sessions structured around small-group participation (approximately five participants per table with one facilitator for every two to three tables). Facilitators observed group interactions and collected qualitative feedback through discussion and structured debrief sessions examining communication dynamics, decision-making processes, and systems-level barriers. Participant reflections and facilitator observations were analyzed to identify key learning outcomes and perceptions of the tool's educational value.

Results

Participants reported increased understanding of the interconnected nature of human, animal, environmental, and agricultural health systems. Gameplay required teams to negotiate cross-sector priorities, allocate limited resources, and rapidly respond to escalating outbreak scenarios. Participants demonstrated improved interdisciplinary communication, strategic thinking, and collaborative problem-solving. Qualitative feedback highlighted the value of the simulation in exposing policy trade-offs, power dynamics, and operational challenges that emerge during real-world public health crises. Participants also emphasized the game's accessibility and adaptability for use in academic training, professional development, and community preparedness programs.

Conclusions

Interactive simulation offers a practical and scalable approach to strengthening One Health competencies and workforce preparedness. By immersing participants in realistic outbreak scenarios that require cross-sector negotiation and systems thinking, the IHLA One Health card game provides an innovative tool for bridging disciplinary divides and advancing collaborative policy and practice. Integrating experiential learning tools such as this simulation into professional training and community education initiatives may enhance global capacity to prevent and respond to zoonotic threats while supporting stronger knowledge exchange across human–animal–environment interfaces.

1264 – Evidence of the impact of chemical pollution on biodiversity

Marta BACCARO, **Eleonora CHINCHIO**, Stephanie BOPP
European Commission, Joint Research Centre (JRC), Ispra, Italy

Background The Kunming-Montreal Global Biodiversity Framework has established a target to reduce pollution risks and mitigate the negative impacts of pollution on biodiversity by 2030. However, despite its significance, the threat of chemical pollution to biodiversity is often underestimated due to a lack of comprehensive evidence linking environmental concentrations of xenobiotics to their effects on biodiversity. A major challenge in establishing this link is the complexity of extrapolating data from individual organism-level studies, typically performed in ecotoxicological studies, to higher biodiversity levels and metrics. From a One Health perspective, it is essential to consider the interconnectedness of human, animal, and environmental health, and to recognize that chemical pollution can have far-reaching consequences for ecosystem services, which are crucial for ensuring human health. This study aims to synthesize an evidence map that summarizes the findings of a large body of eco-toxicological research, exploring the effects of chemical exposure on biodiversity across different biological organization levels.

Methods The evidence map includes field studies, multi-species laboratory studies (e.g., mesocosm studies), and single-species laboratory studies in which direct extrapolation to higher biological organization levels was performed (e.g., population modeling). The focus was on studies where the specific substance and its concentration were explicitly identified. The outcome of interest was defined as any biodiversity measure (e.g., loss of individuals in a wild population, loss of a functional trait). Peer-reviewed publications were obtained from Scopus and Web of Science Core Collection databases, covering the period 2003-2025. After a screening step, the extraction of approximately 5,500 papers was performed using an AI tool.

Results The data extraction focused on the following key information: type of chemical(s), type of study (lab, semi-field, field), biological organization level(s), and toxicological endpoint(s) tested, as well as the method of extrapolation to higher biological organization levels and the associated biodiversity effects.

Conclusions The summary of the outcomes of the evidence map will include details on chemicals, taxa, and methods for which evidence of the impact of chemical exposure on biodiversity exists, highlighting potential knowledge gaps.

1267 – Carbapenem-resistant Gram-negative bacteria in UAE farm animals: evidence from camels of NDM-producing Enterobacterales with potential for zoonotic transmission.

Ashrat MANZOOR (1), Akela GHAZAWI (1), Nikolaos STREPIS (2), Mushtaq KHAN (1)
1: United Arab Emirates University, United Arab Emirates; 2: Erasmus University Medical Centre, Rotterdam, The Netherlands

Background

Antimicrobial resistance (AMR) among Gram-negative bacteria poses a critical global health threat, with carbapenem- and colistin-resistant organisms representing last-resort treatment failures. While the United Arab Emirates (UAE) has documented carbapenemase- and mcr-harboring Enterobacterales in clinical and poultry settings, comprehensive data on their prevalence in farm animals and agricultural

environments remain limited, hindering evidence-based policy evaluation within the national One Health framework.

Methods

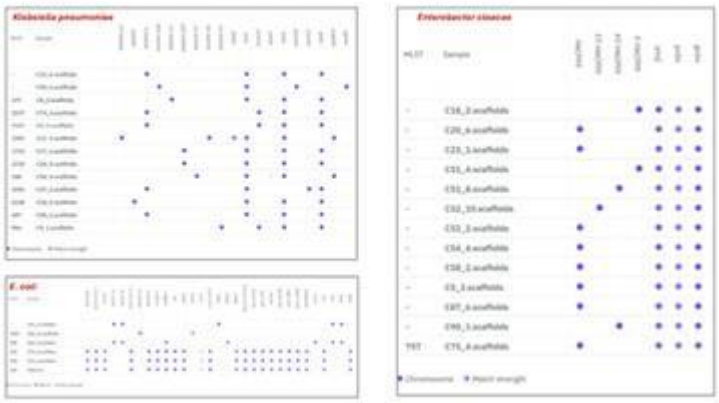
Between June 2024 and February 2025, 352 specimens (349 animal fecal samples and 3 pooled wastewater composites) were collected from three Dubai farms using stratified random sampling. Carbapenem-resistant isolates were recovered using selective chromogenic media, confirmed via broth microdilution, and identified by MALDI-TOFMS. Molecular characterization included plasmid profiling and whole-genome sequencing (Illumina NovaSeq) with bioinformatics analysis. Animal feed samples underwent antimicrobial residue screening via optimized extraction protocols and LC–MS/MS analysis.

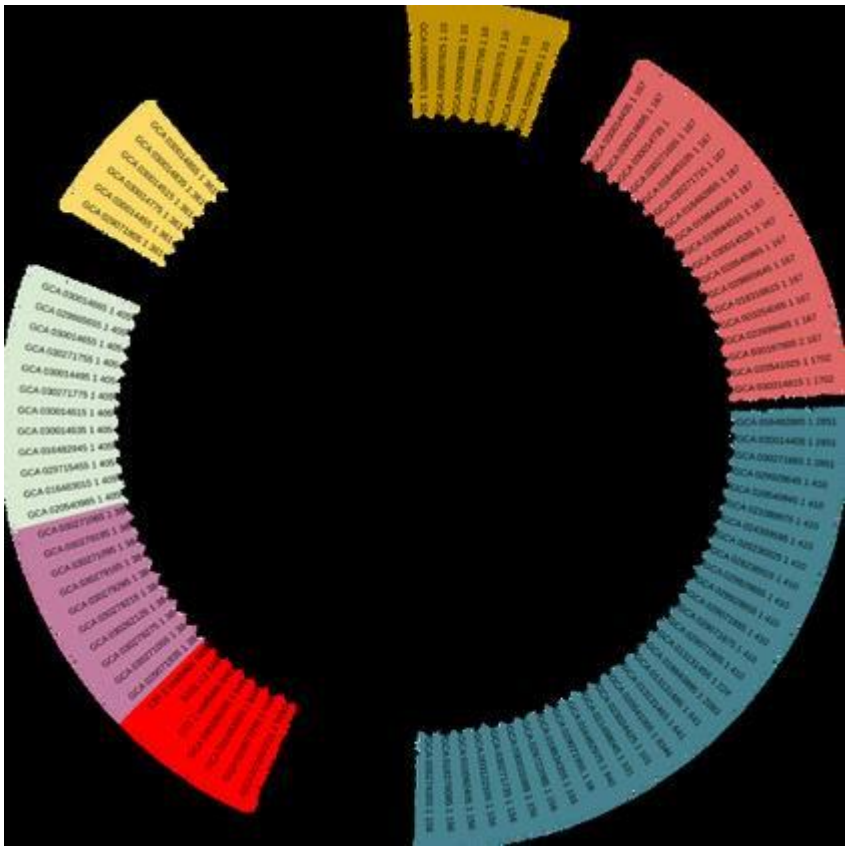
Results

Carbapenem-selective growth was detected exclusively in camel samples (36/125; 28.8%; 95% CI: 21.6–37.3%), yielding 81 phenotypically confirmed carbapenem-resistant isolates across multiple species, including *Escherichia coli, Klebsiella pneumoniae, Enterobacter cloacae, Morganella morganii,* and *Providencia rettgeri*, of which 49 were identified as non-duplicate isolates based on plasmid profiling analysis. Genomic analysis revealed diverse antimicrobial resistance gene profiles spanning β-lactams, aminoglycosides, fluoroquinolones, sulfonamides, and polymyxins, along with chromosomal point mutations conferring colistin (pmrB), tigecycline (acrR, oqxR), fosfomycin (glpT), and fluoroquinolone resistance (gyrA, parC, parE). Multiple plasmid replicon types were identified, including Col-, IncF-, and IncX-family plasmids. Preliminary phylogenetic analysis demonstrated close genetic relatedness of *bla*NDM-5-positive camel isolates to globally distributed human clinical strains, suggesting potential cross-host transmission pathways. Pilot LC–MS/MS optimization successfully recovered spiked meropenem from feed samples and detected multiple putative antimicrobial compounds in the feed matrix.

Conclusions

This study establishes the first baseline characterization of carbapenem-resistant Gram-negative bacteria in UAE farm animals, identifying camels as a significant reservoir. The detection of NDM-producing *E. coli* with genomic similarity to international clinical strains underscores zoonotic transmission risks and highlights the interconnectedness of animal, environmental, and human health sectors. These findings will directly inform targeted surveillance strategies, biosecurity measures, antimicrobial stewardship policies, and post-ban evaluation of the 2024 veterinary colistin restriction, strengthening AMR preparedness within the UAE's One Health framework.





1270 – Bridging fragmented resistance management at district level: Lessons from crop-livestock clinics in Uganda

Annet NAMBOOWA (1), Lilian OWEMBABAZI (2), Micheal JONGA (3), Carolyne NYAMOR (4), Musa SEKAMATTE (4), Christine ALOKIT (2), Kenneth ODONG PRAS (5), Nicholas MUHUMUZA (3), Francis EJOBI (6), Solveig DANIELSEN (7), **Georgina GRELL** (8)

1: Department of Animal Health, Ministry of Agriculture, Animal Industry and Fisheries, Uganda; 2: CAB International, Uganda; 3: Department of Disease Control and Environmental Health, School of Public Health, Makerere University, Uganda; 4: National One Health Platform, Ministry of Health, Uganda; 5: Independent Research Fellow, Uganda; 6: Soroti University, Soroti, Uganda; 7: CAB International, The Netherlands; 8: CAB International, UK

Background. Antimicrobial and pesticide resistance is rising in Uganda due to widespread misuse of drugs and chemicals across human, animal, crop and environmental sectors. Although AMR management is a national priority, district-level implementation remains limited. Crop–livestock “joint clinics” have been introduced in six districts to provide integrated advisory services on crop and livestock health.

While the joint clinics promote disease prevention and prudent pesticide and veterinary drug use, they are not formally recognised within the AMR landscape. This study examines how the clinics are perceived as platforms for strengthening resistance management and how their contributions align with national AMR priorities.

Methods. The study draws on 25 in-depth interviews with farmers and multisectoral district representatives from Hoima and Kayunga districts. Interviewees included extension workers operating the clinics, health workers who participated in clinic sessions, district officers from One Health–related sectors, and farmers who had attended clinics. We explored perceptions of clinic roles in resistance management, key resistance issues in the districts, how these issues are addressed across sectors, and opportunities to strengthen cross-sector synergies.

Results. Interviewees identified clinic contributions under all objectives of Uganda's National Action Plan on AMR (NAP-AMR) (Table 1). However, the clinics were weakly connected to other sectors and not viewed as part of the formal AMR implementation structure. This mirrors a broader pattern of fragmented systems: resistance management remains siloed by sector and resistance type—antibiotics, acaricides or insecticides.

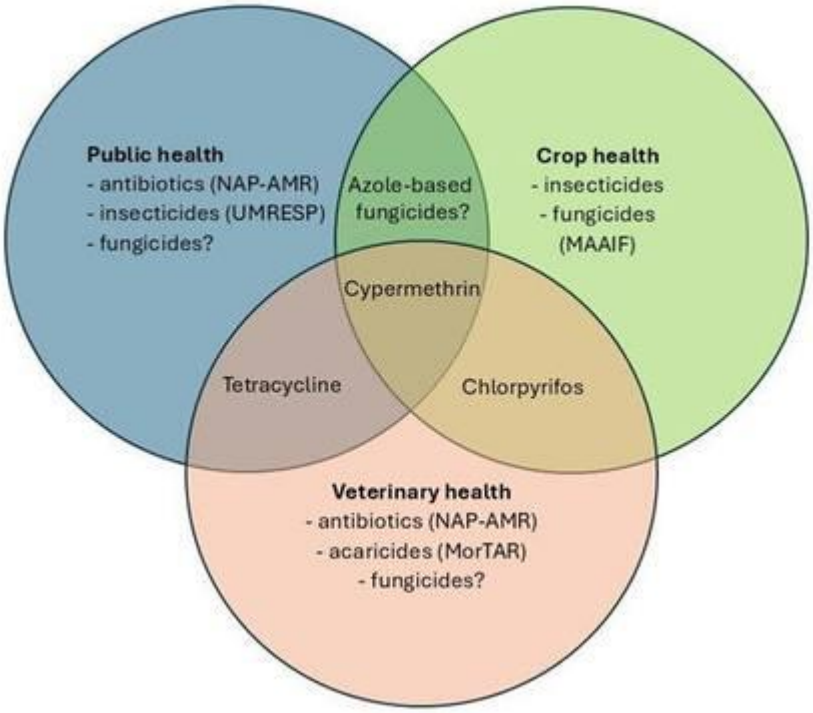
Table 1. Joint clinic actions contributing to NAP-AMR objectives (as perceived by interviewees).

Crop health	Livestock health
Objective 1. Promote public awareness, training and education	
Demonstrations on safe pesticide use; IPM	Training on prudent antibiotic/acaricide use
Objective 2. Improve infection prevention and control	
Promotion of field sanitation, resistant varieties	Vaccinations, biosecurity measures
Objective 3. Promote optimal access to and use of antimicrobials	
Advice on prescriptions; safe pesticide purchases	Promotion of prescriptions, monitoring drug stores
Objective 4. Strengthen AMR surveillance	
Referrals; records of queries and pesticide failure	Referrals; records of drug resistance/ treatment failure
Objective 5. Research and innovation	
Co-learning and exchange across sectors; demonstration-based extension and dissemination	

Several increasingly ineffective compounds, including tetracycline (antibiotic), cypermethrin (pyrethroid) and chlorpyrifos (organophosphate), are used across multiple sectors (Fig. 1), yet resistance challenges are addressed through separate strategies and structures. This compartmentalisation limits recognition of shared risks and leaves cross-resistance insufficiently addressed.

Figure 1. Resistances by sector, highlighting compounds associated with cross-over resistance (overlapping circles). Acronyms indicate national strategies or institutions addressing each resistance issue (reproduced with permission from CABI).

Conclusions. Two key insights emerge. First, the resistance-related contributions of crop–livestock clinics have been overlooked and could be strengthened by formally integrating them into district One Health actions. Second, resistance management is highly fragmented across sectors, undermining synergies, efficient resource use and coordinated responses to cross-sector resistance. A more holistic, aligned approach is needed across interventions and health domains.



1275 – Building a Transdisciplinary Brazilian One Health Research Team: Lessons from a Collaborative Scoping Review on Integrated Health Evidence Production

Jéssica MEDEIROS (2), Verônica GINANI (2), Leonor SANTOS (2), Christina PACHECO (3), Renata FERREIRA (2), Sindy SILVA (1)

1: Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, Portugal; 2: Universidade de Brasília, Brasília, Brazil; 3: Universidade Federal da Paraíba, João Pessoa, Brazil

Background: The One Health approach requires collaboration across disciplines to address complex health challenges involving humans, animals, and ecosystems. However, most evidence synthesis processes remain within disciplinary boundaries. This experience report aims to describe the creation of a Brazilian transdisciplinary research team, established to conduct a scoping review on Socioecological Interconnections in One Health. The protocol for this review was previously published and subsequently adapted, to better reflect the Brazilian context and the emerging priorities of the agenda.

Methods: The team was composed of 21 Brazilian investigators from different backgrounds. Among them are collective health, veterinary medicine, biology, medicine, pharmacy, nutrition, law, librarianship, and art education. The group conducted a scoping review following the international methodology from the Joanna Briggs Institute (JBI). The review process included protocol development, database searches, study screening, and data extraction. The search strategies identified 7.972 records in the databases. During the eligibility phase, blind, and based on title and abstract, team members worked independently, evaluating studies and assigning thematic labels related to six One Health dimensions. In the full-text stage, 496 studies were evaluated for eligibility. Subsequently, the articles were distributed among thematic subgroups for data extraction and analysis. There were plenary meetings, with the full research teams and, and subgroup meetings to facilitate interdisciplinary dialogue, methodological alignment, and shared decision-making.

Results: The formation of a diverse team allowed for the integration of different disciplinary perspectives in the production of evidence in One Health. The researchers actively participated in the stages of the review, contributing to the development of the protocol, the screening of studies, and the elaboration of data extraction tools. The collaborative process allowed the records to be analyzed and interpreted from different disciplinary perspectives. Team meetings fostered knowledge exchange between areas and strengthened the collective understanding of the One Health concept. Among the main challenges identified were differences in methodological approaches between disciplines, varying levels of

familiarity with the One Health concept, institutional limitations, and the coordination of researchers with diverse professional agendas.

Conclusion: The formation of transdisciplinary research teams represents an important strategy for operationalising the One Health approach in the production of scientific evidence. Although collaboration across disciplines increases the complexity and duration of the research process, it enhances analytical depth and the relevance of findings for decision-making. This experience suggests that research programs and public policies that encourage interdisciplinary and interinstitutional teams can strengthen evidence production and contribute to the training and development of the One Health workforce, while also supporting more evidence-informed decision-making processes. The experience in the context of collective health allowed for a discussion with different perspectives, indicating that it is a promising area to leverage One Health as a key point in public policies.

1284 – Solitary bees (Osmia spp.) as novel bioindicators of environmental antimicrobial resistance

Laura CIOT (1), Giovanni CILIA (2), Anselm RODRIGO (1), Jordi BOSCH (1)
1: CREAF, Spain; 2: CREA-AA, Italy

Background

Antimicrobial resistance (AMR) is a major global public health threat associated with increasing morbidity, mortality and healthcare costs. Antimicrobial resistance genes (ARGs) are widely distributed across natural and anthropogenic environments, forming a complex environmental resistome. Monitoring environmental AMR remains challenging because current surveillance approaches are often fragmented and limited to specific matrices or point sources, while ARGs can originate from multiple sources and circulate across interconnected environmental compartments. Integrative bioindicator systems capable of capturing ARG exposure across matrices are therefore needed. Solitary bees of the genus *Osmia* exhibit ecological, behavioural and physical traits that make them promising biological samplers. Through interactions with soil, plant material and airborne particles, together with their limited foraging range and nesting behaviour, *Osmia* bees enable localized, multi-source environmental sampling. In this study, we investigated whether *Osmia* bees can serve as integrative biosamplers of environmental ARGs and explored how resistome composition varies across environmental contexts.

Methods

Small populations of two *Osmia* species (*O. cornuta* and *O. bicornis*) were released at 26 sites across Catalonia (NE Spain). Sites were classified into seven environmental types: agricultural, coastal, farm-adjacent, hospital-adjacent, natural parks, river environments and urban parks. ARGs were screened in four bee matrices: the bee itself, the bee's body surface, mud used for nest construction and pollen-nectar food provisions. In total, 224 samples were analysed and 34 ARGs were targeted using PCR detection. Rarefied ARG richness was used to describe the diversity of ARGs within each environment, and negative binomial models to investigate drivers of ARG burden. Differences in resistome composition were evaluated using Jaccard dissimilarity, principal coordinates analysis (PCoA) and PERMANOVA. Indicator analysis (ISA and SIMPER) were used to identify ARGs associated with specific environmental categories.

Results

ARGs were detected across all sites and sample matrices, confirming the widespread distribution of resistance determinants. Resistance genes belonging to eight antibiotic classes were detected, with tetracycline resistance genes representing the most prevalent group. ARG richness varied across environmental types but was primarily driven by sample matrix, with pollen-nectar provisions and bee samples showing significantly higher numbers of ARGs. Resistome composition was significantly shaped by the interaction between environmental category and matrix, indicating that the influence of environmental context varies across bee-associated matrices. ARG profiles showed substantial overlap across environments and did not form discrete clusters. A limited number of ARGs showed strong associations with specific environments.

Conclusions

Solitary bees can serve as integrative environmental AMR bioindicators, capturing ARG signals from multiple environmental compartments. While environmental context influences resistome composition, ARG profiles largely overlap across environments, reflecting the widespread distribution of resistance. Bee-associated matrices provide a promising tool for localized, multi-compartment monitoring of environmental AMR, with pollen-nectar provisions and bee samples emerging as the most informative matrices.

1295 – Construction of an integrated data collection network in the context of multi-hosts zoonoses persistence communities

Alexis PEUTOT (1,2), Florence AYRAL (1), Dominique BICOUT (2)

1: USC 1233-RS2GP, VetAgro Sup, Université de Lyon, Marcy L'Etoile 69280, France ; 2: Univ. Grenoble Alpes, CNRS, UMR 5525, VetAgro Sup, Grenoble INP, EPSP - TIMC, 38000 Grenoble, France

Background:

The rapid expansion of human-animal interfaces has increased the risk of zoonotic outbreaks worldwide. Most zoonotic agents are multi-host pathogens whose persistence depends on the host-environment assemblage within an ecosystem, referred to as the pathogen maintenance community. However, the absence of structured surveillance for many emerging multi-host diseases, combined with socio-ecosystem diversity, limited access to key host species, logistical constraints, and restricted environmental monitoring, limits comprehensive field investigations. Addressing these challenges requires integrated ecosystem approaches and participatory surveillance. Stakeholders not traditionally engaged in health surveillance, particularly within the environmental sector, may provide critical insights on specific nodes of the maintenance community. This study develops a visual and analytical tool to map and analyze ecosystem-related information shared among stakeholders to better characterize maintenance communities and support investigations of multi-host pathogen outbreaks.

Methods:

We developed an approach built on available eco-epidemiological knowledge, structured around the source–pathway–target framework, combined with interactions driven by socio-economic activities, political context and legal framework. From that detailed picture of pathogen cycle and drivers, relevant local stakeholders can be identified and engaged through semi-structured interviews. These interviews allow to collect information on the nature, strength, and frequency of links between stakeholders. Those links are then modelled as an information flow (cases notification, data ...) network, enabling detailed analysis of communication patterns and coordination related to multi-host disease risk. This network modelling was also used to investigate many scenarios of information transmission.

Results and discussion:

This method was applied to the context of leptospirosis risk in a mountainous ecosystem and 45 stakeholders were identified of which 26 were interviewed. From stakeholders involved in animal management, water use and management, land practices, economic activities and public health, network analysis identified connected or isolated ones. It revealed strengths and weaknesses in inter-sectoral linkages, thereby highlighting potential gaps in surveillance, prevention, or control systems. In addition, it showed uncovered discrepancies between risk exposure and information flow that will require special attention or information hub that concentrates data. It also reveals sectorial compartmentalisation that needs to be addressed.

Eventually, this framework will provide comprehensive data on the ecosystem which could lead to a higher level of knowledge on the studied multi-host pathogen. These standardized, reproducible approach and method can be applied to any multi-host disease and represents a foundational step toward operationalizing a multisectoral One Health approach. By strengthening cross-sectoral understanding and collaboration, it contributes to co-benefits across human, animal, and environmental health sectors, supporting more resilient and context-adapted One Health systems and responses.

1306 – Comparing temporal and regional patterns of H5Nx avian influenza virus detections through wildlife and domestic bird surveillance in Canada, 2021-2025

Samantha DOBSON (1), David L. PEARL (2), Jolene GIACINTI (3), Manon RACICOT (4), Claire JARDINE (1,5)

1: Department of Pathobiology, Ontario Veterinary College, University of Guelph, Canada; 2: Department of Population Medicine, Ontario Veterinary College, University of Guelph; 3: Ecotoxicology and Wildlife Health Division, Science and Technology Branch, Environment and Climate Change Canada, Government of Canada; 4: Animal Health Epidemiology, Surveillance & Laboratory Services Section, Science Branch, Canadian Food Inspection Agency; 5: Canadian Wildlife Health Cooperative

Background:

The incursion of highly pathogenic avian influenza (HPAI) H5Nx viruses into North America in late 2021 renewed emphasis on wildlife surveillance for avian influenza viruses (AIVs). In Canada, wildlife detections are reported through Canada's Interagency Surveillance Program for Avian Influenza Viruses in Wild Birds, which includes passive morbidity/mortality surveillance and active sampling of live and hunter-harvested wildlife. Concurrently, infections in domestic bird premises (IPs) are identified through the Canadian Notifiable Avian Influenza Surveillance System (CanNAISS). Although these systems operate in parallel, their components capture different aspects of HPAI virus epidemiology and reflect distinct surveillance objectives and sampling strategies. Consequently, temporal and regional patterns observed in wildlife and domestic birds require careful contextualization. Herein, we examined temporal and regional patterns of HPAI H5Nx virus detections across wildlife surveillance components and in IPs throughout Canada from 2021 to 2025.

Methods:

Wildlife surveillance data were compiled for sick and dead wild birds and mammals, live birds, and hunter-harvested birds sampled across Canada from 4 November 2021 to 15 May 2025. IPs during the same period were identified through the Canadian Food Inspection Agency (CFIA). Wildlife test-positives were defined as confirmed HPAI- or H5-subtype virus-positive samples. Weekly wildlife test-positive proportions and sampling counts were plotted by surveillance component alongside weekly IP counts, stratified by region and study year. Retrospective temporal scan statistics were used to identify periods of elevated wildlife test-positive proportions and elevated commercial IP counts. Analyses were conducted nationally and regionally where denominator data were available.

Results:

A total of 53 111 wildlife samples were analyzed (n = 51 593 birds; 1518 morbidity/mortality mammals), with an overall proportion of test-positives of 8.8% (95% CI: 8.6–9.0). Positivity was highest in British Columbia (14.2%) and lowest in the Northern Canada (0.7%). Test-positive proportion varied by surveillance component: morbidity/mortality birds 21.6%, live birds 2.7%, hunter-harvested birds 3.3%, and morbidity/mortality mammals 15.3%. A total of 528 IPs were identified, of which 73.1% were commercial. The largest number of IPs occurred in British Columbia (n = 238), followed by Alberta (n = 84) and Ontario (n = 61). Nationally, wildlife detections and IPs showed recurrent seasonal waves from 2021-2025, with the largest increases in spring and autumn 2022. Scan statistics identified significant clusters of elevated commercial IP counts and multiple significant clusters of elevated wildlife test-positive proportions across surveillance components.

Conclusions:

Wildlife and domestic bird surveillance systems captured recurrent, seasonally structured waves of HPAI H5Nx virus activity that were broadly temporally aligned across Canada. Differences in magnitude and timing across wildlife surveillance components highlight the value of maintaining complementary sampling streams, while integrating signals across surveillance systems may strengthen situational awareness and support adaptive surveillance during prolonged HPAI virus circulation.

1315 – Exploring Zoonotic Pathogens and Contact Networks in Backyard Production Systems: Early Insights for Integrated Prevention and Control Strategies.

Raúl ALEGRÍA-MORÁN (1), Victor NEIRA (2), Galia RAMÍREZ-TOLOZA (3), Catalina ALFARO-GODOY (3), Alexis ORTEGA (2), Javiera SILVA-CERDA (3), Tury SEPULVEDA-ZAMORANO (3), Antonia PONCE (3)

1: Escuela de Medicina Veterinaria, Facultad de Medicina, Facultad de Ciencias Biológicas y Facultad de Agronomía y Sistemas Naturales, Pontificia Universidad Católica de Chile, Santiago, Chile.; 2: Laboratorio de Virologia Animal, Departamento de Medicina Preventiva Animal. Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile.; 3: Laboratorio de Parasitología y Enfermedades Parasitarias, Departamento de Medicina Preventiva Animal, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile.

Background: Backyard production systems (BPS) are vital food sources in low-income areas, yet their limited biosecurity and veterinary oversight pose significant public and one health risks. In Chile, these systems facilitate the circulation of zoonotic pathogens such as *Salmonella enterica*, Avian Influenza (AIV), Newcastle disease virus (NDV), *Chlamydia psittaci*, Shiga toxin-producing *E. coli* (STEC), and parasites. As potential sites of emergence for new diseases, BPS represent a silent threat. Understanding the interactions within these systems is crucial for preventing the spread of zoonotic pathogens between animals and humans. Thus, this study aims to determine how BPS contact networks influence pathogen circulation and risk factors in central Chile. We will characterize the zoonotic patho-biome, identify infection drivers, explore spatial risk clusters, and define system structures through network analysis to enhance regional prevention.

Methods: A total of 381 BPS, from the Valparaíso and Metropolitana regions, will be sampled within the project. Previously validated real-time PCR assays are being used to detect and quantify targeted zoonotic pathogens (*Salmonella* spp., STEC, C. psittaci, NDV, and AIV), and direct diagnostic and conventional PCR will be used for parasite diagnostics. If possible, Positive samples will be attempted for pathogen isolation for molecular diagnostic purposes. A logistic multivariable regression model (LRM) will be used to identify risk factors, and the Kulldorff Scan Statistics will be applied to detect spatial clusters. KAP + epidemiological survey, plus BPS georeference, will be used to plot and estimate network parameters.

Results: To date, a total of 151 samples have been collected, corresponding to 15 BPS from the Metropolitana region (3.9% of the project, and 10.4% of the region). Samples from poultry, small ruminants, swine, equine, pets (dogs and cats), and other poultry species have been collected. Ninety-two (62.3%) samples have been analyzed by real-time PCR. For AIV, 7 samples (7.6%) have been reported as suspicious, from 5 BPS in the southern part of the region. No positive samples have been detected for NDV. Among parasite species, Ancylostoma-like, *Toxocara canis,* and *Cryptosporidium* spp. were reported in 1 BPS in dog samples, respectively; in poultry, *Capillaria* spp. (5/15), *Eimeria* spp. (6/15), Ascaridia-like eggs (6/15), Strongylid-like eggs (1/15), and Raillietina spp. (2/15) were reported. Bacteria have not yet been analyzed. In terms of the network structure, a common source of animal food and live animals was detected, as well as the exchange of live birds among BPS at the local and extra-regional levels.

Conclusions: This study will provide the first evidence of the wider circulation of zoonotic and non-zoonotic pathogens among animals from BPS in the Valparaíso and Metropolitana regions of Chile, and of the potential of BPS's highly connected network structure in central Chile, helping future One Health surveillance design.

1322 – Does One Health governance reduce pandemic impact? A global analysis of excess mortality across 90 countries during COVID-19

Marisa PEYRE (1,2), Othilie RADWAN (1,2), Daan VINK (1,2)

1: CIRAD, UMR ASTRE, F-34398 Montpellier, France.; 2: ASTRE, Université de Montpellier, CIRAD, INRAE, Montpellier, France.

BackgroundThe COVID-19 pandemic revealed important gaps in global pandemic preparedness and challenged the reliability of existing preparedness indicators. The One Health (OH) approach, integrating human, animal and environmental health, has increasingly been promoted as a framework for preventing and managing emerging health threats. However, empirical evidence assessing its effectiveness in real-world crises remains limited. This study explores whether countries that had established One Health governance structures prior to the COVID-19 pandemic experienced different pandemic outcomes.

MethodsWe conducted a cross-country analysis covering 90 countries, using data on national OH governance. Pandemic impact was assessed using maximum excess mortality (ExM_Max) between 2020 and 2022, calculated from World Bank mortality data. Expected mortality trends were projected from 2010–2019 using a log-linear model. ExM_Max was analysed in relation to One Health governance level, degree of operationalization, economic development level, and the Global Health Security Index (GHSI).

Non-parametric statistical tests (Spearman correlations, Kruskal-Wallis, Dunn post-hoc tests) were performed. A principal component analysis (PCA) followed by cluster analysis was used to identify country typologies.

ResultsNo significant correlation was found between ExM_Max and conventional preparedness indicators, including the GHSI, OH governance level, or operationalization of the OH approach. However, pandemic impact varied significantly across economic development levels. Upper-middle-income countries (UMICs) experienced significantly higher excess mortality than lower-middle-income (LMICs) and high-income countries (HICs). Multivariate analysis identified three distinct country profiles: (i) high ExM_Max associated with weak OH governance in UMICs; (ii) moderate ExM_Max with moderate OH governance in HICs; and (iii) low ExM_Max with moderate-to-strong OH governance in low-income countries (LICs).

ConclusionOur findings highlight the limits of conventional preparedness indicators in explaining pandemic outcomes and emphasize the complexity of factors shaping health system resilience. While no direct statistical relationship was observed between OH governance indicators and pandemic mortality, the results suggest that governance structures, intersectoral coordination, and broader socio-institutional dynamics play a key role in shaping crisis responses. Strengthening operational and governance dimensions of One Health may therefore be critical to improve preparedness and resilience to future pandemics.

1328 – Large-scale genomic analysis of Salmonella enterica reveals circulating virulence and antimicrobial resistance genotypes in food chains in the Philippines

Thomas Michael ROBERTS (1), Jonah Feliza B. MORA (2), Alyzza Marie B. CALAYAG (2), Jacob Anderson C. SANCHEZ (3), Jody PHELAN (1), Woranich HINTHONG (1,5), Julius C.R HAFALLA (1), Martin L. HIBBERD (1), Susana CAMPINO (1), Geraldine C. SANCHEZ (3), Windell L. RIVERA (2), Taane G. CLARK (1,4)

1: Department of Infection Biology, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Street, London, UK; 2: Pathogen-Host-Environment Interactions Research Laboratory, Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City, Philippines; 3: College of Veterinary Medicine, Pampanga State Agricultural University, San Agustin, Magalang, Pampanga, Philippines; 4: Faculty of Epidemiology and Population Health, London School of Hygiene and Tropical Medicine, Keppel Street, London, UK; 5: Princess Srisavangavadhana Faculty of Medicine,Chulabhorn Royal Academy, 906 Kamphaeng Phet 6 Road, Talat Bang Khen, Lak Si, Bangkok 10210, Thailand

Salmonella enterica, a zoonotic pathogen and leading cause of foodborne illness, is readily transmitted from animals to humans through the consumption of contaminated food. Understanding the transmission routes of *S. enterica* along the farm-to-table continuum, as well as the spread of antimicrobial resistance genetic variants through pathogen sequencing, is critical for improving infection control. In the Philippines, the increasing demand for chicken and pork products, coupled with limited regulation of antibiotic use in farming, poses a significant risk of foodborne *Salmonella* infections caused by antibiotic-resistant and multidrug-resistant (MDR) strains. This concern is particularly acute in Metropolitan Manila, where wet markets serve as a major source of meat products for the public. Using Illumina whole-genome sequencing, we analysed the genomic diversity of 1,139 *S. enterica* isolates collected between 2019 and 2022. These isolates were sourced from chicken (*n*=662; 58.1%) and pork (*n*=477; 41.9%) in wet markets and slaughterhouses in Metro Manila, as well as veterinary clinics in Pampanga. A total of 45 serovars were identified, with four - *S.* Infantis (*n*=220, *S.* Anatum (*n*=179), *S.* Uganda (*n*=121), and *S.* London (*n*=83) - accounting for over half (52.9%) of the isolates. Globally significant serovars associated with severe illness, such as *S.* Typhimurium (*n*=51; 4.5%) and *S.* Enteritidis (*n*=26; 2.3%), were also detected (**Figure 1**). Over half of the isolates encoded resistance to at least one antibiotic class, with seven isolates being genotypically resistant to the last-resort antibiotic colistin. We also found that chicken and markets saw higher proportions of resistant isolates as well as a wider range of genes encoding genotypic resistance to a wider range of antibiotic classes compared to pork and slaughterhouses (**Figure 2**). All isolates harboured 10–15 virulence factors, with higher counts of resistance genes and virulence factors observed in isolates from chicken and wet markets. By integrating publicly available *S. enterica* data (*n* = 1,323), we identified more than 100 potential transmission chains, including 10 clusters comprising 20 to 124 isolates across 7 serovars, suggesting shared sources among samples (**Figure 3**). This one-health approach to pathogen surveillance highlights the increasing prevalence of MDR *Salmonella* in the Philippines, particularly in chicken samples, and underscores the heightened virulence of isolates originating from chicken and wet markets. Furthermore, the transmission

chains point to common sources of these MDR and potentially virulent pathogens, emphasising the urgent need for an integrated, sequencing-based diagnostic approach to mitigate their spread along the farm-to-table continuum.

Figure 1. A phylogenetic tree of the collected isolates from Metro Manila cities and Pampanga province (n=1,139). The ten most common serovars found in the dataset have been numbered. The bands surrounding the clades detail the sampling locations around Metro Manila, and if the samples were collected from the Pampanga province, as well as if the samples were from chicken and pork (type of meat) and what environment they were sourced from (Markets being wet markets, slaughterhouses specialising in pigs, and vet clinics being regular clinics in Pampanga).

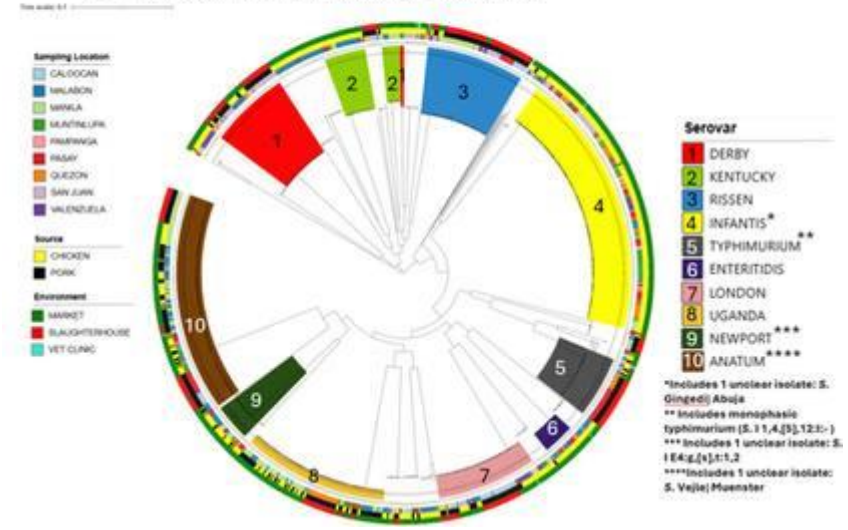
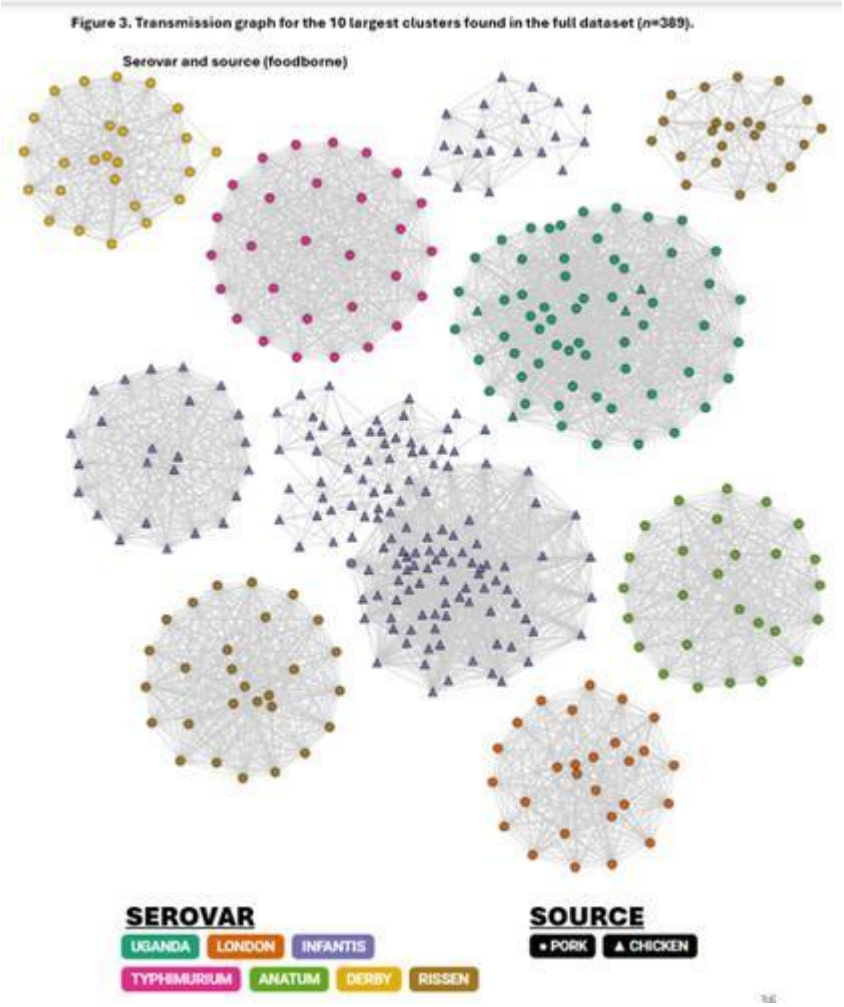


Figure 2. Heatmaps of the presence of genes encoding genotypic resistance to different detected classes of antibiotics in the dataset. To be accepted as present, the detected gene must resemble at least 80% of a known resistance gene and achieve a minimum of 80% coverage.



1335 – Investigating Avian Influenza Viruses in Mammals to Assess Zoonotic Threats

Veronica LEHTINEN (1,2), Eda ALTAN (1,2), Kirsi AALTONEN (1,2), Pamela ÖSTERLUND (1), Tarja SIRONEN (1,2)

1: Department of Virology, University of Helsinki, Finland; 2: Department of Veterinary Biosciences, University of Helsinki, Finland

Background: The recent spread of highly pathogenic avian influenza (HPAI) H5N1 across birds and mammals highlights the importance of understanding how avian influenza viruses circulate at the wildlife-livestock-human interface. This doctoral project takes a One Health approach to investigate potential mammalian reservoirs, their role in transmission, factors influencing viral persistence, and early host-virus interactions in human airway cells. The work combines international and national studies across three main research areas: (1) surveillance of influenza viruses in fruit bats in Kenya, (2) development of human airway cell models to study early events of infection, and (3) virome analysis of animals affected during the 2023 Finnish fur-farm H5N1 outbreak. The overall goal is to clarify the role mammals play in the circulation and cross-species transmission of avian influenza viruses. **Methods:** Field sampling of fruit bats is conducted in caves near Shimoni, Kenya. Bats are captured, sampled, and released after collection. Oral and rectal swabs are screened using influenza A RT-qPCR and a bat-specific H9N2 RT-real-time PCR, while blood samples are analyzed using bat H9/N2-specific ELISA. Human primary nasal epithelial (HNE) cells are expanded and differentiated at air-liquid interface (ALI) to create a physiologically relevant model of the upper airway for infection and early host-virus interaction studies. In parallel, lung, intestinal, and fecal samples collected from fur-farm animals during the 2023 H5N1 outbreak will undergo RNA/DNA extraction and next-generation sequencing to characterize the full virome and detect possible co-infections that could influence susceptibility. **Results:** Between 2023 and 2025, 350 fruit bats were sampled in southeastern Kenya. Collaborators reported high seropositivity in

2023-collected blood samples from Egyptian fruit bats in the Shimoni region, suggesting previous exposure to influenza-like viruses circulating in bats. Specifically, 73% reacted positive in the Bat H9-spicific ELISA, and 65% reacted positive in the Bat N2-specific ELISA. However, all swabs tested negative in PCR assays. HNE ALI cultures have been successfully established and differentiated into a pseudostratified, ciliated epithelium suitable for infection experiments. Preliminary assays show that HPAI H5 can enter these cells. Ongoing experiments will assess viral replication and innate immune responses between seasonal and avian type viruses. Virome sequencing of Finnish fur-farm animals is underway to determine whether cocirculating viruses contributed to the severity or spread of the 2023 outbreak. **Conclusions:** Together, these three research studies provide a broader understanding of how influenza viruses circulate in wildlife, how they interact with the human upper airway, and how coinfections may shape outbreak dynamics in mammals. The findings support improved surveillance, biosecurity, and pandemic preparedness within a One Health framework.

1343 – Community, Youth Engagement and Cultural Integration in Advancing One Health: Experiences from COHESA, Kenya

Mosbei JEPTOO (1), Marianne W. MUREITHI (1), Moses MASIKA (1), Lillian OMUTOKO (1), Joshua ONONO (1), Salome BUKACHI (1,2)

1: University of Nairobi, Kenya; 2: Durham University, UK

Background

Human, animal, and environmental health have become increasingly intertwined. Engaging communities, especially the youth is critical to turning One Health principles into practical action in addressing complex health issues. Youth play a key role in shaping sustainable health and environmental practices, yet their participation in One Health initiatives is often underutilized. The Capacitating One Health Eastern and Southern Africa (COHESA) project in Kenya has supported initiatives aimed at strengthening awareness, interdisciplinary learning, community and youth participation in One Health implementation. This abstract describes experiences from two such initiatives: a community and youth tree planting activity in Mathare North, Nairobi, and University of Nairobi Faculty of health Sciences cultural week, which used cultural expression to promote One Health awareness.

Methods

COHESA Kenya supported awareness activities that were implemented through participatory community and youth engagement in collaboration with academic institutions. The Mathare North activity involved various university environmental clubs, community youth groups, and local stakeholders who participate in environmental discussion around urban greening through planting of indigenous tree seedlings. During the activity, short environmental education sessions were held to discuss how ecosystem health, climate resilience, and human well-being are interconnected. To enhance community engagement, awareness messages were communicated through culturally relevant methods like traditional songs and dance performances that translated One Health concepts into locally accessible narratives. A series of webinars by COHESA provided a knowledge-sharing platform for students and the faculty on One Health principles, interdisciplinary collaboration, and the role of culture in health promotion. Insights from these webinars inspired medical school students to adopt One Health as the central theme for its annual cultural week.

Results

The Mathare North initiative resulted in the planting of over 100 indigenous tree seedlings while fostering dialogue on environmental conservation and public health among community members and students. The use of songs and dance enhanced community participation and improved the accessibility of environmental and health messages. The faculty cultural week further expanded awareness by bringing together students from diverse disciplines (Anthropology, Medicine and Veterinary Science) to showcase their cultural backgrounds in sharing their understanding of one health through various forms of knowledge sharing- music, art, fashion and panel discussions. Through exhibitions, cultural performances and discussions, students explored how cultural values influence health behaviors and environmental interactions.

Conclusion

These experiences demonstrate that youth are critical players in the One Health conversations and dissemination as well as in advancing its debate and implementation through youth appropriate channels. These initiatives provide an example of how community-driven and youth-led interventions can enhance knowledge translation and capacity building. The COHESA Kenya experience highlights the potential of culturally grounded and community-driven approaches to advance sustainable and inclusive One Health implementation in urban and academic settings and among the youth.

1348 – What's in the Water? A Metagenomic Exploration of the One Health Risks of Antimicrobial Resistance in a Scottish Wild Swimming Site.

Silken TSCHOFEN (1), Natalie RING (1), Scott HAMILTON (2), Eleanor WATSON (2), Ross FITZGERALD (1), Inaki DEZA-CRUZ (1), Lynsey MELVILLE (2), Jessica MITCHELL (1)

1: University of Edinburgh, Edinburgh, United Kingdom; 2: Moredun Research Institute, Penicuik, United Kingdom

Background: Freshwater environments are increasingly recognized to be reservoirs and disseminators of antimicrobial resistance (AMR) which are influenced by anthropogenic activities. Despite this, and amongst growing concerns of poor water quality in the United Kingdom (UK), there remains limited surveillance of AMR in freshwater sites. The wild swimming community, who actively participate in their activity within the natural environment and often adjacent to agricultural spaces, present an ideal population to engage with regarding concerns of AMR across multiple One Health dimensions. Herein we use a metagenomic approach to explore the resistome of a freshwater wild swimming site in Scotland and inform a future wider surveillance study which seeks to better understand the risk relationship of AMR between humans, animals, and the environment.

Methods: Sediment and water samples were collected from a freshwater reservoir in Scotland. DNA was extracted for metagenomic sequencing and pooled samples were prepared and sequenced using Oxford Nanopore Technologies ligation sequencing gDNA-Native barcoding kit on a PromethION FLO-PRO114M flow cell with Dorado super-accurate basecalling. Bioinformatic analyses included basic read quality control with NanoStat and antibiotic resistance gene (ARG) prediction with DeepArg. Additional bioinformatic analyses will involve assembly with Flye and taxonomic classification and estimated species abundance with Kraken2 and Bracken with the GTDB database (release 226).

Results: In total, 66.94 Gb and 48.02 M reads were generated, with a N50 of 3.02 kb, and a median Q-score of 25. Water samples generated an average of 1.736 Gb, and 1.07 M reads, and sediment samples generated an average of 1.78 Gb, and 14.47 M reads. 43 and 146 unique AMR genes were predicted from water and sediment samples respectively, encompassing multiple drug classes including aminoglycosides, beta-lactams, and fluoroquinolones.

Conclusions: This pilot surveillance study identified the presence of AMR genes, which when combined with final bioinformatic analysis, is anticipated to provide greater contextualized insight into the distribution and diversity of AMR genes in freshwater. These findings emphasize the importance of monitoring freshwater sites, especially those which act as intersections of One Health spheres, such as wild swimming sites.

1351 – Surveillance of HPAI H5Nx in clinically healthy wild birds and mammals in Ukraine

Nataliia MUZYKA (1), Oleksandr RULA (1), Ann Kathrin Ahrens ANN KATHRIN AHRENS (3), Francesco BONFANTE (4), Siamak ZOHARI (5), Anne POHLMANN (3), Martin BEER (3), Jonas WALDENSTRÖM (2), Denys MUZYKA (1,2)

1: NSC Institute of Experimental and Clinical Veterinary Medicine, Ukraine; 2: Linnaeus University, Kalmar, Sweden; 3: Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany; 4: Istituto Zooprofilattico Sperimentale delle Venezie, Italy; 5: National Veterinary Institute, Swedish Veterinary Agency, Uppsala, Sweden

Background. Influenza A viruses (IAVs) continue to pose a serious threat for the health of humans and animals, affecting both public health and food safety. The capacity of IAV to cross species barriers, and ability for rapid genetic change makes these viruses significant pathogens. Of particular concern is the repeated spillover infections of highly pathogenic avian influenza (HPAI) viruses to wild and domestic carnivores in Europe, seals and other marine mammals in the Americas, and cattle in the USA. These

examples emphasize the importance of research into IAV biology and epidemiology, particularly in natural animal reservoir species, and to develop preparedness plans for future outbreaks.

Methods. Active and passive surveillance for IAV was carried out in Ukraine for two decades (2005-2025), generating more than 40,000 samples from wild birds, and more than 5000 wild and domestic mammals. Samples were screened for presence of virus RNA and/or antibodies to IAV and HPAI H5 2.3.4.4b viruses, before further characterization using subtyping, genome sequencing and virus neutralization and hemagglutinin inhibition assays. Research was funded by NAAS, R&D Joint project of MES of Ukraine, NRFU (#2021.01/0006; #2025.07/0063), STCU (P444a-b P777).

Results. Ukraine lies at the intersection of different migratory flyways and host a large number of migratory birds during autumn, winter and spring. From 2005-2025, H5N1 and H5N8 HPAI viruses were isolated from wild birds, including Great Cormorants, Great Crested Grebes, Ruddy Shelduck, White-fronted Goose, Mallard, and Eurasian Teal. The epidemiologically important HPAI virus H5Nx clade 2.3.4.4b has been circulated in wild birds in Ukraine since 2016, originally only in dead wild birds. An increased circulation of clade 2.3.4.4b H5Nx in wild birds has been registered since 2020 and since 2021 these viruses have been detected in clinically healthy wild birds (0.82–3.42%). Concomitant serological surveillance of wild waterfowl showed high seroprevalence to HPAI H5Nx clade 2.3.4.4b in ELISA (69.4–71.4%). Evidence of circulation of HPAI was detected in wild mammals in Ukraine. The wide serological surveillance of domestic and wild carnivores detected antibody to influenza A (1.57–11.88%) in 2023-2024. Further research has shown seroprevalence to HPAI H5 in 0.78–10.2% of red foxes and domestic cats. At the same time wide surveillance of domestic swine, horses, wild boars didn't detect any H5 positive cases.

Conclusion. Our findings highlight the importance of continued surveillance efforts in Ukraine. As disease knows no borders, surveillance in Ukraine has regional significance, including for the European Union. This region serves as a crucial hotspot for early detection of new IAV variants including HPAI viruses prior to their incursion into Europe. Detection of seropositivity to H5 HPAI virus in wild and domestic carnivores indicates expansion of this epidemiologically important variant in a new territory in Europe.

1355 – Mapping Progress: Milestones and Outcomes in the EU's Cross-Agency One Health Task Force

Maya CARVALHO-EVANS (1), **The CROSS-AGENCY ONE HEALTH TASK FORCE** (1,2,3,4,5)

1: European Food Safety Authority; 2: European Environment Agency; 3: European Centre for Disease Prevention and Control; 4: European Chemicals Agency; 5: European Medicines Agency

Background: As Europe advances toward operationalising a One Health approach, cross-sector cooperation has become indispensable. Recent years have demonstrated that silos can be bridged, and agencies can act together under a shared purpose. Since 2022, the global governance landscape has accelerated. The Cross-agency One Health Task Force, uniting ECDC, ECHA, EEA, EFSA, and EMA, was established to implement the One Health approach, making the EU and its Member States better able to prevent and respond to health threats. The Task Force agreed on a joint framework for action, which aimed to be implemented over a period of three years (2024–2026) providing a basis for addressing One Health challenges [1]. This presentation aims to increase awareness of the tangible outcomes to date, illustrated graphically, depicting progress across the five strategic objectives.

Methods: The task force's activities were monitored throughmonthly walk-in calls involving members of the task force from the five EU agencies. A shared living document was maintained to collect relevant data and updates on projects. Reporting lines were established, designating lead and supporting agencies for each activity and documenting activities. Elements of the Network for Evaluation of One Health (NEOH) framework provided guidance, through systems thinking methods, on how to define the initiatives and evaluate outcomes [2]. Progress was assessed using milestone classification and status-tracking, enabling early identification of delays, resource needs, and transition between development phases. These processes provided a structured approach to converting strategic objectives into measurable outputs.

Results: The outcome of this exercise presents tangible deliverables and a stronger understanding of the progress that has been made by the EU agencies collaborating to implement the One Health approach. A figure was developed to illustrate the three main milestones, and their implementation status, under each of the five strategic objectives. The 2026 projection indicates targeted completion or substantial

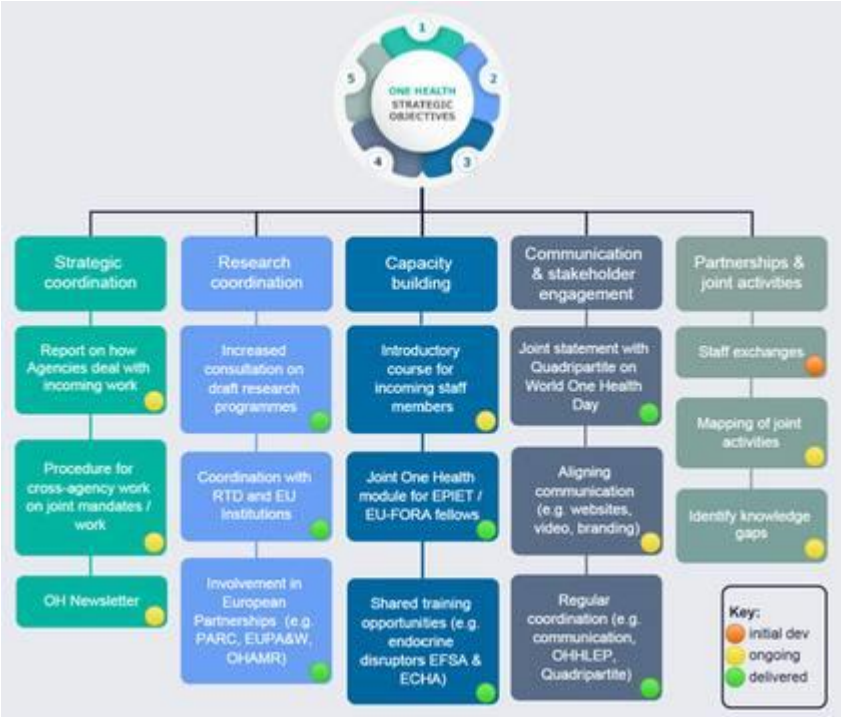
advancement across most actions. Collectively, these milestones demonstrate the added value of cross-agency cooperation and reflect substantive progress toward embedding One Health implementation within EU institutional practice.

Conclusions: As the EU prepares its next steps, the evolving work of the Cross-agency One Health Task Force offers lessons on structured collaboration, coordinated implementation, and system-level enablers. These insights can support the future evolution or renewal of the Framework for Action and contribute to a more resilient and integrated One Health landscape for Europe.

References:

[1] Bronzwaer, S., de Coen, W., Heuer, O., Marnane, I., & Vidal, A. (2024). The framework for action of the Cross-agency One Health Task Force. One Health, 19, 100925.

[2] Rüegg, S. R., Häsler, B., & Zinsstag, J. (Eds.). (2018). Integrated approaches to health: a handbook for the evaluation of One Health. Wageningen Academic Publishers.



1360 – One Health participatory theatre for gender transformative Taenia solium control in Southern Rwanda: A pilot study

Prince RWAGASORE (1), Tayechalem MOGES (1), Ruth Zihiga UWASE (1), Anne DECKERT (2), Catherine DEWEY (2), Anselme SHYAKA (1), Janna SCHURER (1)

1: University of Global Health Equity, Rwanda; 2: University of Guelph, Canada

Background

Taenia solium is a zoonotic cestode endemic to Southern Rwanda where it causes significant human and economic losses. In this region, men and women generally occupy complementary roles along the smallholder pork value chain, accessing different resources, and exercising different levels of agency. This pilot project aimed to explore the value of participatory theatre in delivering integrated One Health and gender-transformative messaging to rural Rwandese communities engaged in reducing the human and swine burden of T. solium. It was part of the Community One Health Empowerment in Senegal and Rwanda (COHERS) program.

Methods As part of the COHERS (Community One Health Empowerment in Rwanda and Senegal) initiative and a broader 1-year One Health curriculum, village One Health Teams in Rwanda were trained to deliver participatory theatre emphasizing mechanisms of T. solium transmission/control and the value of shared household decision making in disease prevention. Over a 3-month period in 2025, One Health Teams in 85 villages across three sectors of Nyamagabe District (Southern Province) presented their skits during regular community gatherings. Each skit ended with a question-and-answer session where audience members could express their views and experiences. Two trained enumerators planned to attend sessions in 20% of villages to observe and document gender-disaggregated attendance, participation and overall uptake using a standardized tool. Thematic saturation was considered the endpoint for data collection.

Results Across the 17 observed villages, approximately 845 female and 555 male residents (N=1400) attended the sessions. Of those,131 voluntarily participated in the theatre or shared questions/experiences. Adolescents were notably absent and older women chose not to voice opinions. In general, attendees agreed that the theatre narrative closely resembled gender norms and pig husbandry practices in their villages, while also prompting reflections on gendered expectations embedded in these practices. The topic of shared roles and decision making between men and women attracted the most commentary. As one male participant commented, “I did not see the benefit of taking the woman to the market or involving her in household financial decisions”. Other attendees demonstrated clear knowledge uptake on T. solium transmission and control.

Conclusions

This participatory theatre intervention was generally welcomed as a fun, informative and inclusive way to learn important One health information as well as to engage in sensitive gender discussions. Such tools have practical applications for low resources settings where community sensitization plays a critical role in managing neglected and zoonotic diseases.

1366 – Integrating Gender into One Health: A Woman’s Perspective on Community Resilience

Tatiana MARRUFO

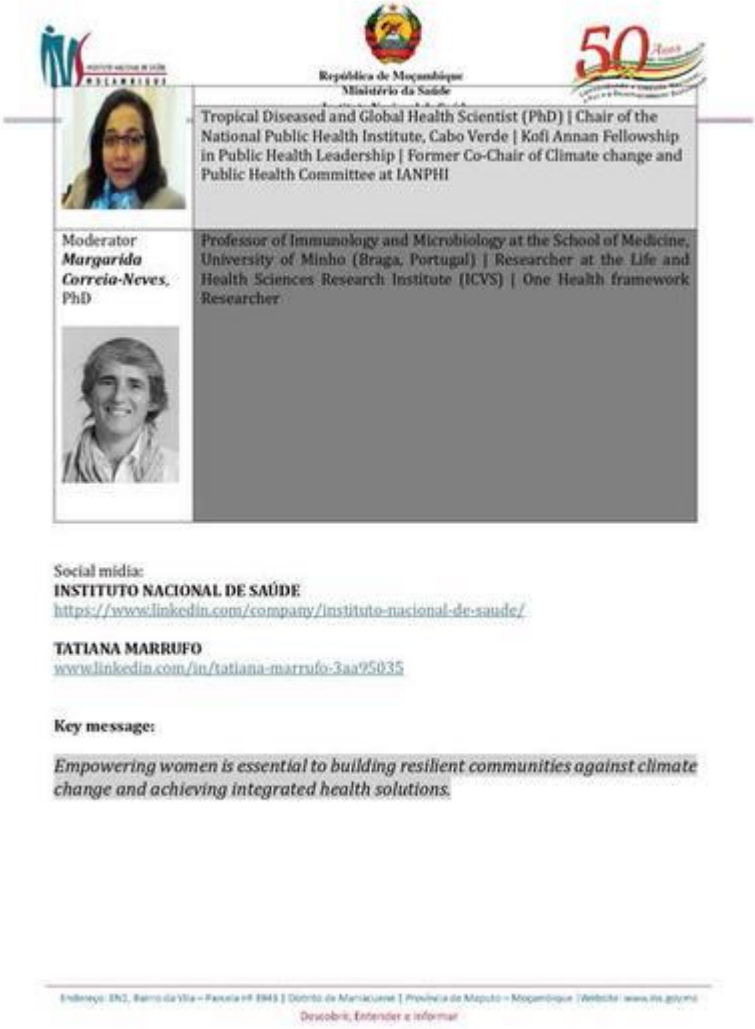
Instituto Nacional de Saúde, Mozambique, Mozambique

Extreme climate events affect human health, environmental stability, and local ecosystems to similar extents, highlighting the need for integrated approaches. These events impact ecosystems, food production, and water availability, increasing the risk of infectious diseases and maternal health problems. Women, particularly in tropical and rural contexts, play central roles in maintaining family well-being, coordinating community resources, and managing immediate responses to disasters. Their experiences and adaptation strategies provide a crucial perspective for understanding how human, animal, and environmental health intersect in times of crisis. The proposed session is innovative in that it combines gender, public health, and climate change, an issue of great relevance and global impact. It will explore how the challenges faced by women after extreme events, such as food insecurity, exposure to disease, and psychological stress, interact with environmental and social factors. This approach focuses on understanding vulnerability and community adaptation, highlighting women as key nodes within integrated health systems and as mediators between human needs and environmental impacts. The expected educational outcome includes increased understanding of the importance of women’s

leadership and participation in maintaining community and environmental health in post-disaster contexts. This integration will help develop more effective and sustainable approaches to addressing the challenges posed by climate change, recognizing the central role of women in promoting health and environmental balance. In this context, the National Institute of Health of Mozambique intends to organize a discussion around this topic with African female researchers who are contributing to this field in the region.

Session structure	
Title	**Integrating Gender into One Health: A Woman's Perspective on Community Resilience**
Venue	*Institute of Hygiene and Tropical Medicine, NOVA University of Lisbon*
Modality	This session is proposed to be a 90-minute in-person session, composed by three female speakers and one female moderator. Each speaker is proposed to talk for about 20 minutes, and at the end the moderator will have 30 min for interaction with the audience and also Q&A for the speakers.
Background	Extreme climate events affect human health, environmental stability, and local ecosystems to similar extents, highlighting the need for integrated approaches. These events impact ecosystems, food production, and water availability, increasing the risk of infectious diseases and maternal health problems. Women, particularly in tropical and rural contexts, play central roles in maintaining family well-being, coordinating community resources, and managing immediate responses to disasters. Their experiences and adaptation strategies provide a crucial perspective for understanding how humans, animals, and environmental health intersect in times of crisis. The proposed session is innovative in that it combines gender, public health, and climate change, an issue of great relevance and global impact. It will explore how the challenges faced by women after extreme events, such as food insecurity, exposure to disease, and psychological stress, interact with environmental and social factors. This approach focuses on understanding vulnerability and community adaptation, highlighting women as key nodes within integrated health systems and as mediators between human needs and environmental impacts. The expected educational outcome includes increased understanding of the importance of women's leadership and participation in maintaining community and environmental health in post-disaster contexts. This integration will help develop more effective and sustainable approaches to addressing the challenges posed by climate change, recognizing the central role of women in promoting health and environmental balance. In this context, the National Institute of Health of Mozambique intends to organize a discussion around this topic with African female researchers who are contributing to this field in the region.

Session objectives	• Discuss how women's roles in households and communities influence adaptation strategies and health outcomes following climate-related disasters. • Analyze the gendered dimensions of vulnerability in post-disaster contexts. • Highlight evidence and experiences from African and international researchers working at the intersection of gender, climate change and One Health. • Identify opportunities for integrating gender-responsive approaches into climate resilience, public health and One Health policies
Speaker 1 ***Delfina Hlashwayo***, PhD	Proposed topic: **Gendered dimensions of vulnerability in post-disasters contexts: the case of Mozambique** Global Health Scientist (PhD) | World Health Organization Advisor UN | UNESCO External Expert | UN fellow '24 | Best young health researcher MZ 2025
Speaker 2 ***Tatiana Marrufo***, MD MPH PhDc	Proposed topic: ***Opportunities for integrating gender-responsive approaches into climate resilience in Mozambique*** Public Health and Environmental Health Scientist | Environmental Health Strategic Program, including the Occupational health Program Lead | Chair of the Resilience and Adaptation sub-group of the Emergency and Response Group of the Ministry of Health, Mozambique | Co-Chair of Climate change and Public Health Committee at IANPHI
Speaker 3 ***Maria da Luz Lima***, MD PhD	Proposed topic: ***ONE-Health approaches and experiences to influence adaptation strategies and health outcomes in a era of changing climate***



1372 – Interventions in informal food markets deliver health and wealth: the Vendor Business School in Nairobi and Quezon City

Silvia ALONSO (1), **Garima SHARMA** (1), Phoebe RICARTE (2), Arma BERTUSO (3), Gordon PRAIN (4)

1: International Livestock Research Institute (ILRI); 2: International Rice Research Institute (IRRI); 3: International Potato Centre (CIP); 4: Freelance; United Kingdom

Background. The informal food sector is a large and essential component of the urban food systems in the Global South. Most people living in urban areas of low- and middle-income countries depend on this sector for their daily food needs. It is also an accessible source of job opportunities for many, especially women and youth. These societal contributions are compromised by widespread public health concerns around food safety. Governments have generally failed to create the enabling conditions needed to support the sector. Improving the handling and safety of foods traded in the informal sector requires not only investments in technologies and infrastructure, but a radical new approach that combines capacity building on food handling with strengthening of entrepreneurial capabilities. We developed the Vendor Business School (VBS), a capacity building program for vendors in the informal sector that combines group training and individual coaching to support the vendors through a journey of transformation towards improved food handling, enhanced business skills, and entrepreneurial drive.

Methods: The VBS was tested among women running dairy businesses in Nairobi, Kenya, and vegetable market vendors in Quezon City, Philippines. We used a quasi-experimental design where a group of vendors enrolled in the program and a comparison group were monitored over time. A team of

intensively trained facilitator-coaches ran the 7-month program through weekly group sessions followed by individual coaching. Baseline and endline surveys were administered to both groups before and immediately after the program. The study evaluated the effect of the program on two primary outcomes: acquisition of food safety knowledge or uptake of food safety practices and monthly business profit. We conducted regression models to explore the effect of the intervention on the outcomes. Adjusted models included the outcome measure at baseline and any variables that were unbalanced between the groups at baseline.

Results: A total of 236 and 271 vendors participated in the study in Kenya and the Philippines, respectively. In Kenya, trained vendors had, at endline, three times the odds of having adopted at least one new milk safety practice compared to the comparison group; the training didn't have a statistically significant effect on profit, although vendors in the intervention group reported higher revenues at endline. In the Philippines, no effect was observed on food safety knowledge, mostly due to high knowledge at baseline. Trained vendors reported substantially higher profits at endline compared to controls.

Conclusions: The study shows how a program that onboards informal sector food vendors on a journey to grow their entrepreneurial mindset can deliver food safety and business outcomes. The effect of the program was markedly different across both countries. Further research using qualitative investigations could help to better understand this variation and identify refinements in the program.

1374 – Working together for better preparedness against Kyasanur Forest Disease (KFD) in Goa, India: Best practices and lessons learnt

Dr Stefanie PREUSS, **Balaji SIVARAMAN**

Deutsche Gesellschaft fuer Internationale Zusammenarbeit (GIZ), India

Kyasanur Forest Disease (KFD) is a tick-borne viral haemorrhagic fever first detected in 1956 in the forest of Kyasanur village in the State of Karnataka, India. In recent years, KFD cases have also been reported in four more States along the Western Ghats (Goa, Kerala, Tamil Nadu, Maharashtra). Forest-adjacent communities and people working in forests and plantations are at highest risk.

Given the tick's multi-host ecology (larvae feed on small mammals, nymphs on medium-sized hosts – including non-human primates and humans, and adults on large animals), effective risk reduction requires coordinated action to align surveillance, risk communication, and interventions across human, animal, and environmental sector.

In the Indian State of Goa, the Directorate of Health Services (DHS), Department of Animal Health and Veterinary Services (DAHVS), Directorate of Agriculture (DoA), Forest Department (FD) and Goa State Biodiversity Board (GSBB) came together within the scope of the project "One Health and Agroecology" to jointly strengthen prevention measures, promote awareness, and reduce the risk of disease transmission. The project is commissioned by the German Federal Ministry for Economic Cooperation and Development (BMZ) and implemented by India's Ministry of Environment, Forest and Climate Change (MoEFCC) in collaboration with the Government of Goa and supported by Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ).

Through this collaborative and innovative approach, stakeholders demonstrate in practice how a One Health approach can reduce the risk of KFD transmission while promoting environmentally sustainable practices that support both community well-being and ecological balance.

In this session, practicing professionals from the human health, animal health, agricultural and environmental sectors in Goa share first-hand information regarding challenges, best practices and lessons learnt while working together towards a KFD-smart Goa.

Participants will learn

Format (90 min session):

Chairs:

Talks and speakers from different sectors:

1379 – Socio-economic indicators and biosecurity barriers in small-scale pig systems: A One Health framework to strengthen resilience against African Swine Fever

Mattia BECCHETTI (1), Elena LAZZARO (1), Stefania CROVATO (1), Giulia MASCARELLO (1), Marco ZAGO (1), Carlo CITTERIO (1), Denis VIO (1), Giacomo NALESSO (1), Serena MILANO (3), Samuele TRESTINI (2), Jacopo GORACCI (3), Federica LOI (4), Pierangelo CASALE (5), Raffaella PONZIO (3), Francesco FELIZIANI (6), **Giorgia ANGELONI** (1)

1: Istituto Zooprofilattico Sperimentale delle Venezie; 2: Dipartimento TESAF, Università degli Studi di Padova; 3: Slow Food Italia APS; 4: Istituto Zooprofilattico Sperimentale della Sardegna; 5: Veterinari Senza Frontiere Italia ETS; 6: Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Laboratorio Nazionale di Riferimento per la Peste Suina Africana

African Swine Fever poses a major threat to animal health and welfare, rural livelihoods and sustainable livestock systems, particularly in small-scale,backyard and outdoor pig farms. In Italy, these farms represent most registered holdings (as of 31 December 2025, farms with fewer than 50 pigs account for 85% of fattening pig farms and 95% of breeding farms). Recent ASF outbreaks have highlighted vulnerabilities related to biosecurity, socio-economic conditions and local governance. This study aimed to: (i)identify socio-economic and territorial indicators to assess the impact of ASF on food systems and local economies;and (ii)analyse barriers limiting the implementation of biosecurity measures in small-scale pig production systems. Human behaviour and socio-economic conditions are key determinants of ASF spread and impacts and should be considered alongside biological factors.

A structured literature review identified socio-economic and territorial variables associated with ASF occurrence and impact, focusing on quantitative analyses based on field data. Variables were grouped into four macro-areas: farming system characteristics, socio-economic factors, environmental infection pressure and wildlife habitat. Statistically significant variables were synthesised into a preliminary set of indicators for assessing ASF impacts. In parallel, a structured review of the scientific literature identified barriers to biosecurity implementation in small-scale pig systems, complemented by consultation of grey and institutional sources. A three-step selection process (identification, title/abstract screening and full-text assessment)defined the studies included in the thematic analysis. Barriers were classified into economic, socio-cultural, knowledge-related, infrastructural, institutional and risk-perception domains. Results will inform a subsequent field phase of the project, including interviews or questionnaires with farmers.

ASF-related impact indicators emerged at multiple scales. At the market level, EU Member States experienced an average 15% reduction in pork exports and a decline in production of more than 4% following ASF introduction. At the farm level, panic sales temporarily increased cash flow while reducing herd value. Social vulnerability indicators, such as the Material Deprivation Index, were associated with a fourfold higher risk of disease persistence in disadvantaged areas. Education level (OR = 3.97) and free-ranging pig keeping (OR = 6.87)were significant risk factors, while improved biosecurity compliance reduced outbreak risk(OR = 0.90).

Barriers to biosecurity implementation were multifactorial. Economic constraints, including costs of fencing, safe feed and disinfection, were frequently reported. Inadequate compensation schemes discouraged early outbreak reporting. Socio-cultural practices such as free-ranging, swill feeding and informal slaughter, together with limited knowledge and low risk perception, reduced compliance. Institutional weaknesses, limited training and communication, and low trust in veterinary and public authorities undermined surveillance and biosecurity adoption.

Integrating socio-economic indicators with participatory and context-specific biosecurity strategies may support more feasible ASF prevention and control within a One Health perspective. Policies should consider the structural characteristics of small-scale pig systems to ensure biosecurity measures remain proportionate and feasible.

1388 – Antimicrobial use in communal livestock systems: Community knowledge and stewardship challenges

Nolwazi NDIMANDE, Rachel WYNBERG, Maya MARSHAK

University of Cape Town, South Africa

Background: Livestock farming is the backbone of rural livelihoods because of its socioeconomic, cultural and ecological value. To boost productivity and support livelihoods, antimicrobials, especially antibiotics have gained popularity in agriculture and aquaculture alike. In Southern Africa, there have been very few studies in communal farming systems exploring Antimicrobial Use (AMU) and the prevalence of Antimicrobial Resistance (AMR), and the associated dangers to human, animal and environmental health. This study investigated antimicrobial use amongst livestock farmers focusing on their knowledge, perspectives and practices.

Methods: A total of 34 livestock farmers and herders, 5 Agri veterinary shop officials, 2 animal health technicians were interviewed in a remote town within the OR Tambo district, Eastern Cape. The study employed qualitative methods, using semi-structured interviews and focus group discussions. Data captured included participant demographics, prescription and access to veterinary antimicrobials, education levels, knowledge of animal diseases and their management, understanding of biosecurity measures and withdrawal periods and their knowledge of AMU and AMR.

Preliminary results: All the participants interviewed had a positive attitude towards use of antimicrobials to manage livestock diseases. Most of the antimicrobials used in the community are available from Agri-veterinary shops without prescription. There is limited understanding amongst farmers on how to use these substances due to literacy barriers. Majority of the staff in the Agri-vet shops did not hold nationally mandated qualifications to advise on or sell veterinary antimicrobials. Antimicrobials are used for both prophylactic and therapeutic measures. Knowledge of AMU amongst all participants was limited.

Conclusion: In this South African village, there is high reliance on antimicrobials for livestock health. The findings of this study highlight several issues concerning access and inappropriate use of antimicrobial substances. Misuse or abuse increases the chances of antimicrobial resistance and calls for development of coordinated antibiotic stewardship protocols, accessible information and knowledge systems on antimicrobials and their uses.

1395 – Perceptions of Climate Change in Older Adults living in Greece

Eleni RODITI, Anastasia PANA, Venetia Sofia VELONAKI, Petros GALANIS, Panagiota SOURTZI

National and Kapodistrian University of Athens, Greece

Background Climate change (CC) and the ageing of the population are in the rise worldwide. Older people are affected by CC, but it has been reported that they do not know about its consequences on their health. The purpose of the study was to explore older people's perception about CC and its impact on health.

Methods The study was designed as a cross-sectional one. Anonymous questionnaires were distributed to older people, through Open Care Centres for Older People in greater Athens area, Greece. The 408 participants were between 65 and 100 years old. The questionnaire included demographic and socioeconomic questions, their perceived knowledge about CC, a questionnaire to assess their knowledge (Salem et al. 2022) and the CC attitude survey developed by Christensen and Knezek (2016). The data were analysed with SPSS.

Results Of the 408 older adults who participated in the study, 57% were women, 66% lived in urban, 21.5% in a semi urban, 8.8% in rural areas. The mean of self-perceived knowledge about CC was 5.87 (range 1-10). Regarding knowledge about CC, 94% answered correctly that CC increases the risk of heat waves, while 74% understood that it affects extreme cold. While 91% answered that global warming affects human health, questions regarding specific health problems had the lowest percentages of correct answers. Self-perceived knowledge about CC was positively correlated (rs=0.229, p0.001) with having answered correctly over 70% of knowledge questions. Age was negatively correlated with self-perceived knowledge (rs=-0.130, p=0.01), correct answers to CC knowledge questions (rs=-0.134, p=0.008), and CC intentions (rs=-0.140, p=0.05). Area of residence was correlated with perceived knowledge (rs=-0.160, p=0.002) but not actual knowledge and perceptions about CC. Educational level was positively correlated with perceived knowledge (rs=0.294, p0.001), CC intentions (rs=0.203, p0.001) and answering over 70% of the knowledge questions correctly (rs=0.127, p=0.011). Being active in organisations and Open Centres for Older People was positively correlated with self- perceived knowledge (rs=0.109, p=0.03) and beliefs about CC (rs=0.128, p=0.01).

Conclusions The majority of older people in Greece seem to be aware of CC and its consequences on health and the planet. They also believe that CC consists an actual problem and they are worried about it. This information can be useful for health and social care professionals to support adequately older people they care for.

1399 – Research Despite the War: Surveillance of Emerging Viral and Bacterial Pathogens in Wildlife in Ukraine, Consequences and Future Perspectives

Denys MUZYKA (1,2), Nataliia MUZYKA (1), Oleksandr RULA (1), Oleksandr MEZINOV (1,3), Anton VLASCHENKO (1), Anastasiia POPOVA (1), Olga MAIBORODA (1), Polina YURKO (1), Oleksandr GAIDASH (4), Jeanne FAIR (6), Martin BEER (5), Jennifer OWEN (7), Jonas WALDENSTRÖM (2)

1: NSC Institute of Experimental and Clinical Veterinary Medicine (IECVM), Kharkiv, Ukraine; 2: Linnaeus University, Kalmar, Sweden; 3: The F.E. Falz-Fein Biosphere Reserve "Askania Nova", Ukraine; 4: The Danube Biosphere Reserve, Ukraine; 5: Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany; 6: Global Conservation Institute, USA; 7: Archbold Biological Station, USA

Introduction. Wild birds and mammals host numerous pathogens that pose risks to humans and domestic animals, including influenza A viruses, flaviviruses, coronaviruses, avian avulaviruses, vector-borne pathogens, and antimicrobial-resistant bacteria. Surveillance of these pathogens is essential for predicting and preparing for future outbreaks and pandemics. The war in Ukraine has created new challenges for the One Health approach, with consequences extending beyond Ukraine to the rest of Europe.

Methods. Studies on emerging wildlife pathogens (virological, serological, PCR-based detection, and sequencing) have been conducted in Ukraine during 2005–2025 with funding from NAAS, NRFU (#2021.01/0006, #2025.07/0063), STCU (P444a-b, P777, P781), U.S. DoD BTRP (UP4, AZDN).

Results. Active wildlife surveillance in Ukraine began in 2005 and has continued despite the war since 2014 and the full-scale invasion in 2022. In total, 207 avian influenza viruses (AIV) belonging to 15 HA and 7 NA subtypes were isolated from wild birds. Most isolates were low pathogenic; however, highly pathogenic avian influenza (HPAI) viruses were also detected in apparently healthy wild birds. The prevalence ranged 0.16–19.65% for AIV and 0.82–3.42% for HPAI (H5Nx). Genetic analysis revealed high diversity and phylogenetic relationships with AIVs reported from Europe, Siberia, and Asia. Evidence of influenza virus circulation was also detected in wild and domestic mammals. Broad serological surveillance of domestic and wild carnivores detected antibodies to influenza A virus (1.57–11.88%); seroprevalence to HPAI H5 in red foxes was 0.78–10.2%. Surveillance of domestic swine, horses, and wild boars did not detect any H5-positive cases. Avian avulaviruses of several serotypes (AaV1,4,6,7,9) were detected in wild birds/ The AaV-13 serotype was detected in Europe for the first time. Extensive surveillance of coronaviruses (CoV), paramyxoviruses (PMV), and orthomyxoviruses (OMV) in insectivorous bats was conducted in 11 regions and included 20 bat species. About 2.7–69.2% and 0.52–33.3% of bats tested positive for CoV and PMV, respectively. All bat samples were negative for OMV, bacterial pathogens. Serological surveillance for West Nile virus revealed high seropositivity in wild birds (9.09–78.57%), bats (33.3–57.9%), domestic horses (87.0%), and deer (33.3%). Bacteriological surveillance showed active circulation of multidrug-resistant *Escherichia coli* (prevalence 10.0–31.8%) and *Salmonella* spp. (1.7–50%) in wild birds.

Conclusions. Several viral and bacterial pathogens of importance to human and animal health were detected in wild and domestic animals in Ukraine, highlighting the potential risk of spillover from wildlife reservoirs to domestic animals and humans. The ongoing war may significantly affect pathogen circulation and reduce the capacity for timely outbreak detection, potentially worsening epidemiological outcomes. Continued surveillance in Ukraine remains critically important. As infectious diseases do not recognize borders, surveillance efforts in Ukraine are regionally important and beneficial for Europe, including the EU.

1401 – Co-Creating Participatory Research through Community Engagement and a Participatory Risk-based Assessment of the Pre-Emergence Phase of Pandemics

Karen SAYLORS
Labyrinth Global Health, United States of America

Background: The National Science Foundation's Center for Pandemic Insights (CPI) engages One Health expertise to understand pre-emergence pandemic phases, focusing on influenza in sea birds and marine mammals, and coronaviruses in bats. Traditional fragmented risk assessment strategies often exclude community knowledge and perspectives, limiting their effectiveness. We hypothesize that participatory risk-based approaches and mixed methods research yield more productive zoonotic spillover risk assessments than conventional strategies. Building on community-based participatory research (CBPR) principles, the Center promotes co-learning and capacity building among academic, non-profit, tribal, and community partners co-responsible for study design, implementation, and analysis. This approach integrates quantitative risk estimates with qualitative insights that elucidate contextual dimensions inaccessible to purely quantitative analysis, yielding more comprehensive risk understanding.

Methods: We developed a community-driven participatory research framework for assessing zoonotic emergence and transmission through integrated mixed-methods risk assessment tools. Participatory research was conducted at three California sites: Pinnacles National Park and Yolo Bypass Wildlife Area (low spillover risk bat monitoring sites) and Año Nuevo State Park (current HPAI outbreak site in marine mammals). The framework integrates semi-structured ethnographic interviews with community leaders, semi-quantitative measures of sociopolitical acceptability for interventions, and socioeconomic determinants through participatory research. Community experts were identified via snowball sampling. At Pinnacles, we conducted participatory risk mapping using proportional piling, where respondents allocated seeds to factors based on perceived transmission risk, followed by focus groups on study design and community priorities for citizen science projects.

Results: The Center engaged diverse communities including indigenous leaders, youth land trust stewards, community college students building sensors, ranchers, and park service professionals (wildlife biologists, cultural resources managers, educators) in monitoring and Citizen Science efforts. Interview themes covered community risk perceptions, receptivity to sensor technology for bat monitoring, expert-based risk evaluation, and public health messaging during outbreaks. Participatory risk mapping revealed community-identified factors not captured in traditional assessments, while focus groups generated locally-relevant Citizen Science priorities. Youth engagement programs trained 45+ participants in sensor technology, while indigenous knowledge integration enhanced understanding of human-wildlife interaction patterns across sites. Community partnerships established ongoing monitoring protocols that combine traditional ecological knowledge with modern surveillance approaches.

Conclusions: In sites where disease threats may be emerging but not clinically documented, integrating local knowledge into risk analyses is essential for estimating risk and strengthening prevention strategies. This participatory framework demonstrates how community engagement enhances One Health surveillance while building local capacity for pandemic preparedness. The mixed-methods approach successfully captured risk dimensions invisible to traditional assessments, creating more comprehensive and culturally responsive prevention strategies that empower communities as active participants rather than passive subjects in One Health initiatives.

1410 – Tracking antimicrobial-resistant Escherichia coli in an urban Kenyan wet market

Erika CANDA (1), Addison DEISHER (2), **Brandie Banner SHACKELFORD** (1), Lolyne GATWIRI (3), Matthew C FREEMAN (1), Ruthie ROSENBERG (4), Wali MWALUGONGO (4), Catherine KUNYANGA (3), Maya L NADIMPALLI (1)
1: Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, Georgia, USA; 2: Hubert Department of Global Health, Rollins School of Public Health, Emory University, Atlanta, Georgia, USA; 3: Department of Food Science, Nutrition and Technology, University of Nairobi, Kenya; 4: Fresh Life, Nairobi, Kenya

Background:

Wet markets in low and middle-income countries are important sources of fresh, affordable food, but often lack appropriate food hygiene controls. Burma Market is Kenya's largest meat market and a key retail poultry supplier in Nairobi. Pervasive contamination in markets like Burma makes it difficult to pinpoint where market interventions should be targeted to reduce transmission of foodborne antimicrobial-resistant (AMR) *Escherichia coli*. Our goals were to (1) understand market risk factors for microbial contamination, (2) assess if and by how much the wet market setting "amplifies" AMR *E. coli*

contamination amongpoultry sold at Burma and (3) quantify strain-level transmission among humans, poultry, and the environment over time.

Methods:

We prospectively enrolled 8 poultry vendors from June-July 2025, each for two days. Vendors were surveyed daily and poultry (cage fecal droppings, rectal swab, pre-evisceration carcass, ready-to-sell carcass) and environmental (vendor hand rinses, slaughterhouse surface, food and water fed to poultry) samples were collected at least once. Human samples, including vendor feces and urine diverting dry toilet (hereafter, "latrine") waste, were collected 2-3 weeks after poultry and environmental sampling was complete. Structured observations were performed at the market level, vendor stalls, and in slaughterhouses. We quantified third-generation cephalosporin-resistant *E. coli* using cefotaxime-supplemented MacConkey agar. Up to five presumptive AMR *E. coli* colonies were pooled from each positive sample, followed by DNA extraction and short-read metagenomic sequencing. We applied the StrainGE toolkit to assess strain sharing within vendors and between latrine waste and all other sample types.

Results:

Of 150 samples collected, most (92%) were positive for AMR *E. coli* by culture. Among poultry and environmental samples collected longitudinally (n=102), AMR *E. coli* contamination was higher on day 2 compared to day 1 (p0.05 by two-way ANOVA). We identified multiple infrastructural barriers and low levels of food safety and hygiene practices that could contribute to contamination, e.g., handwashing was never practiced by vendors during customer interactions (n=24) or by slaughterhouse staff (n=32). AMR *E. coli* predominantly harbored the *bla*CTX-M-15 gene. We identified 101 within-vendor strain-sharing events. The most commonly implicated sample types were ready-to-sell chicken carcasses (79/101 events), pre-evisceration carcasses (49/101), and chicken rectal swabs (31/101). There was substantial heterogeneity in within-vendor strain sharing rates, ranging from 0 to 0.37 observed/total possible events per vendor. Latrine waste sampling mostly captured AMR *E. coli* strains from vendor feces, pre-evisceration carcasses, and ready-to-sell carcasses. Despite being emptied daily, latrines harbored AMR *E. coli* variants detected up to 3 weeks prior, suggesting a market reservoir of AMR *E. coli*.

Conclusions: Wet market conditions may lead to the amplification of AMR *E. coli* contamination with multiple hotspots identified. Developing and testing market interventions could reduce AMR transmission from markets to communities.

1419 – Population-based cohorts as integrated One Health data platforms for infectious disease dynamics and epidemic preparedness in Africa: A Scoping Review

Lydiah KISOO (1,2), Filipe DIAS (3), Guash Abay ASSEFA (1,2), Yaw AWUKU-LARBI (1,2), Torben HEINSOHN (1), Manuela HARRIES (1), Fabian LEENDERTZ (3), Carolina J. KLETT-TAMMEN (1), Fee ZIMMERMANN (3), Berit LANGE (1,4)

1: Department of Epidemiology, Helmholtz Centre for Infection Research, Braunschweig, Germany; 2: PhD Programme "Epidemiology" Braunschweig, Hannover, Germany; 3: Helmholtz Institute for One Health, Greifswald, Germany; 4: German Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Braunschweig, Germany

Background: Emerging infectious diseases are a major global threat, especially in Africa, where recent outbreaks show the role of zoonotic spillovers. Population-based cohorts represent critical data integration platforms, linking human, animal, and environmental interfaces for studying infectious disease dynamics over time using the One Health approach. This study maps African population-based cohorts integrating ≥2 One Health domains, including data integration patterns to support decisions for optimizing epidemic preparedness and early spillover detection strategies.

Methods: Following PRISMA-ScR guidelines, we conducted a scoping review to map population-based cohorts in Africa integrating at least two One Health domains (human-animal and/or human-environment). Searches of PubMed, Scopus, Web of Science, and grey literature were performed from database inception to July 2025, and eligibility was defined using the Population Concept Context (PCC) framework. Data extraction used standardized forms to capture cohort characteristics, settings, outcome and One Health exposure domains, biospecimens, and diagnostics. A composite data integration matrix and score were derived by summing the presence of key data domains. Descriptive analyses summarized

study characteristics while determinants of higher scores for data integration were assessed using multivariable Poisson regression analyses.

Results

Of the 4,473 records examined, 190 publications representing 174 unique cohorts were included. The cohorts were geographically concentrated in Eastern (37%), Western (29%) and Southern Africa (26%), with Central Africa (3%) and Northern Africa (6%) being the least represented. The initiation of cohorts peaked in the 2010's (37%), which coincided with major One Health policy milestones such as the 2010 Tripartite Concept Note. Nearly half (47.1%), of the cohorts were embedded within Health and Demographic Surveillance Systems (HDSS), and more than half participated in data-sharing networks such as INDEPTH (52.3%). Infectious outcomes were dominated by high-burden diseases such as malaria (39.3%), diarrhoeal diseases (30.6%), HIV/AIDS (26.0%) and tuberculosis (19.1%). Human-environment interfaces predominated (64.6%), whereas in 61/174(35%) of cohorts, where animals were studied, the environment was also examined. There was limited direct animal sampling (12.0%), despite the inclusion of animal domains. Spatial data integration was common (84.0%), whereas clinical data linkage was rare (9.0%). In multivariable Poisson regression, HDSS cohorts had higher data integration scores (RR = 1.18, 95% CI 1.06–1.32). Only five cohorts (2.9%) explicitly referenced the One Health framework.

Conclusions: Population-based cohorts are critical instruments for integrated One Health surveillance in Africa. Despite substantial multi-domain integration in several cohorts, direct animal sampling, clinical data linkage, and reference to the One Health framework remain limited. To improve their contribution to epidemic preparedness, efforts may need to prioritise standardised integration protocols, strengthened animal and environmental monitoring, and multisectoral data-sharing mechanisms.

1424 – Multi-layered incentives for zoonotic surveillance:A participatory paradigm shift from fear to identity across three biodiversity hotspots

Alex SMAJGL (1), Thaweepol NUANGNONG (1), John WARD (1), Julien CAPPELLE (2,3)

1: Mekong Region Futures Institute (MERFI), Bangkok, Thailand; 2: ASTRE, CIRAD, INRAE, Univ Montpellier, Montpellier, France; 3: CIRAD, UMR ASTRE, F-34398 Montpellier, France

Background:

Zoonotic spillovers threaten global health, the COVID-19 pandemic, caused by a sarbecovirus likely originating in bats, and the 2014–2016 West Africa Ebola epidemic, both underscored the fragility of current surveillance and prevention systems in biodiversity hotspots. Furthermore, conventional fear-based interventions fails to sustain long-term adoption of prevention measures due to risk habituation.

Methods

Within the framework of the BCOMING project, we employed a transdisciplinary approach that combined participatory co-design with computational simulation in three biodiversity hotspots: Guadeloupe (tropical arboviruses transmitted by Aedes and Culex mosquitoes); Cambodia (SARS-related bat coronaviruses involving guano and bushmeat pathways); and Guinea (Ebola virus involving bat-to-bridge-to-human transmission at the forest-savanna interface).

Results

By synthesising the results of the three case studies, we have uncovered an emergent 'incentive ecology': a multi-layered incentive scheme comprising community benefits and individual rewards (with no direct cash payments) that aligns with cultural identity and social norms. This scheme has produced simulated zoonotic risk reductions of 50–83%. Household survey data (n ≈ 1,500 per site) reveal correlations between livelihoods and income, and health behaviours (e.g. higher levels of protective hygiene in households with diversified income), quantifying the health–poverty–biodiversity nexus. Shifts in causal belief from fatalism to agency explain the endurance of these behaviours. Agent-based models demonstrate that combining ecological interventions (e.g. reforestation and cave closures) with social interventions creates positive feedback loops, achieving better results than single measures alone.

Conclusions

This transdisciplinary approach, which integrates psychology, disease ecology, participatory co-design and computational modelling, provides a framework for achieving the Sustainable Development Goals through prevention. It transforms the way we approach zoonotic risk, creating resilient systems that protect human health, alleviate poverty and conserve biodiversity in emerging disease hotspots.

1429 – Heartland and Bourbon viruses - Emerging tick-borne pathogens in Virginia USA, as evidenced via wildlife and cattle serology, and a novel duplex RTqPCR assay

Gillian EASTWOOD (1), Thomas EDWARDS (2), Alexandra CUMBIE (1)

1: Virginia Tech, United States of America; 2: Liverpool School of Tropical Medicine, United Kingdom

Background: Emerging tick-borne pathogens include serious arboviral agents capable of causing severe clinical illness and even death. Viruses know to be vectored by *Amblyomma americanum* (Lone star tick) include Bourbon virus (Thotogovirus, family Orthomyxoviridae) and Heartland bandavirus (Family Phenuiviridae). Methods: Both viruses have been evidenced to circulate in the Commonwealth of Virginia in the United States, with exposure in over 800 wildlife and agricultural hosts serologically demonstrated by our group using plaque reduction neutralization tests, along with recent detection of Bourbon virus in several local tick species. Here we also describe a molecular duplex assay to efficiently simultaneously detect Bourbon and Heartland viruses in field specimens using a RT-qPCR methodology targeting the PB1 and Small gene of each virus respectively. Results: Validation of the assay showed strong reproducibility and replicability, with a limit of detection down to 1 genome copy, and a specificity unique from similar viruses. Using the assay with RNA extracted from N=1000 field-collected ticks from Virginia, we evidence both Bourbon and Heartland viruses in *A.americanum*, building further data to support to active circulation of these tick-borne viruses in the region. Conclusion: Ticks represent a serious One Health threat, with association with viral agents evidenced to be present in Virginia, with exposure in a range of wildlife and in cattle. The molecular assay described here to screen ticks can be performed at half reaction volume providing a low cost testing mechanism for field surveillance of emergent viral pathogens of public health significance.

1433 – Community Engagement in One Health: Narrowly Applied but Broadly Needed

Jill JOHNS, **Jessica SCHWIND**

Institute for Health Logistics & Analytics at Georgia Southern University, United States of America

BACKGROUND

Community engagement methodologies, including Knowledge, Attitudes, and Practices (KAP) surveys, Participatory Asset Mapping (PAM), Community-Based Participatory Research (CBPR), and Asset-based Community Development, have well-established track records across public health and development. Within One Health, community engagement is acknowledged as essential; however, recent evidence reveals a striking methodological narrowness in how it is applied. Systematic reviews confirm existing engagement is largely limited to disease-specific KAP studies targeting occupational groups in low- and middle-income countries, with broader community populations and strengths-based approaches remaining absent. Implementation of the One Health Joint Plan of Action continues to be governance-driven, with local and indigenous communities underrepresented in design and agenda-setting. What does broad-spectrum, strengths-based community engagement yield when applied within a One Health frame, and what does it reveal that narrower approaches miss?

METHODS

We draw on two independent projects applying established community engagement methodologies within an One Health lens in two high-income settings. In County Wexford, Ireland, a cross-sectional mixed-methods KAP study recruited community members using structured surveys and focus groups with inferential analysis of demographic correlates. In 18 rural counties in southeast Georgia, USA, a strengths-based PAM initiative applied an asset-based approach through a "Prepare, Engage, Report" process over two years, using stakeholder interviews and environmental scans to identify and map One Health

resources across nine domains. Both studies positioned community members as content experts and were designed to translate findings into education, workforce development, and policy action.

RESULTS

In Wexford, KAP assessment revealed low formal One Health literacy, yet a large majority recognized strong human-environment health connections, and AMR awareness varied significantly by occupation, a pattern most surveillance systems are not designed to capture. Qualitative findings surfaced actionable barriers including policy fragmentation, absence of plain-language resources, and demand for youth-led engagement. In rural Georgia, strengths-based PAM revealed extensive previously unmapped One Health assets alongside critical workforce gaps in emergency preparedness, veterinary access, and harm reduction. In both contexts, community-centered design produced richer, more actionable intelligence than disease-specific or expert-led approaches would have captured.

CONCLUSIONS

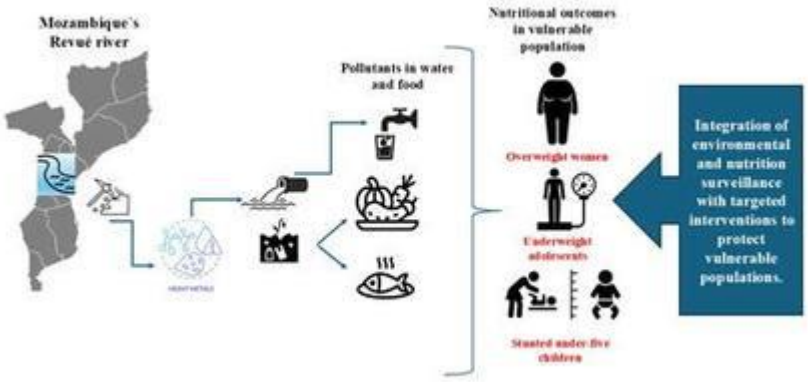
Limitations in One Health community engagement relate not only to scale, but to methodology, geography, and design philosophy. Engagement is happening, but narrowly focused on single diseases, professional cohorts, and deficit-based framing. Evidence from Ireland and the USA demonstrates that methodological expansion is feasible and productive, consistently surfacing knowledge, assets, and readiness that narrower approaches miss. KAP surveys targeting general populations, PAM adapted to One Health domains, and CBPR principles should be recognized as a complementary methodology suite embedded in national action plans. While One Health recognizes the importance of communities, translating that understanding into sustained engagement requires methodological tools and deliberate effort

1435 – Nutritional profile of children, adolescents and women seasonally exposed to chemical environmental pollutants from the Revuè river in the Manica Province, Mozambique

Tatiana MARRUFO (1,2,3), Osvaldo INLAMEA (1), Márcia XAVIER (1), Celso CUMBULA (1), Filipe MURGORGO (4), Cristovão PEREIRA (5), Ivalda MACICAME (1), Bettencourt CAPECE (6), Maria-Raquel SILVA (7,8,9,10)

1: Instituto Nacional de Saúde, Mozambique, Mozambique; 2: Faculty of Science and Technology, University Fernando Pessoa, 4249-004 Porto, Portugal; 3: RISE-Health, Faculty of Health Sciences, Fernando Pessoa University, Fernando Pessoa Teaching and Culture Foundation, 4249-004 Porto, Portugal; 4: Research Centre of the Health Directorate, Manica, Mozambique; 5: University of Zambeze, 670, Alfredo Lawley Avenue, Beira, Sofala, Mozambique; 6: Faculty of Veterinary Medicine, University Eduardo Mondlane, Av. de Moçambique, Km 1,5, Maputo city, Mozambique; 7: FP-I3ID, FP-BHS, and Faculty of Health Sciences, University Fernando Pessoa, 4200-150 Porto, Portugal; 8: Molecular Oncology and Viral Pathology Group, Research Center of IPO-Porto (CI-IPOP) &RISE@CI-IPOP (Health Research Network), Portuguese Oncology Institute of Porto (IPO-Porto)/Porto Comprehensive Cancer Center Raquel Seruca (Porto. CCC), 4200-072 Porto, Portugal; 9: CHRC, Comprehensive Health Research Centre - Group of Sleep, Chronobiology and Sleep Disorders, Nova Medical School, Nova University of Lisbon, 1150-090 Lisbon, Portugal; 10: CIAS, Research Centre for Anthropology and Health – Group of Human Biology, Health and Society, Uni-versity of Coimbra, 3000-456 Coimbra, Portugal

The global nutrition crisis continues to disproportionately affect vulnerable populations, particularly in environmentally hazardous regions where artisanal mining heightens health risks. This study assessed the nutritional status of children, adolescents, and women attending health facilities in the Revuè sub-basin, alongside measurements of chemical contaminants in drinking water sources. Using an observational, cross-sectional design, researchers combined anthropometric and sociodemographic data with laboratory analysis of heavy metals in the river and groundwater. Results showed a high prevalence of stunting among children under five (28.4% in males and 19.9% in females), while female adolescents exhibited levels of underweight, especially during the rainy season. In contrast, women demonstrated elevated rates of overweight (17.5–19%) and obesity (2.8–3.1%). Early introduction of complementary foods ($p=0.03$) and mercury exposure ($p\ 0.01$) were strongly associated with adverse nutritional outcomes in children, whereas higher educational attainment among husbands appeared protective for women ($p\ 0.001$). Mercury's attributable fraction varied widely across regions and seasons, reaching up to 75%. Water analyses revealed arsenic and mercury concentrations exceeding national and international safety standards. Overall, the findings highlight the substantial nutritional and environmental burdens linked to artisanal mining and emphasize the urgent need for continuous monitoring and targeted interventions in affected communities.



1444 – Preparing the next generation One Health workforce in southern and eastern Africa

Flora PULE-MEULENBERG (1), Florence MUTUA (2), Simon ANGOMBE (3), Lucinda DE ARAUJO (4), Shauna RICHARDS (5), Buke WAKO (6), Shafi Abdullahi MOHAMED (7), Yusuf HARED (8), Pamela WAIRAGALA (9), Justine OKELLO (10), Alexandre CARON (11), Theodore KNIGHT-JONES (12), Simon BROOKER (13)

1: Botswana University of Agriculture and Natural Resources, Gaborone, Botswana; 2: International Livestock Research Institute, Nairobi, Kenya; 3: University of Namibia, Windhoek, Namibia; 4: Eduardo Mondlane University, Maputo, Mozambique; 5: International Livestock Research Institute, Nairobi, Kenya; 6: International Livestock Research Institute, Nairobi, Kenya; 7: Shaffi Abduhalli Mohamed, Somaliland; 8: Amoud University, Somalia; 9: International Livestock Research Institute, Kampala, Uganda; 10: Makerere University, Kampala, Uganda; 11: CIRAD ASTRE - ILRI, ILRI, Nairobi, Kenya; 12: International Livestock Research Institute, Addis Abeba, Ethiopia; 13: International Livestock Research Institute, Nairobi, Kenya

Background: The preparation of future One Health (OH) workforce is essential for strengthening global resilience against emerging and re-emerging health threats. Embedding the OH concept into national and regional planning frameworks is therefore critical, and education and training must play a central role. Capacitating One Health in Eastern and Southern Africa (COHESA) project built an inclusive research and innovation ecosystem that accelerates the uptake, adaption and adoption of OH solutions. A core component of this effort involved equipping education and research institutions across ESA to train future OH practitioners and strengthen OH curricula. A assessment conducted earlier highlighted several gaps in higher education OH programming in the region, including: 1) the need for curriculum reform, 2) inadequate awareness of existing OH opportunities and limited development of cross-cutting OH competencies In response, COHESA supported regional and national OH capacity development initiatives to strengthen OH education and institutional functionality across ESA.

Methodology: To address the identified gaps, COHESA supported national and regional capacity development initiatives. These included supporting the Inter University Council of East Africa to develop benchmarks for a OH Masters focussing on cross-cutting competencies and training in developing short term OH courses. Each country developed a targeted plan to advance OH education within education and research, capacity development of existing workforce, and mentorship. At a regional level the COHESA project considered priority shared learning opportunities and regional strategies within the same thematic areas.

Results: One health modules were integrated into existing qualifications after review of curricula by countries. In Ethiopia, OH incourses across 8 universities. At the University of Nairobi, the revision of OH curricula took place through COHESA. While some countries developed Masters programs (Namibia, Zambia), others developed courses for continued professional development (Botswana). In Zimbabwe, OH was introduced into curricula of 19 teacher training colleges. Regional approaches to OH education initiated by COHESA included training of trainers on the World Health Organization's Workforce Development Operational Tool Databases of OH training tools and resources. ESA participants utilized existing tools instead of duplicating efforts. Furthermore, two pedagogy workshops on the use of technology and integration of cross-cutting competencies through training of lectures at tertiary

institutes were conducted. While conventional education strategies were often used, gamification was a novel approach introduced into OH teaching strategies.

Conclusions: COHESA produced examples of integrating OH education into existing frameworks by utilizing existing trainings, tools, and resources. This approach recognized that curriculum change is challenging on short term and that in the interim there were other ways to integrate OH education. Using this experience, these solutions can be extended to the rest of the continent to advance OH education and the integration of core competencies needed for the workforce to advance OH institutionalization and operationalization.

1451 – Healthy Parks: Mobilizing participatory science to implement the One Health approach in peri-urban natural parks in Canada

Cécile AENISHAENSLIN (1), Manon BOITEUX (1), Catherine BOUCHARD (2), Frédéric BUSSIÈRE (3), Camille DESBIENS (4), André-Philippe DRAPEAU PICARD (3), Serge DROLET (5), Ariane DUMAS (2), Jessica HAINAULT (1), Gabriel TEJ (6), Martin LECLERC (4), Patrick LEIGHTON (1), Ariane MASSÉ (7), Jean-Philippe ROCHELEAU (1), Mélanie DAPPEN-COUTURE (1)

1: Université de Montréal, Canada; 2: Public Health Agency of Canada, Canada; 3: Ville de Montréal, Canada; 4: Université Laval, Canada; 5: Ville de Granby, Canada; 6: Société des établissements de plein air du Québec, Canada; 7: Ministère de l'Environnement, de la Lutte contre les changements climatiques, de la Faune et des Parcs

Background: Peri-urban natural parks provide a range of benefits to society, including ecosystem services such as lower temperatures and biodiversity conservation, as well as direct effects on the physical and mental health of citizens who visit them. However, In the Canadian context, climate change and deer abundance promote the establishment of *Ixodes* tick populations in these parks, which are the main vectors of several zoonotic pathogens. This situation is a classic example of a One Health issue, requiring a rebalancing of human, animal and ecosystem health. The objective of this project was to co-develop an intervention research programme enabling the creation of an integrated, sustainable and socially acceptable strategy to protect the biodiversity of Canadian peri-urban nature parks while reducing the risk of tick-borne diseases for the humans and domestic animals that frequent them.

Method: A transdisciplinary team was formed, comprising academic, community and government stakeholders from different sectors (human health, animal health, environment) and levels of governance (municipal, provincial, national). The team included decision-makers responsible for six peri-urban nature parks in Quebec (Canada), which were experiencing the targeted issues. Three co-construction workshops were held to develop a systems map of the issues and identify the main levers for synergistic action. Based on this map, the programme was determined, including the objectives, approaches and expected results agreed upon by consensus.

Results: The project resulted in the formation of a formal partnership between four universities and thirteen Canadian partner organisations, in the form of a project called Healthy Parks. The systems map identified three priority areas for intervention: (1) monitoring deer populations and their impact on biodiversity and the risk of tick-borne diseases, (2) evaluating integrated environmental interventions aimed at controlling white-tailed deer and reservoirs of tick-borne diseases, such as small wild rodents, and (3) evaluating citizen science as a means of reinforcing preventive and pro-environmental behaviours. The resulting programme was funded by a federal funding agency, which combines funding from the partner organisations and the agency (total = CAD$2.5 million). It is governed by a transdisciplinary scientific committee, which is responsible for the project's overall direction, facilitating its implementation, and providing training for twelve graduate trainees. The citizen science component has recruited over 200 park users, who are currently undergoing training to become ambassadors for healthy Canadian parks.

Conclusion: Healthy Parks is a concrete example of research development that is consistent with the principles of the One Health Approach. From its inception, it has innovated by applying systems thinking, transdisciplinarity and participatory science to combat biodiversity loss and the emergence of tick-borne diseases in Canadian parks. The programme will enable the development of an integrated intervention strategy that can be implemented in all parks facing similar issues.

1454 – ZooHumano Preschool Series - Bringing One Health into Kindergarten

Alice MATOS, Rita LARANGINHA, Rosário BOBONE, Catarina LAVRADOR
Veterinários Sem Fronteiras Portugal, Lisbon, Portugal

Background: Ages 2 to 7 are the most important years for internalizing empathetic behaviors, with higher potential for shifting important societal paradigms. By realizing that animals also experience cold, hunger, fear, joy and illness, children develop a more mindful attitude toward animals, humans, and their shared environment. Additionally, communication is a core OH competency, requiring veterinarians to translate complex concepts for diverse audiences, including children. Therefore, ensuring that veterinary students have opportunities to practice communication is essential. In this context, Veterinarians Without Borders Portugal (VSF Portugal) created the initiative "ZooHumano - Uma Só Saúde: da Escola para a Vida". This initiative aims to increase OH awareness among preschool children (ages 2-5) while providing opportunities for veterinary students to interact with this audience, contributing to the development of healthier communities through education at different levels.

Methods: The program consists of three sequential sessions:

Activities were developed by veterinarians and a veterinary student with education training; they are delivered by this team, along with additional students. Each session includes a brief topic introduction followed by hands-on activities: books, games, drawings, and a collaborative mural where children display their work throughout the school year to reinforce learning. An assistance dog participates, enabling real-time observation of animal body language and enhancing engagement. Sessions are evaluated through collaboration with teachers, analyzing children's work and interactions. This assessment is supplemented by teacher feedback surveys. Sessions 2 and 3 begin with recall activities to strengthen retention.

Results: Sessions 1 and 2 were administered in two pilot schools between October 2025 and March 2026. Informal feedback from the first session was very positive, with schools demonstrating high interest in continuing the series. In the second session one school educator indicated that it was “well adapted to the context”, using a “sensitive and constructive pedagogical approach” that “proved to be very meaningful”. OH series is scheduled to begin in four additional preschools, and sessions will be delivered by the end of the school year.

Conclusions: While results are still limited, our experience shows that there is a clear interest from schools to conduct this type of activities. Considering the importance of the OH approach, the impact of individual level behaviors in promoting the global good, and the urgency in creating competent veterinary graduates that can clearly communicate complex issues with different audiences, this series represents an important, well-designed initiative, with potential to be replicated.

1463 – Consequences of zinc oxide withdrawal in UK weaner piglets: a shotgun metagenomic analysis of the faecal microbiome and resistome

Donald DUNBAR (1), Sebastien GUIZARD (1), Andrew BEASE (1), Nicky CRAIG (1), Bryan WEE (1), Adrian MUWONGE (1), Sara PITA (1), Ricardo CORONA-TORRES (1), Jade DAVIES (2), Yasmin SABINO (3), Linda OYAMA (3), Ilias KYRIAZAKIS (3), Muna ANJUM (2), Manal ABUOUN (2), Mark STEVENS (1), Andy LAW (1), Abel EKIRI (4), Roberto LA RAGIONE (4), Nick WHEELHOUSE (5), Sam BEECHENER (6), Amy TAYLOR (7), **Deborah HOYLE** (1)
1: Roslin Institute, R(D)SVS, University of Edinburgh, United Kingdom; 2: Animal and Plant Health Agency, United Kingdom; 3: Queen's University Belfast, United Kingdom; 4: University of Surrey, United Kingdom; 5: Edinburgh Napier University, United Kingdom; 6: Scotland's Rural College (SRUC), United Kingdom; 7: AB Neo, United Kingdom

Background

Weaning is stressful for piglets and may result in development of a gut microbiome favouring colonisation with enterotoxigenic *Escherichia coli* (ETEC), the primary cause of post-weaning diarrhoea (PWD). PWD is a welfare and economic concern, and until recently was managed by zinc oxide (ZnO) supplementation in feed. However, concerns that zinc as a metal may select for antimicrobial resistance (AMR) due to common resistance mechanisms, contributed to the UK and EU banning ZnO in feed above 150ppm. Understanding the effect of ZnO on the weaner gut microbiome and resistome is critical to inform on new strategies for managing PWD.

Methods

This study involved 29 commercial UK pig herds recruited to a longitudinal study (2022- 2025) and two additional herds both running parallel trial groups of weaner pigs with/without ZnO in feed. Illumina 150 bp shotgun metagenomic sequencing was performed on DNA extracted from pen-floor faecal samples, pooled at herd level for longitudinal herds, for pre-withdrawal, 6-months and 12-months post-withdrawal time-points. The with/without ZnO trial groups were sequenced as individual pen samples.

For taxonomical analysis, reads were processed with the taxprofiler nf-core pipeline1, used with Kraken2 and Bracken to assign taxa from the GTDB R226 database2 to sequence reads. Taxapasta and Krona were used to merge and visualise data. For gene-based analysis to detect AMR, metal and virulence genes, reads were assigned by mapping with KMA to three databases: MEGARes, ResFinder, and a curated panel of *E. coli* virulence genes (APHA)3. Read counts for each gene variant were scaled to hits per million reads and compared between trial groups, and for pre- versus post-ZnO withdrawal time-points, using ALDEX2.

Results

Data from with/without trial groups revealed one herd exhibited significantly higher differences (p 0.05) in relative abundance of specific AMR genes e.g. *narA* and *ermB,* for the with-ZnO group. Without ZnO, a higher abundance of ETEC heat-stable toxin virulence genes (*sta*, *stb*; p 0.05), and higher relative abundance of *Enterobacteriaceae* were observed. Analysis of the pre-withdrawal within-herd pools showed consistent relative abundance of certain taxa across the 29 herds, for example *Faecalibacterium*, *Segatella* and *Blautia*, but widely varied abundance of other genera, such as *Escherichia* and *Streptococcus*. A wide diversity of AMR genes was detected in pre-withdrawal samples, of differential abundance across herds. Further analyses are ongoing to compare pre- and post-ZnO withdrawal time-points for microbial diversity, taxonomical composition, gene composition and gene diversity.

Conclusion

Removing ZnO from weaner diets may alter resistome profiles and microbiome diversity, however, differences may be dependent on individual farm characteristics. Further comparison of pre- and post-ZnO withdrawal data from longitudinal study herds is ongoing and will reveal whether any differences identified are consistent across herds, suggesting findings of broader relevance to the wider industry.

1466 – Evaluation of One Health Integration in Medical School Curricula: A Case Study from the University of Global Health Equity, Rwanda

Ursin BAYISENGE (1), Maria ALBIN (1), Kelsey RIPP (1,2), Phaedra HENLEY (1)

1: University of Global Health Equity, Rwanda; 2: Alaska Native Tribal Health Consortium

Background: Amid global health threats such as pandemics, antimicrobial resistance, and climate-driven disease emergence, the need for health professionals with systems thinking and intersectoral collaboration skills is urgent. One Health (OH), recognising the interdependence of human, animal, and environmental health, offers a framework to prepare such leaders, yet its integration into undergraduate medical education remains rare and under-evaluated. The University of Global Health Equity (UGHE) in Rwanda is among the first institutions worldwide to embed OH longitudinally into its medical curriculum across preclinical and clinical years. This study presents the first formal evaluation of this model, undertaken after the inaugural cohort completed training.

Methods: We conducted a mixed-methods cross-sectional study. A structured questionnaire assessed OH knowledge, perceived relevance to patient care and basic medical sciences, and perceptions of teaching and assessment methods. Quantitative data were complemented by focus group discussions (FGDs) with medical students and faculty exploring experiences of learning, teaching, and applying OH. Ninety-three participants took part: 45 (48.4%) students, 36 (38.7%) clinical medicine faculty, 11 (11.8%) basic sciences faculty, and 1 (1.1%) OH faculty member.

Results: Two quantitative patterns were particularly salient. First, reported OH knowledge spanned the full spectrum but clustered toward the middle and upper levels: 20 (21.5%) participants rated their knowledge as basic/very basic, whereas 33 (35.5%) rated it as advanced/very advanced, including 17 (18.3%) students and 16 (17.2%) faculty. This suggests that longitudinal exposure can foster substantial self-rated competence while still revealing ongoing faculty learning needs. Second, most 58 (62.4%) and

62 (66.7%) respondents including both faculty and students respectively viewed OH as relevant to basic medical sciences and to patient care and public health, supporting its inclusion within the MBBS curriculum. Qualitative findings added important nuance. Across FGDs, both students and faculty consistently identified community- and field-based experiences, case-based learning, and structured OH history-taking as the most effective strategies for translating abstract OH concepts into clinical reasoning, particularly for zoonotic and environmentally linked conditions. At the same time, participants highlighted limited faculty competence, weak alignment of assessments with OH content, and the perception of OH as a parallel "add-on" rather than a fully integrated thread as key barriers to deeper integration.

Conclusion: Longitudinal integration of OH into an MBBS curriculum is feasible, valued by learners, and associated with perceived gains in knowledge and clinical relevance. Realising the full potential of this approach will require sustained investment in faculty development, stronger alignment between assessments and OH competencies, and clearer expectations within clinical training environments. The UGHE model offers a practical template for medical schools seeking to mainstream OH within core medical education.

1476 – Participatory sciences in One Health

Cécile AENISHAENSLIN
Université de Montréal, Canada

Background. The One Health (OH) approach is grounded in the integration of diverse forms of knowledge across sectors, disciplines, institutions, and communities. Yet, recent analyses indicate that many OH initiatives still struggle to meaningfully engage external stakeholders and to bridge knowledge systems effectively. Participatory sciences - including participatory research, community-based research, and citizen science - offer structured methodologies to address these shortcomings. These approaches foster shared learning, reduce power asymmetries among actors, strengthen intersectoral collaboration, and support the co-design of context-specific solutions.

Educational outcomes. This 90-minute special session aims to demystify participatory sciences within the OH field and to critically examine their added value for addressing complex, systemic challenges.

Participants will (1) gain a clearer conceptual understanding of the spectrum of participatory approaches and their relevance to OH; (2) identify practical design features, enabling conditions, and common pitfalls in implementing participatory OH projects; and (3) develop a more coherent vocabulary to describe participatory approaches. The session will promote peer-to-peer learning and critical reflection, equipping researchers, practitioners, and policymakers with actionable insights to strengthen stakeholder engagement and co-development processes in future OH initiatives.

Format (90 minutes): The session will be co-chaired by Cécile Aenishaenslin, professor at Université de Montréal and by junior researchers Jessica Hainault, Manon Boiteux (Université de Montréal) and Camille Desbiens (Université Laval, Canada). It will showcase five concrete case studies from diverse geographic areas and reflect on how participatory sciences contribute to One Health training for post-graduate students.

Each case study will be presented in 10 minutes, followed by a 20-minute facilitated discussion focused on cross-cutting lessons and future directions (10mn for questions). Each presentation will illustrate how participatory methodologies were operationalized at different stages of the research or policy cycle, the challenges encountered (e.g., governance, equity, resource constraints), and the impacts on knowledge integration and decision-making.

Case studies

1479 – ResAlert: A UK One Health Early Warning and Coordinated Response System for Antimicrobial Resistance of Potential High Risk to Human or Animal Health

Manal ABUOUN, Beth ANDERSON, Fraser BROADFOOT, Aisling GLENNIE, Kitty HEALEY, Tamsin DEWÉ, **Sophie SPALDING**

Veterinary Medicines Directorate, United Kingdom

Background: Antimicrobial resistance (AMR) poses a risk to human, animal and environmental health, therefore early detection of emerging or unusual resistance is essential to support harmonised One Health action. In 2015, the United Kingdom established the ResAlert system to identify, assess and respond to resistant bacterial isolates from animals, their environments, feed, or foods of animal origin(1). Led by the Veterinary Medicines Directorate (VMD) and brings together experts across government, public health, animal health, food safety and environment agencies to ensure rapid, risk-based action for AMR across the four UK nations.

Methods: A ResAlert is triggered when UK laboratories (Animal and Plant Health Agency, Agri-Food and Biosciences Institute or Scotland's Rural College) detect resistant bacteria considered to be high risk to human or animal health. The identifying laboratory submits a standardised form to VMD, who coordinate circulation of the case to the ResAlert membership, which represent the four nations, one health sectors and government policy leads. The group undertakes a risk assessment, agrees risk management and communication actions, and assigns cross-sector actions. Policy decisions that arise from a ResAlert are made by the policy lead from the relevant nation.

Results: To date, 60 ResAlerts have been raised in the UK, most originating from pigs, followed by poultry and cattle. Alerts were triggered by detections of AMR of public or animal health concern, including methicillin resistant *Staphylococcus aureus*, colistin resistant *Escherichia coli* and *Salmonella enterica* and extended-spectrum beta-lactamases and carbapenem resistant Enterobacterales. Incidents triggered action across One Health sectors, including field investigations, enhanced microbiological and genomic analysis, and information sharing with public health and food safety partners. Over time, the development of whole genome sequencing (WGS) has improved in-depth characterisation, enabling detailed comparison between isolates from different sectors, underpinning risk assessment. Novel findings, of higher concern, or with wider industry implications are also escalated to the Chief Veterinary Officer and/or the Veterinary Risk Group.

Recent examples have demonstrated how ResAlerts drive improvements and adapt surveillance approaches. The detection of carbapenem-resistant *Salmonella Agona* in poultry led to cross-sector investigation, reinforcing the importance of early genomic confirmation and coordinated response (2). A ResAlert triggered by amikacin-resistant *E. coli* and *Salmonella* harbouring *rmtB* in pigs resulted in targeted surveillance to better understand emerging risks in livestock populations (3).

Conclusions: The UK ResAlert system demonstrates a functional One Health early warning mechanism for AMR threats arising from animals or their environment, enabling timely cross-sector data sharing, and proportionate actions across the UK. ResAlert provides a model for integrated AMR surveillance and response, improving preparedness against zoonotic and environmental AMR risks and strengthening the interface between animal and human health systems.

1485 – One Health Education in a Fragile State: A Multi-Level Knowledge Assessment Across Schools in Somalia

Yusuf Abdi HARED (1,5), Farah I. MUMIN (2,4), Shafii Abdullahi MOHAMED (3), Abdisalam Mahdi HASSAN (1), Knight-Jones THEO (2), Siobhan M. MOR (2,4)

1: Amoud University, Borama, Somalia; 2: International Livestock Research Institute, Nairobi, Kenya; 3: Somali National University, Mogadishu, Somalia; 4: Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Neston, United Kingdom; 5: Dalarna University, Falun, Sweden

Background

One Health (OH) education, integrating human, animal, and environmental health perspectives, remains largely absent from school curricula in low-resource and fragile-state settings. Somalia presents both a critical need and a meaningful test case: millions of households depend on livestock, children grow up in close contact with animals, with high exposure to zoonotic diseases including brucellosis, anthrax, and rabies. Despite these risks, 88.4% of the national school curriculum lacks OH content (Hassan-Kadle et al., 2025). Decades of conflict have fragmented health and education systems, limiting conventional health

promotion. Schools are increasingly recognised as strategic platforms for behaviour change, yet evaluations of OH education in East African or fragile-state school systems are scarce. This study evaluates the effectiveness of a Training of Trainers (ToT)-based OH education programme across primary (Grades 5–8) and secondary (Grades 9–12) schools in Somalia.

Methods

A pre–post evaluation design was used. Assessments were administered in 19 schools (14 primary, 5 secondary) across Awdal and Benadir regions between June and October 2025. Amoud University and Somali National University trained 196 teachers through intensive five-day ToT workshops; trained teachers then delivered structured weekly OH lessons. Primary students completed an 8-item knowledge assessment tool (zoonoses, hygiene, AMR, environmental health); secondary students completed an 18-item multiple-choice questionnaire covering OH concepts, zoonotic disease, AMR, WASH, and community collaboration. Both instruments were administered in Somali language via KoBoToolbox. Scores (% correct) were compared pre–post disaggregated by gender, grade, and region.

Results

A total of 2,738 pre-post assessments were collected (1,523 primary; 1,215 secondary paired samples). Among secondary students, mean knowledge scores increased from 38.1% to 76.7% (+38.6 percentage points). Gains were consistent across all domains: One Health concepts (+42.6 pp), zoonotic disease and AMR (+39.7 pp), WASH and sanitation (+33.9 pp), and community collaboration (+38.3 pp). Among Benadir primary students, scores rose from 12.7% to 74.6% (+61.9 pp); 89% of matched individual students improved, with a mean individual gain of 30.5 pp. Knowledge gains were equitable across gender and grade levels. Awdal secondary schools showed higher pre-intervention baselines (59.8%) compared to Benadir (27.7%), consistent with prior programme exposure, yet both regions demonstrated comparable knowledge gains (+35.4 pp vs +41.5 pp). The weakest gains were in AMR at primary level (+5.7 pp).

Conclusions

A teacher-led, ToT-based OH curriculum produced substantial and broadly equitable knowledge gains across school levels in a fragile-state context. The programme successfully extended OH education to primary school children for the first time in this setting and demonstrates a replicable, cost-efficient model for scaling OH education in low-resource settings. These findings provide a validated pathway for national curriculum reform and a transferable model for comparable contexts across East Africa and beyond.

1498 – Strengthening early detection of emerging health threats: Localization of One Health Community event-based surveillance and response (CESR) in Navotas City, Philippines

Maricar SILVA (1), Kenn Manuel PALMARES III (3), Armel BERIÑO (4), Ian Christian GONZALES (2), Mark Romel MONTEVIRGEN (1), Ingrid MAGNATA (1), Christia PADOLINA (4), Eric DAVID (4), Cheney Ville GABRIEL (4), Ysabela Bernardina NAZAL-HABUNAL (4)

1: Jhpiego Philippines, Philippines; 2: Department of Health - Epidemiology Bureau, Philippines; 3: Department of Health - Metro Manila Center for Health Development Regional Epidemiology and Health Statistics Section; 4: Local Government Unit (City Administrator, Health, Agriculture, and Environmental Offices) of Navotas City, Philippines

Background

The Philippines' public health surveillance system is established to support efforts to ensure population health and safety through case- and event- based approaches, with event-based surveillance and response (ESR) as an essential mechanism to detect and verify rare, unusual, or unexpected events that may not be captured through case-based reporting and traditional monitoring.

Community participation in early detection, reporting, response, and monitoring of health events is significant to prevent potential public health impacts. As such, the Department of Health (DOH) Epidemiology Bureau (EB) and the Task Force for Global Health developed the community ESR (CESR) and implemented it in selected sites. CESR involves reporting of signals detected by frontline health workers. However, the current CESR focuses on signals related to general symptoms or clusters of illnesses in humans and animals. Cognizant of distinct issues faced by localities in addition to diseases under surveillance, Jhpiego initiated the development of locally relevant signals for CESR.

Navotas City is an urban-poor, narrow coastal city facing environmental vulnerabilities and public health risks such flooding and chemical spread. These conditions led to its selection as implementing site for this initiative.

Methods

In close collaboration with DOH-EB, Metro Manila Center for Health Development, and Navotas City, Jhpiego facilitated focused group discussions to determine key events of public health significance in Navotas. These were complemented by desk reviews of related implementation models to develop a localized CESR signal.

The localized signal will be incorporated into existing training modules for regional and Navotas City personnel, including disease surveillance focal points, representatives from agriculture and environmental offices, and human, animal, and environmental health workers at the community level, for implementation.

Trained community health workers will report CESR signals using a digital platform, KoboToolbox. Monitoring visits will be conducted after initial implementation to determine if the system was effectively utilized and to gather lessons from the implementation.

Results

Navotas City hosts numerous ice plants, and previous incidents of ammonia leaks raised concerns about potential chemical exposures. Thus, the development of an environmental signal related to possible chemical hazards is highly relevant for the locality. The localized signal focuses on "*sudden environmental occurrences that may cause health issues*."

Examples include *unexplained/unusual pungent smell causing any of the following: difficulty in breathing, irritation to eyes/skin, sudden coughing/choking*; or *unexplained death/dying vegetation, gasping fish in nearby water, white "mist" appearing in pipes, loud hissing/whistling sounds from industrial tanks/pressurized systems*.

Conclusion

The localization of CESR highlights the importance of adapting surveillance systems to local contexts through a One Health approach. By integrating an environmental signal relevant to Navotas City, CESR enhances community capacities to prevent, detect, and respond to potential public health threats that may otherwise go unnoticed.

1501 – Linking rodent-borne zoonotic virus exposure to human mobility and rodent ecology in degraded forest landscapes

Emilia JOHNSON (1), Andrina NANKASI (2), Isaac WESTLAKE (1), Elizabeth WILLEMS (3), Joachim MARIEN (3), Sarah CLEAVELAND (1), Christina FAUST (1)

1: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, United Kingdom; 2: Vector Control Division, Ministry of Health, Uganda; 3: Institute of Tropical Medicine Antwerp, Belgium

Background

Land use change and forest fragmentation is implicated in the emergence of zoonotic disease. Rodents host a disproportionate number of pathogens, including human-infecting viruses. With rapid life history and adaptive traits, *Mastomys spp.* readily occupy ecological niches that emerge following landscape conversion. Although spatial overlap between rodentsand humans is likely to drive exposure to rodent-borne viruses, the impact of land use and individual space use in determining infection risk is unclear.

Methods

A cross-sectional serological survey was conducted in 18 villages in Western Uganda between July-August 2025 around Bugoma and Budongo Forests (Figure 1A). Sites were classified using remote sensing data, with 6 households randomly selected per village. Multiplex immunoassays were used to detect serum antibodies against zoonotic RNA viruses. A nested movement study was conducted in July 2025 and February 2026, with GPS devices deployed to a subset of participants for 7 days with 3-minute fixes continuously. Forest edges were defined as +/-50m around patches >1.8-hectares and beta mixed-effects

models were fit to individual exposure metrics. At a subset of sites, a 6.76-hectare grid was monitored for rodent abundance and diversity using longitudinal capture-mark-recapture (CMR). Relative abundance of key reservoirs (*Mastomys)* was estimated using a GLMM. Ongoing analyses are investigating space use relative to *Mastomys* distributions and formulating step selection models to evaluate the contributions of spatial and sociodemographic drivers on seropositivity to zoonotic viruses.

Results

785 individuals were enrolled, balanced by gender (n=352 males, 44.8%; n=433 females, 55.2%) and reflecting a young population (mean age of 20.9, 1–85.0 years). GPS data were collected from 85 participants over 12 years of age. Individuals near protected forests have lower odds of time spent in edge habitat (aOR=0.18, CI95 0.09-0.36, p0.001) than those near degraded forests, while men have 4.5-fold higher odds of high edge use (aOR=4.48, CI95 1.58-14.6, p=0.007). Odds of a rodent being *Mastomys* are 3-fold higher in degraded sites than in matrix sites (OR=2.81, CI95 1.45-5.45, p0.001). Serocatalytic models will be used to estimate force of infection by sociodemographic status and land use motifs. Screening of serum collected from individuals >8 years (N=568) for antibodies against a panel of arboviruses and poxviruses is ongoing.

Conclusions

Individual exposure to forest edges varied strongly by land use. Recent forest conversion and high fragmentation concentrate human exposure through idiosyncratic behaviour and underlying rodent reservoir hazard, while stable ecological boundaries appear to reduce exposure. Serological surveys paired with human mobility data, longitudinal rodent ecological data and participatory mapping exercises provide a novel framework to evaluate emergent hotspots of rodent-human contact and epidemiological risk in dynamic landscapes. This underscores land use and landscape management strategy as a key determinant and intervention point for exposure pathways at the human-rodent disease interface.

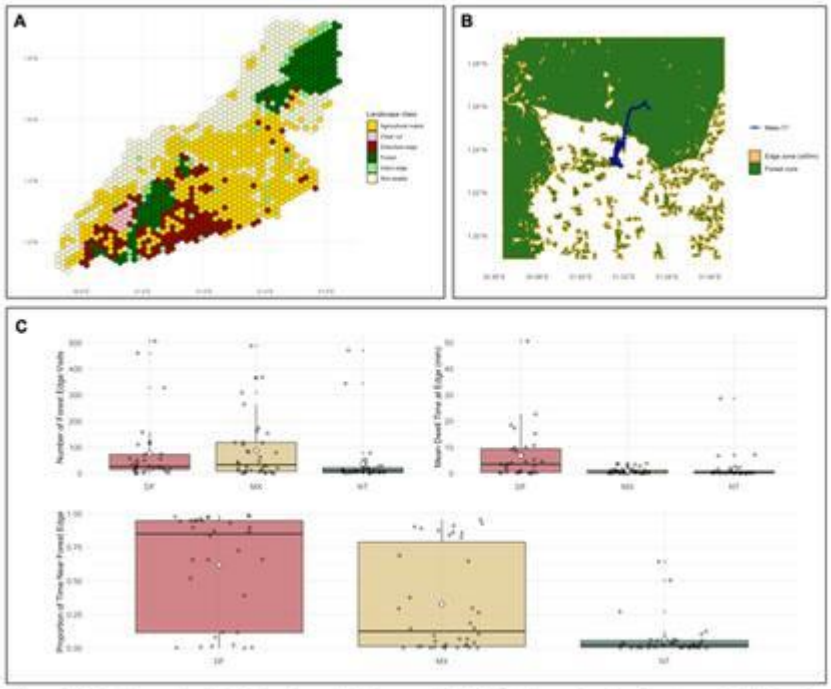


Figure 1. A) Study area classified by landscape (2km hexagons). B) GPS track overlayed on forest core (≥1.8ha) and edge (±50m). C) Space use metrics across disturbed forest (DF), intact forest (NT) and agricultural matrix (MX).

1505 – Investigating risk factors for rodent-borne zoonoses exposure in rural Madagascar

Niamh MCAULEY (1), Soanandrasana RAHELINIRINA (2), Rado RAKOTONANAHARY (2), Ines VIGAN-WOMAS (2), Minoarisoa RAJERISON (2), Sandra TELFER (1,2)

1: University of Aberdeen, United Kingdom; 2: Institut Pasteur de Madagascar, Antananarivo, Madagascar

Background

Emerging and re-emerging zoonoses present a growing public health concern. Exposure risk to zoonoses is influenced by environmental and socioeconomic variables. Risk is often believed to be highest in tropical, rural regions, where the prevalence of agricultural occupations tends to increase contact between humans and reservoirs. Lower socioeconomic status can also increase exposure due to reduced access to infrastructure such as clean water and robust household materials. Rodents are important reservoirs of a range of zoonotic pathogens. For some zoonotic diseases, rodents are the main reservoir, whilst for others alternative animals, including livestock, may also play a role. In addition to their role as disease reservoirs, rodents can negatively impact food security and have indirect effects on health due to their role as pests of crops and stored foods. This study aimed to assess the prevalence of exposure to four rodent-borne zoonoses and investigate the relative importance of environmental, demographic, socioeconomic and behavioural risk factors in rural communities.

Methods

A cross-sectional study was conducted across 20 villages in Moramanga, Madagascar. Serum samples were collected and tested using IgG ELISAs for antibodies to *Leptospira*, *Yersinia pestis*, spotted fever group rickettsia (SFGR), and typhus group rickettsia (TGR). Questionnaire surveys were conducted to collect demographic and socioeconomic data, as well as information on , contact with potential reservoirs. Associations between serological status and potential risk factors were analysed through multivariate analyses using generalised additive mixed models.

Results

Seroprevalence was 8.0% (95/1190) for *Leptospira*; 24.5% (291/1188) for SFGR; 6.6% (78/1188) for TGR; and 0.8% (9/1190) for *Y. pestis*. The multivariate analysis was only conducted for *Leptospira*, SFGR, and TGR due to low prevalence of *Y. pestis* exposure.

Contact with rodents was associated with exposure to all three pathogens, though notably *Leptospira* exposure was predominantly associated with contact with mice as opposed to rats. *Leptospira* exposure was also positively associated with ownership of cows, a potential reservoir for *Leptospira*. SFGR and TGR exposure seemed more associated with socioeconomic variables such as education, where a higher education increased risk of TGR exposure and decreased risk of SFGR. In contrast, *Leptospira* exposure appeared more driven by specific activities such as contact with potentially contaminated water and livestock. Notably, both *Leptospira* and SFGR exposure was significantly higher in males than females.

Conclusions

This study highlights the role multiple reservoirs can play in zoonotic exposure, with *Leptospira* exposure linked to rodents, livestock, and environmental contamination. Exposure to the three pathogens studied were influenced by demographic, socioeconomic, and behavioural variables. Current work is further investigating the role socioeconomic status plays in zoonotic exposure, and a longitudinal study aims to improve our understanding of the incidence of exposure and disease in rural Malagasy communities.

1513 – Airborne Livestock Microbiomes and Community-Acquired Pneumonia Risk: Metagenomic Investigation around Goat Farms using a One Health approach

Alex BOSSERS (1,2), Myrna M.T. DE ROOIJ (1), Wouter LOKHORST (2), Jan VERKAIK (2), Inge M. WOUTERS (1), Albert WINKEL (2), Lidwien A.M. SMIT (1), Thomas HAGENAARS (2)

1: Utrecht University - Institute for Risk Assessment Sciences, The Netherlands; 2: Wageningen BioVeterinary Research, part of Wageningen University & Research, The Netherlands

Background: Dutch Epidemiological studies have consistently shown associations between living in proximity to goat farms and community-acquired pneumonia (CAP) between 2009 and 2019. It was hypothesized that airborne transmission of microbial agents from goat farms could explain this finding. By comprehensive farm and environmental investigations combined with sequencing approaches, we aimed to identify relevant micro-organisms.

Methods: Within the Dutch Livestock Farming and Neighboring Residents' Health study (VGO3, 2018-2024), a multi-faceted approach was adopted to identify potential causes underlying the increased risk of CAP. This included research among pneumonia patients, non-farming residents and goat farm workers. It also involved intensive sampling at and around goat farms assessing a large variety of matrices, including

stable air, manure, feed, direct goat-derived samples, and outdoor air. During 31 visits (between November 2019 and December 2021) of 16 goat farms, we collected >3,300 samples. At residential sites at varying distances from goat farms, we collected >280 outdoor air samples (April – November 2021). Initially, based on sampling completeness, 880 samples were analyzed by multi-target meta-barcoding approaches (16S rRNA and ITS), 400 samples by shot-gun metagenomics sequencing, and 260 samples were analyzed for the goat virome using virome-enriched metagenomics. Source-attribution analyses were used to obtain insights into the contribution of micro-organisms from and to various matrices and their spread and accumulation inside the stable.

Results: Observed community compositional differences in bacteria, fungi and viruses aligned with farming related practices. Using a literature-based list of 94 bacterial, fungal or viral pathogens present in goats that can cause CAP, we found 36 (32 bacteria, 4 fungi and 0 viruses) to be present in stable air of at least 25% of goat farms in our study. Of these, 18 bacterial pathogens were also detected in outdoor air. Nine of these matched the top-10 highest prevalent pathogens in stable air samples. In line with meta-barcoding results, metagenome-assembled-genomes confirmed the presence of several of the higher abundant micro-organisms and facilitate on-going strain-level investigations.

Source attribution analyses on the total microbiome compositions revealed that manure from the barn was the major contributor (median ~36% (IQR:19-54%) to the microbiota measured in stable air. Bedding, feed and goat feces contributed 18% (IQR:10-33%), 2% (IQR:1-5%) and 8% (IQR:1-13%) respectively.

Conclusions: We identified bacterial pathogens in the air in and around goat farms that may provide an explanation for the higher incidence of CAP in neighboring residents. Given the high abundances of airborne pathogens in goat farming overall, our outcomes support the development of practical measures (such as altered manure management) in goat husbandry. Reduction of bio-aerosol concentrations inside the farm and its emissions, is expected to contribute to improved public health and likely beneficial to goat farmers themselves and their animals.

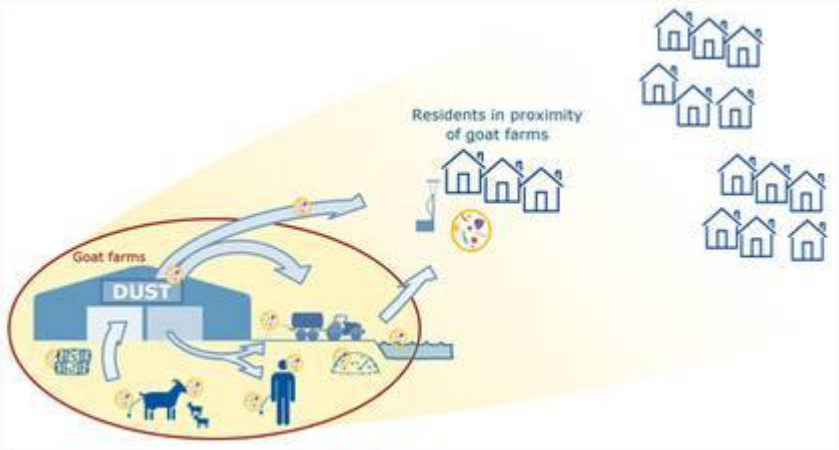


Figure 1. Metagenomics measurements on and around goat farms.

1522 – Mapping Complexity: A One Health Approach to Socio-Economic Impacts of Vector-Borne Zoonotic Diseases in Canada

Sarah J. ROBINSON (1), Simran PUREWAL (1), Jolene A. GIACINTI (2), Murray GILLIES (3), Damien JOLY (4), Kelley LEE (1), Andrea OSBORN (5), Rackeb TESFAYE (1), Kaylee A. BYERS (1,4,6)

1: Faculty of Health Sciences, Simon Fraser University; 2: Science and Technology Branch, Environment and Climate Change Canada; 3: Canadian Animal Health Surveillance System, Animal Health Canada; 4: Canadian Wildlife Health Cooperative; 5: Community for Emerging and Zoonotic Diseases; 6: School of Population and Public Health, University of British Columbia

Background: Vector-borne zoonotic diseases (VBZDs) pose a growing threat to the health of humans, domestic animals, and wildlife. This evolving challenge is compounded by socio-economic factors, notably housing insecurity, rising poverty, employment precarity, and changing land-use and agricultural practices that influence exposure, vulnerability, and capacity to respond. Recognizing the complexity of the social and economic dimensions of VBZDs, this project applies a One Health lens to develop

foundational evidence to guide research and policy for mitigating climate-related impacts of these diseases in Canada.

Methods: We conducted a modified Horizon Scan to identify research and policy priorities related to the socio-economic impacts of VBZDs and the factors shaping those impacts. The approach integrated three components: 1) a scoping review collating evidence on socio-economic impacts and influencing factors in the Canadian context; 2) semi-structured key informant interviews with VBZD experts (n=6) to identify priority diseases, populations most affected, and barriers to participation in decision making; and 3) fuzzy cognitive mapping (FCM) to develop literature-informed and interest-holder-derived maps. Interest-holder sessions included participants from forestry and conservation (n=7), outdoor programs and recreation (n=7), and veterinary staff working with vulnerably housed individuals (n=6), who mapped and weighted relationships among factors and impacts drawing on their lived experiences with VBZDs.

Results: Key informant interviews highlighted that VBZD impacts are shaped by socio-economic context and unevenly distributed across populations. Marginalized groups, vulnerably housed residents, outdoor workers, and Indigenous communities were identified as priority populations. Informants emphasized addressing mental well-being, institutional trust, and culturally appropriate risk communication.

The literature-informed FCM revealed diverse and interconnected factors spanning occupational, economic, social, and behavioural dimensions. Facilitators included access to reliable information, knowledge of disease risks and prevention, stable housing, community-based interventions, shared decision making with healthcare providers, and tailored communication strategies. Barriers included medical stigma, unclear messaging, and misinformation.

Interest-holder-derived maps emphasized interconnections among mental health impacts (fear, anxiety, uncertainty), the burden of preventative behaviours, changing relationships with nature, and concern for animal health. Facilitators included trusted information sources and reliable healthcare access, while cost, time constraints, mistrust in public health, and diagnostic challenges amplified impacts. Climate change was identified as a cross-cutting factor expected to intensify impacts and compete with other public health priorities.

Conclusions: Addressing VBZD socio-economic impacts requires integrated approaches that recognize the reciprocal relationship between disease dynamics and socio-economic context. FCM provides a visual framework to capture community knowledge and guide research and decision making. Factors with higher perceived weight among priority populations highlight potential intervention points and avenues for future research. Findings underscore the need for tailored risk communication, community-driven interventions, and locally relevant strategies, while shared trends across groups point to high-priority signals for timely research and policy action under the pressures of climate change.

1527 – The One Health Landscape of Antibiotic Stewardship: What Works, What Hinders, and What's Next

Marion BORDIER (1), Leo DELPY (2)

1: ASTRE, University of Montpellier, CIRAD, INRAE, Montpellier, France; 2: Center for Sociological and Economics Studies and Research (CLERSE), CNRS, University of Lille, Villeneuve-d'Ascq, France

Background:

Antibiotic resistance (ABR) is a global health threat that is mainly driven by the overuse and misuse of antibiotics. As interactions between humans, animals, and the environment are central to the emergence and spread of ABR, adopting a One Health approach is essential to effectively address the issue. A large panel of antibiotic stewardship (ABS) interventions has been developed to optimize the use of antibiotic. However, we lack a comprehensive overview of the landscape of antibiotic stewardship interventions from a One Health perspective, in terms of scope and effectiveness. To address this gap, we conducted a scoping review of existing interventions and identified future directions.

Methods:

A systematic literature search was applied to retrieve interventions meeting our study definition. We purposefully sampled some of these interventions to illustrate the diversity of existing interventions. These sampled interventions were then assessed using 26 variables related to their general

characteristics, development and implementation mode, scope, One Health dimensions (including equity), and impacts. We conducted a descriptive analysis on the data extracted to summarize the characteristics of the antibiotic stewardship interventions.

Results

The study selected and described 29 interventions. They focused on information and education, access to antibiotics and their usage, and antibiotic disposal. Regarding their One Health aspects, they vary in terms of intersectoral collaboration, engagement with the private sector, and equity. Strong livestock industry engagement, efficient legal and institutional framework, and provision of alternatives to antibiotics act as facilitators to intervention success. Interventions demonstrated effects in terms of changes in antibiotic use and resistance, awareness and practices, as well as effects on animal health and productivity. Our synthesis of One Health interventions also highlighted the important role of policy diffusion, from one country to others, on shaping interventions. The policy framework is rapidly evolving, with countries learning from and reacting to each other as they attempt to curtail the global threat of ABR. However, ABS intervention efficacy remains highly dependent on the implementing context. This study underlined the persistent dominance of human health objectives in the design and implementation of One Health antibiotic stewardship interventions and the continuous need to strengthen evaluation approaches of such interventions to better understand facilitators and barriers to their implementation as well as the impacts they are contributing to.

Conclusion

This review highlights the diversity of antibiotic stewardship interventions within a One Health framework. Strengthening cross-sectoral integration, context-sensitive design, and robust evaluation is essential to enhance effectiveness and address the global challenge of antibiotic resistance.

1541 – Invasive wild boar management through a One Health approach: intersectoral surveillance experiences from Argentina

Maria MESPLET (1,2,3), Soledad BARANDIARAN (2,3,4), Agostina TAMMONE (5,6), Ezequiel CONDORI (5,6), Andrea MARCOS (7,8), Kurmanzhan DASTANBEK KYZY (1), Francisco D'ALESSIO (1), Chadia WANNOUS (1)

1: WOAH, World Organisation for Animal Health; 2: Universidad de Buenos Aires, Facultad de Ciencias Veterinarias, Cátedra de Enfermedades Infecciosas; 3: Universidad de Buenos Aires, Instituto de Investigaciones en Epidemiología Veterinaria (IIEV); 4: CONICET-Universidad de Buenos Aires. Instituto de Investigaciones en Producción Animal (INPA). Buenos Aires. Argentina.; 5: Universidad Nacional del Centro de la Provincia de Buenos Aires, Facultad de Ciencias Veterinarias; 6: Centro de Investigación Veterinaria de Tandil (CIVETAN - CONICET-UNCPBA-CIC); 7: Universidad de Buenos Aires, Facultad de Ciencias Veterinarias, Cátedra de Salud Pública; 8: Dirección Nacional de Sanidad Animal, SENASA. Argentina.

Background

The Quadripartite (FAO-WHO-UNEP-WOAH) One Health Joint Plan of Action (2022–2026) highlights wildlife-livestock-human interfaces as critical spaces for preventing zoonotic emergence and biodiversity loss. Despite this, wildlife health surveillance systems remain fragmented in many countries of the Americas. In Argentina, invasive wild boar (*Sus scrofa*) is present in nearly 45% of the national territory and serves as a reservoir of zoonotic pathogens including tuberculosis, trichinellosis, brucellosis, and leptospirosis. We present two Argentine case studies demonstrating how One Health principles, supported by intersectoral collaboration and links with national epidemiological surveillance systems, can be operationalized at territorial level in both protected and productive landscapes.

Methods

Two complementary initiatives implemented between 2016–2025 were examined through a One Health governance lens.

In El Palmar National Park, the Invasive Exotic Mammal Control Plan brought together park authorities, academic institutions (University of Buenos Aires-UBA, and National University of the Center of the Province of Buenos Aires-UNICEN), hunters' associations, and the National Service for Agri-Food Health and Quality (SENASA). Systematic inspection and laboratory diagnosis were conducted in 320 culled wild boars between 2016 and 2022, generating valuable pathogen data. Training strengthened food safety practices and reduced occupational health risks.

In Tandil, a collaborative network led by the Faculty of Veterinary Sciences (UNICEN) established participatory governance mechanisms for invasive wild boar management through strong intersectoral coordination among academic, governmental, and producer stakeholders. Activities included camera-trap monitoring (27 units across 5,000 hectares), pilot testing of multi-capture traps, development of sanitary management protocols to reduce spillover risk at the wildlife–livestock interface.

Results

In El Palmar, integrated monitoring generated the first structured local dataset on zoonotic pathogens in invasive ungulates and enabled the distribution of meat tested negative for *Trichinella* spp. to community institutions, linking conservation with animal health, and public health. The data generated is integrated in the national surveillance system, supporting animal disease and public health programs.

In Tandil, cross-sector collaboration improved territorial mapping, risk perception assessment, and regulatory dialogue for integrated capture–slaughter–sanitary circuits.

Both cases operationalized OH JPA pathways on multisectoral integration (Pathway 2) and data generation (Pathway 3), while contributing to Action Tracks on zoonotic disease control, food safety, and environmental integration.

Conclusions

These experiences demonstrate that invasive wildlife management can serve as an entry point for strengthening wildlife health surveillance, food safety systems, and biodiversity protection under a One Health approach. Argentina's territorial models illustrate how intersectoral collaboration and integration of multiple actors in national epidemiological surveillance systems can translate WOAH-aligned wildlife health strategies into actionable, scalable practices across the Americas.

1546 – Towards pathogen fingerprint profiling of human viruses for Biosecurity

Gloria Grace AKURUT, Bilal KHAN, Mariana ULINICI, Ursa SUSNJAR, Tea CARLETTI, Alessandro MARCELLO
Molecular virology Laboratory, International Centre for Genetic Engineering and Biotechnology, Trieste,Italy

Introduction; Accurate genomic characterisation of pathogens stored in a high-containment laboratory is critical for biosecurity. Beside characterising viruses in store and their possible mutations upon passaging, it is important to verify pathogens against information shared during exchange of laboratory material with collaborators. Furthermore, in a situation where an infection caused by spillover or laboratory leakage is suspected, it is crucial to trace the cause and source of the pathogen thus giving confidence in the reliability of laboratory procedures. Fingerprinting by genomic sequencing is a reliable way to deduce identity and source. Moreover, genomic information from biorepositories in addition to curated biosecurity genomic databases can be used to promote responsible research and implement biosecurity measures.

Methods; We are developing procedures for fingerprinting viral pathogens using the Molecular virology laboratory at ICGEB as a pilot by creating and validating primer schemes for amplicon-based sequencing using Oxford Nanopore Technology (ONT) platform but are compatible with other sequencing platforms. The viruses being fingerprinted include; Dengue (DENV), Zika (ZIKV), Chikungunya (CHIKV), Tick borne encephalitis (TBEV), Yellow fever virus (YFV), Usutu virus (USUV), West Nile virus (WNV), Influenza virus (H1N1) and Oropouche virus (OROV). We are also creating an institutional biosecurity genomic database containing a curated collection of viral genome sequences based on the viruses held in the biorepositories along with the meta-information like: number of tubes, viral loads, source of the virus, lab passage.

Results; Using stock viruses, at a sequencing depth of 10x, genome coverage achieved is as follows; DENV (1-4); 91.3% to 95%, comparable to serotype-specific protocols , ZIKV ≥ 97%, CHIKV ≥99%, TBEV ≥99%, Usutu virus ≥93%, YFV ≥95% and OROV ≥99%. Limit of detection for Virus specific primer schemes was at a ct ≥ 30, furthermore, most primer schemes are optimized to work at the same annealing temperature which is useful for multiplexing. An updated institutional biosecurity genomic database facilitates screening high-through put sequencing (HTS) data against viruses held in the biorepositories.

Discussion and conclusion; This approach generates near whole genome sequences, even directly from samples with ct ≥ 30 and clinical samples, without requiring prior serotyping especially for DENV. The

same annealing temperature allows for assays to be multiplexed hence simplifying use and increasing robustness of the assay. Leveraging on the ONT platform, this approach is both cost effective and adaptable for implementation in the field or low resources settings, enhancing genomic surveillance and biosecurity through fingerprint profiling of pathogens within laboratory repositories. However, the approach is compatible with other sequencing platforms. To circumvent the complexities of processing HTS data on large, non-curated public databases, an internal biosecurity database curated specifically to the institution eases data processing, institutional accountability through internal probes during disease outbreaks, biosecurity event.

1550 – Prevention is the best protection: Sherpabody-based inhibitors against SARS-related betacoronaviruses for pandemic preparedness

Petja SALMINEN (1), Anna MÄKELÄ (1), Hasan UĞURLU (1,2), Riku FAGERLUND (1), Kalle SAKSELA (1,3)

1: Department of Virology, Faculty of Medicine, University of Helsinki, Finland; 2: Department of Molecular Biology and Genetics, Faculty of Sciences, Erzurum Technical University, Turkey; 3: HUS Diagnostic Centre, HUSLAB, Clinical Microbiology, Helsinki University Hospital, Finland

Background

Numerous bat species across Europe, Africa and Asia are natural reservoirs for SARS-related betacoronaviruses (sarbecoviruses), a subgenus of *Betacoronavirus* which contains the epidemic SARS-CoV-1 and pandemic SARS-CoV-2. Environmental and anthropogenic changes globally have increased interactions between humans and these bat species, leading to increased risk for sarbecovirus spillover. To address this public health and pandemic threat, we utilized sherpabodies (Sb), small, modular targeting scaffolds, to develop broadly neutralizing inhibitors against sarbecoviruses.

Materials and Methods

Affinity selection was performed for a large Sb phage display library (diversity ~1011) using alternating RBD variants as baits. The binding specificities and relative affinities of discovered RBD-binding sherpabodies were analyzed by ELISA. Soluble sherpabody trimers were efficiently produced in bacteria. Lenti-based reporter viruses were generated based on the spike glycoproteins of ACE2-utilizing sarbecoviruses, and pseudovirus neutralizations were performed to assess the neutralizing potencies of the developed Sb trimers.

Results

Over 50 unique sherpabody clones were discovered. From these, sherpabodies with broad binding specificities were assembled into trimers and successfully produced in high yields. These Sb trimers were assessed for their neutralization potencies against seven SARS-CoV-1 and SARS-CoV-2 related sarbecoviruses in pseudovirus neutralization assays. Consequently, all tested Sb trimers neutralized the pseudoviruses at low-to-subnanomolar IC50 (half-maximal inhibitory) values, while also retaining a highly potent neutralization capacity of immunoevasive SARS-CoV-2 Omicron subvariants.

Conclusions

The development of Sb-based inhibitors capable of broadly and potently neutralizing diverse sarbecoviruses solidifies the ability of sherpabodies to engage highly conserved sarbecovirus RBD epitopes. This also demonstrates the ease at which broadly binding sherpabodies can be discovered. Multimeric sherpabodies can be economically produced in high amounts and they exhibit remarkable biophysical robusticity. Taken together, these findings further highlight the multi-purpose applicability of the sherpabody technology for pandemic preparedness against sarbecoviruses.

1552 – Virus–host associations of bat coronaviruses along a land-use gradient in the Yucatán Peninsula, Mexico

Marco Antonio JIMÉNEZ-RICO (1,2), Ana Laura VIGUERAS-GALVÁN (1), María José TOLSÁ-GARCÍA (1,2), Paola MARTÍNEZ-DUQUE (1,2), Erika HERNÁNDEZ-VILLEGAS (1), Laura I. LÓPEZ-APODACA (1,2), Audrey ARNAL (1,3), Benjamin ROCHE (1,3), David ROIZ (3,4), Rosa Elena SARMIENTO-SILVA (1), Gerardo SUZÁN (1,2)

1: Facultad de Medicina Veterinaria y Zootecnia (FVMZ) - UNAM, Mexico; 2: International Joint Laboratory IRD/UNAM, Yucatán, México; 3: MIVEGEC, IRD, CNRS, Université de Montpellier, 34090 Montpellier, France; 4: Grupo Sanidad y Biotecnología (SaBio), Instituto de Investigación en Recursos Cinegéticos, IREC (UCLM-CSIC), Ciudad Real, Spain

Background: Coronavirus (CoV) spillover from wildlife to humans is increasing and has caused major global epidemics, driven in part by human-induced habitat alteration that promotes zoonotic emergence. This highlights the need to better understand transmission dynamics within wildlife reservoirs, such as Neotropical bats, which harbor a highly diverse CoV community. Despite this diversity, the host and ecological drivers of CoV circulation, as well as virus–host associations such as genotype-level host range, remain poorly characterized.

Methods: During 2021-2023, we conducted extensive bat sampling across an anthropogenic land-use gradient in the Yucatan Peninsula, Mexico, to characterize bat community diversity. We then detected bat-associated CoVs and studied the association between CoV detection and intrinsic host traits as well as ecological variables. Detected CoVs were subsequently sequenced and phylogenetically characterized. Using publicly available databases and host phylogenetic diversity metrics, we further analyzed the host range of each CoV genotype to identify specialist–generalist patterns and their distribution along the gradient.

Results: Bat diversity was significantly lower in urban sites. Although overall CoV positivity was low (3.2%), we identified eight divergent genotypes, including two novel Alphacoronavirus sequences and the first CoV reported from *Lophostoma brasiliense*. Juvenile bats were more likely to be CoV-positive, a pattern particularly pronounced in *Sturnira parvidens,* but absent in *Artibeus jamaicensis*. We found a specialist-generalist gradient in CoV genotype host range, supported by differences in host phylogenetic distances, suggesting variation in circulation success and cross-species transmission potential. Notably, low-diversity sites harbored CoVs with broader host ranges.

Conclusions: Our findings expand the known diversity of Neotropical bat CoVs and demonstrate that virus–host associations vary across bat host species and anthropogenic land-use gradients. Habitat alteration reduces bat diversity while favoring CoVs genotypes with broader host ranges, potentially increasing the opportunities for cross-species transmission. Maintaining ecological integrity through bat conservation, alongside sustained viral surveillance may help mitigate the risk of future zoonotic emergence.

1562 – “I don't trust them, we vaccinate dogs and they still come to kill them.", culling undermines One Health: a case study amongst animal health officers and communities living with rabies

Tasmin ALEXANDER (1), Kennedy LUSHASI (1,2), Lwitiko SIKANA (1,2), Anna CZUPRYNA (1), Nicholas HANLEY (1), Nai RUI CHNG (1), Sarah CLEAVELAND (1), Katie HAMPSON (1)

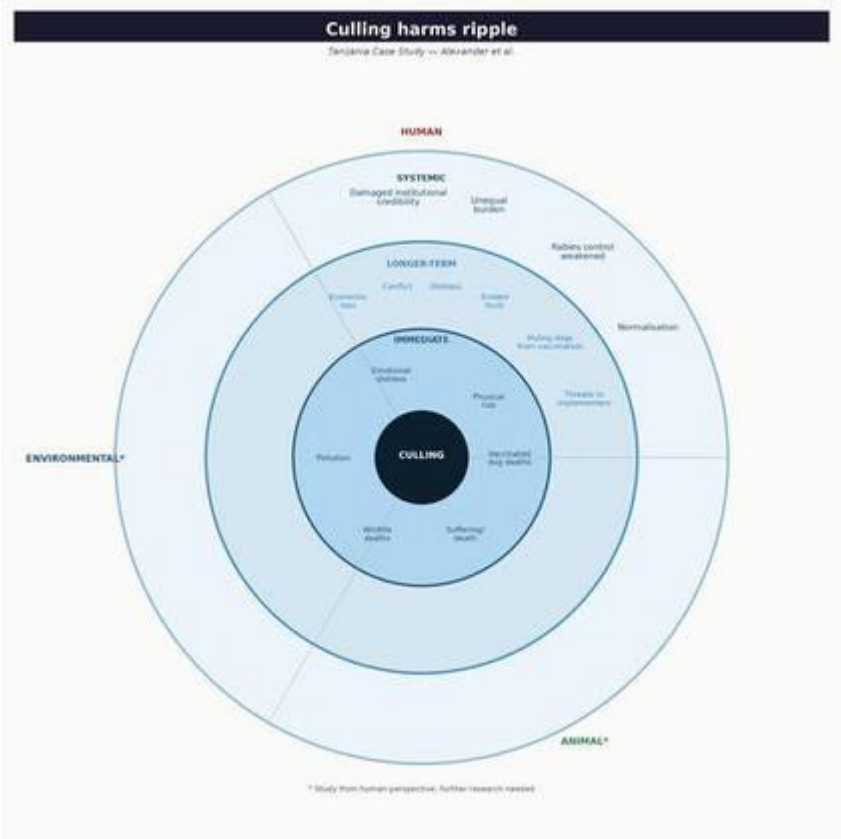
1: School of Biodiversity, One Health & Veterinary Medicine, Univeristy of Glasgow, United Kingdom; 2: Ifakara Health Institute

Background: One Health approaches are recommended for controlling zoonotic diseases, aiming to improve health outcomes across human, animal, and environmental sectors through coordinated action. Rabies**,** a deadly viral zoonosis,is widely regarded as a model for One Health implementation. By vaccinating dogs both animals and the communities that live alongside them are protected. Yet, culling of free-roaming dogs is common in many endemic settings, aiming to control rabies. Harms arising in the context of culling for rabies control remains poorly examined.Here, using Tanzania as a case study, we characterise dog culling practices and examine their potential harms to people, animals and the environment.

Methods: Data were collected across Tanzania, through questionnaires, in-depth interviews and focus group discussions with government-employed animal health officers, community members and a non-governmental animal welfare practitioner. Quantitative data on reported culling procedures were described, and qualitative data were analysed using an interpretive grounded theory approach to identify themes related to harm, governance, and implementation.

Results: Government officers reported shooting and poisoning as methods for culling free roaming dogs and participants described several harms resulting from these practices. Participants across all stakeholder categories described: the unintended killing of livestock and wildlife; prolonged animal suffering following poison ingestion and gunshot injuries, as well as environmental contamination from poison and abandoned carcasses. Additionally, participants reported physical risks to bystanders and implementors, including injuries requiring hospitalisation. Government implementers reported disliking culling dogs and facing hostility from the community but felt unable to refuse due to fear of job insecurity and that they had few other available options for rabies control. Dogs were described by owners as "night watchmen", and their loss was linked to increased theft, sadness and anger. Harms fell disproportionately on poorer households, whose dogs were more likely to be free roaming and therefore culled, and children, who formed close bonds with dogs. Across all groups, stakeholders considered that culling was ineffective for long term rabies control and produced only temporary reductions in dog populations. The culling of owned and vaccinated dogs led some owners to hide dogs during vaccination campaigns, fearing the government planned to kill their dogs. As one community member stated: "I really don't trust them because we vaccinate dogs and you still come to kill them".

Conclusions: Dog culling causes multiple harms affecting human, animal, and environmental health, erodes community trust, and undermines vaccination. These practices, and their associated harms, reflect a broader failure in implementation of effective One Health approaches to rabies, whereby practitioners lack the tools and support to vaccinate at scale, creating conditions in which culling and rabies persists. Achieving rabies control and elimination requires collaborative cross-sectoral investment and action with strong community engagement.



Tables

Table 1. In-depth interview and focus group topics of enquiry and prompts used to investigate culling practices, experiences and perceptions among community members, animal health officers and animal welfare practitioner.

Topics of enquiry	Example follow-up prompts
Culling practices	How, when, where, who is involved; dog selection
Relationships with dogs	Dogs' roles; perceived benefits; challenges; care practices
Culling support/opposition	Why cull; effectiveness; risks; supporters and resistors
Impacts of culling	Social, emotional, economic, physical; impact on rabies
Cultural impacts	Trust in authorities; community cohesion; fears and rumours

Table 2. Example of illustrative quotes representing One Health harms of culling from the perspective of community members, animal health officers and animal welfare practitioner, within culling districts in Tanzania. Edited to ensure fit to word limit, meaning remains.

One Health domain	Illustrative quote
Human harm	
	" child picks it [poison], puts it in his mouth.", community
	" [culling] works left to you. So, you feel pity.", officer
	"vaccinated dogs lack identification, you end up killing them", officer
Animal harm	
	"after poison, dog crawled, dragging… five minutes to die.", community
	"we got dogs in with multiple shot wounds", welfare practitioner
	"killed a goat thinking that it was a dog", officer
Environmental harm	
	"they throw [carcasses] in the rivers, may decompose there.", community
	"Eagle passed by and it was affected [by poison].", officer
	"[officers] never followed up to ensure dead dogs buried", community

1565 – Barriers and Facilitators to Cross-Sector Communication in One Health: An Implementation Science Analysis of Practitioner Perspectives in Canada

B. Amarachi EZEOCHA (1), Sarah J. ROBINSON (1), Julia H. SMITH (8), Claire M. JARDINE (2,3), Anne-Marie NICOL (1), Chelsea G. HIMSWORTH (4,5), Emily NEWHOUSE (4,6), Esther A. PRIETO (7), Kaylee A. BYERS (1,2)

1: Faculty of Health Sciences, Simon Fraser University, Burnaby, British Columbia, Canada; 2: Department of Pathobiology, Ontario Veterinary College, University of Guelph, Ontario, Canada; 3: Ontario node, Canadian Wildlife Health Cooperative, Ontario Veterinary College, University of Guelph, Ontario, Canada; 4: School of Population and Public Health, University of British Columbia, British Columbia, Canada; 5: British Columbia node, Canadian Wildlife Health Cooperative, Animal Health Centre, Abbotsford, British Columbia, Canada; 6: Fraser Health Authority, British Columbia, Canada; 7: Northern Health Authority, British Columbia, Canada; 8: College of Health Sciences, Vin University, Ocean Park, Hanoi, Vietnam

Background: Effective One Health action depends on timely communication across human, animal, and environmental health sectors. However, cross-sector information sharing often occurs through fragmented and under-resourced channels, making it difficult for practitioners to identify, interpret, and act on emerging issues. Despite growing recognition of communication as a key implementation challenge, little research has examined how information actually moves among practitioners in practice or what conditions support effective cross-sectoral information exchange. This study addresses that gap by examining practitioner-defined information needs and the conditions required to support One Health communication.

Objective: This study aimed to examine barriers and facilitators to practitioner-to-practitioner information sharing, how practitioners conceptualize and apply One Health in their work within Canada's decentralized public health system, and how Implementation Science frameworks can be used to analyze and inform improvements in intersectoral communication.

Methods: A qualitative study was conducted using virtual focus groups and semi-structured interviews with over 70 health practitioners, including veterinarians, physicians, nurse practitioners, and environmental health officers, across three health authority regions in Canada: Fraser Health and Northern Health in British Columbia, and Wellington-Dufferin-Guelph Public Health in Ontario. Data were analyzed using thematic analysis informed by Implementation Science frameworks, with the Exploration, Preparation, Implementation, Sustainment (EPIS) framework used to identify barriers and facilitators within and across sectors.

Results: Practitioners described cross-sector communication as fragmented across multiple channels, leading to missed signals and inconsistent distribution of critical information. Heavy workloads, differences in terminology, and uneven access to sector-specific information further complicate how signals are interpreted and shared across sectors. Without clear or consistent communication pathways across sectors, practitioners often rely on informal professional relationships to clarify information and coordinate responses, making information flow vulnerable when roles change or key individuals are unavailable. Participants also identified conditions that improve communication, including trusted cross-sector relationships, clear points of contact, shared information resources, and communities of practice.

Conclusion: Understanding how cross-sector communication works is essential for strengthening One Health implementation. Using Implementation Science frameworks to analyze these systems can help identify context-specific solutions and support more realistic planning for sustainable One Health coordination. This study provides one of the first Implementation Science based analyses of cross-sector regional One Health communication in Canada.

1583 – Nature-based solutions with potential co-benefits for antimicrobial resistance and the triple planetary crisis: a scoping review

Gloria RUKOMEZA (1), Zoe BERMAN (4), Hai Tuan HOANG NGO (2), Tea SKRINJARIC (3), Pablo IMBACH (3), **Sonia LEWYCKA** (1,2)

1: University of Oxford, United Kingdom; 2: Oxford University Clinical Research Unit, Vietnam; 3: CATIE - Tropical Agricultural Research and Higher Education Centre, Costa Rica; 4: Princeton University, United States

BackgroundAntimicrobial resistance (AMR) and the triple planetary crisis of climate change, pollution, and biodiversity loss are interconnected global challenges shaped by overlapping environmental, agricultural, and health-system pressures. Nature-based solutions (NbS), broadly defined as actions that protect, restore, sustainably manage, or emulate natural ecosystems and processes, are increasingly recognised for their potential to generate cross-sectoral co-benefits for both environmental and human health. However, evidence on how NbS may simultaneously contribute to AMR mitigation and planetary health remains fragmented across disciplines. This scoping review aims to map the global evidence on NbS with potential co-benefits for AMR and one or more dimensions of the triple planetary crisis, and to categorise the intervention types, implementation areas, and reported co-benefits, considering the One Health framework.

MethodsThe review follows Joanna Briggs Institute scoping review methodology and is reported in line with the PRISMA extension for scoping reviews. A comprehensive search strategy was developed and applied across multiple databases, including Ovid MEDLINE, Embase, CAB Abstracts, Global Health, Scopus, and Web of Science Core Collection. Eligible peer reviewed papers included papers describing nature-based or nature-inspired interventions relevant to both AMR and at least one pillar of the triple planetary crisis. Two reviewers independently screened records and extracted data using a standardised form. Data charting focused on intervention type, implementation context, reported co-benefits, barriers, and recommendations.

ResultsPreliminary mapping suggests that the literature spans a diverse range of Nature-based and nature-inspired interventions implemented across water, wastewater, agricultural, aquaculture, and soil-related systems. Early screening indicates that relevant solutions include ecosystem-based interventions, such as constructed wetlands and biochar-based systems, and modified nature-inspired practices, including biologically derived treatment and remediation approaches. Reported co-benefits include AMR-relevant outcomes such as antibiotic removal, reduction or inactivation of resistant or pathogenic microorganisms, and decreased environmental antimicrobial pressures, alongside triple planetary crisis-related benefits including pollution reduction, wastewater or waste reuse, ecosystem restoration or management, and climate-relevant gains such as nutrient cycling, carbon-related benefits, or other environmental improvements. Preliminary screening also shows important variation in how NbS are defined and adapted for each specific intervention, reinforcing the need for broad but transparent considerations when examining environmental pathways linking AMR and planetary health.

ConclusionsThis review provides an emerging overview of how NbS may support integrated responses to AMR and the triple planetary crisis. By identifying NbS intervention types, their implementation settings, and their potential co-benefits, it contributes evidence to support more joined-up One Health research, policy, and practice at the environment–health interface.

1590 – Leveraging the Competencies for One Health Field Epidemiology (COHFE) framework to strengthen multisectoral biosecurity capacities: results from prioritization workshops in Nigeria and Bangladesh

Stacie DUNKLE (1), Oladipo OGUNBODE (2), TABM Muzaffar OSMANI (3), Hana ABDELSATTAR (4), Hasan Mohiuddin AHMED (3), Ravi DISSANAYAKE (5), Anthony ESHOFONIE (3), Irene ISIBOR (3), Mushtofa KAMAL (6), Tahmina KARIM (7), Daniel Damilola KOLADE (2), Immamul MUNTASIR (8), Shakila NARGIS (9), Oyeladun OKUNROMADE (2), Md. Omar QAYUM (8), Md. Sohel RANA (8), Tahmina SHIRIN (8), Barbara ALESSANDRINI (4), Julio PINTO (5), Catherine SMALLWOOD (1)

1: World Health Organization, Health Emergency, Preparedness and Response Division; 2: Nigeria Centre for Disease Control and Prevention; 3: World Health Organization, Bangladesh; 4: World Organisation for Animal Health; 5: Food and Agriculture Organization of the United Nations; 6: World Health Organization, South East Asia Regional Office; 7: Bangladesh Department of Livestock Services; 8: Institute of Epidemiology, Disease Control and Research, Bangladesh Ministry of Health; 9: Bangladesh Forestry Department

Background

Effective biosecurity requires coordination across the public health, animal health, and environment sectors to prevent, detect, and respond to biological threats. However, countries often struggle to operationalize multisectoral biosecurity objectives within existing workforce development and capacity building mechanisms. The Competencies for One Health Field Epidemiology (COHFE) framework was developed by FAO, WHO and WOAH in support of the Quadripartite Joint Plan of Action on One Health and

provides a shared reference for building multisectoral field epidemiology capacities. The framework offers a structured approach to defining, prioritizing, and strengthening the knowledge, skills, and competencies (KSC) needed by field epidemiologists working across sectors. This assessment examines how multisectoral prioritization of COHFE KSC supports context-specific alignment and collaboration to address One Health biosecurity threats.

Methods

Two multisectoral workshops were conducted to develop national level, customized field epidemiology competency frameworks using the COHFE framework. In February 2024, in Abuja, Nigeria, participants representing the public health, animal health, and environment sectors ranked the optional One Health KSC for the frontline training level using pairwise comparison. In November 2025, in Dhaka, Bangladesh, participants from the three One Health sectors used simple ranking to prioritize optional One Health and sector-specific KSC for the advanced training level. In the Dhaka workshop, participants had the option to eliminate KSC that they deemed non-essential. At both workshops, participants worked in multisectoral groups to enable cross sector discussion during the ranking process. Results were reviewed and debated in plenary sessions following the prioritization exercise.

Results

In Nigeria, participants produced a ranked list of optional One Health KSC for frontline training. The group agreed not to set universal cut-off criteria for inclusion or exclusion; instead, they evaluated each domain individually and selected the most highly ranked and feasible KSC, ensuring that all core One Health KSC were already included in the curricula. In Bangladesh, the option to eliminate KSC created clearer thresholds for inclusion. Following the workshop, a multisectoral working group reviewed the preliminary results and refined them before finalizing the customized framework. In both settings, participants emphasized that a coordinated training approach strengthens the capacity of individual sectors while also improving multisectoral collaboration during health emergencies.

Conclusions

The COHFE framework provides a standard yet flexible, competency-based approach for One Health field epidemiology training. Systematic prioritization of KSC in multisectoral workshops promotes a shared understanding of cross sectoral priorities and helps identify opportunities for collaboration and synergy. Countries can use these customized frameworks to assess existing training curricula or to design new multisectoral One Health programs. By fostering alignment across public health, animal health, and the environment sectors, the COHFE framework helps build integrated capacities essential for safeguarding global health security.

1592 – Knowledge, Attitudes, and Practices Regarding Rabies and Free-Roaming Dogs Among Schoolchildren in Urban Guwahati, Assam, India

Parimala MOHANTY (1), Bikash KHURA (2), Dilwar HUSSAIN (3), Achyut PATHAK (4), Satwik CHALASANI (4), Geetika KUJUR (4), Ganesh DAIMARY (4), Salome DÜRR (1), Harish Kumar TIWARI (3,4,5)

1: Veterinary Public Health Institute, University of Bern; 2: International Institute for Population Sciences, Mumbai 400088, India; 3: Jyoti and Bhupat Mehta School of Health Science and Technology, Indian Institute of Technology Guwahati, Guwahati, Assam, India; 4: JH CreIndia Foundation, Bhetapara, Guwahati, Assam, India; 5: DBT-Wellcome Trust India Alliance Intermediate Fellow, Hyderabad, Telangana, India

Abstract

Background: Rabies is a major public health concern in India, particularly in urban settings with high densities of free-roaming dogs (FRDs). Schoolchildren are among the most vulnerable to dog bites, yet data regarding their knowledge, attitudes, and practices (KAP) on rabies are limited. Understanding these factors is crucial for designing effective prevention and education strategies.

Methods: A cross-sectional, school-based survey was conducted in 2024 among 1,028 students in grades VI-IX across 11 schools (nine public, two private) in Guwahati, Assam. A structured, self-administered questionnaire in the local language was used to assess KAP related to rabies and FRD. Composite scores for knowledge, attitudes, and practices were dichotomised at the median, and multivariable logistic regression identified factors associated with positive KAP outcomes.

Results: Most students, 66% (n=678), reported prior awareness of rabies, but detailed knowledge was variable. While 56% (n = 576) identified animal bites as a primary transmission route, fewer were aware of risks from licks, scratches, or saliva. Knowledge regarding prevention was higher: 68% (n = 699) recognised the importance of prompt post-bite vaccination, and 80% (n = 822) understood the need to complete the full vaccination course. Awareness of FRDs and rabies vaccination for dogs was moderate (52% (n = 535) and 62% (n = 637), respectively). Positive attitudes were reported by 39% (n = 401) of students and were strongly influenced by personal exposure; students with pets at home were more likely to exhibit favourable attitudes (OR = 1.5, 95% CI: 1.1-2.0, p = 0.008). Appropriate practices were demonstrated by 45% (n = 463) of participants. Factors associated with better practices included private school attendance (OR = 0.4, 95% CI: 0.3-0.6, p 0.001), higher class levels (Class VIII: OR = 1.6, Class IX: OR = 2.1), female gender (OR = 0.5, 95% CI: 0.3-0.6), Hindu religion (OR = 1.6, 95% CI: 1.0-2.5), and absence of prior dog-bite experience (OR = 0.6, 95% CI: 0.4-0.9).

Conclusion: While general awareness of rabies exists among urban schoolchildren, significant gaps remain in detailed knowledge and preventive practices. Attitudes and practices are shaped more by personal experience and pet ownership than by socio-demographic factors alone. Targeted school-based educational interventions, particularly in public schools and lower grades, are needed to improve understanding of rabies transmission, appropriate post-bite care, and safe interactions with FRDs, thereby supporting rabies prevention in urban communities.

Table 1. Summary of Key Results on Knowledge, Attitudes, and Practices Regarding Rabies and Free-Roaming Dogs Among Schoolchildren in Guwahati, Assam, India (N = 1,028)

Domain	Indicator	Findings
Knowledge	Heard of rabies	66% (n = 678)
	Recognized animal bites as primary transmission route	56% (n = 576)
	Recognized importance of prompt post-bite vaccination	68% (n = 699)
	Aware that full vaccination course must be completed	80% (n = 822)
	Correctly identified free-roaming dogs (FRDs)	52% (n = 535)
	Aware that dogs can be vaccinated against rabies	62% (n = 637)
Attitudes	Students demonstrating positive attitudes toward dogs and rabies prevention	39% (n = 401)
	Pet ownership associated with positive attitudes	OR = 1.5, 95% CI: 1.1-2.0, p = 0.008
Practices	Students demonstrating appropriate practices when encountering FRDs or responding to dog bites	45% (n = 463)
	Private school attendance	OR = 0.4, 95% CI: 0.3-0.6, p < 0.001
	Higher grade level	Class VIII: OR = 1.6; Class IX: OR = 2.1
	Female gender	OR = 0.5, 95% CI: 0.3-0.6
	Hindu religion	OR = 1.6, 95% CI: 1.0-2.5
	No prior dog-bite experience	OR = 0.6, 95% CI: 0.4-0.9

1598 – Application of Systems mapping as a tool to unpack the socio-ecological drivers of Rabies in Geita District, Tanzania

Janeth George LAUREAN (1), Mourice MBUNDE (2), Loveness KIMARO (2), Given Sam SAM (2), Mkunde CHACHAGE (3,4), Gilbert FOKOU (5), Bassirou BONFOH (5), Nicolas ANTOINE-MOUSSIAUX (6), Japhet KILLEWO (2)

1: The Open University of Tanzania, Tanzania; 2: Muhimbili University of Health and Allied Sciences, Dar es salaam, Tanzania.; 3: University of Dar es Salaam - Mbeya College of Health and Allied Sciences, Mbeya, Tanzania; 4: National Institute for Medical Research-Mbeya Medical Research Centre, Mbeya, Tanzania; 5: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, Cote d'Ivoire; 6: University of Liège, Liège, Belgium

Background: Rabies is a viral disease and a significant public health threat, often underreported in tropical regions. Despite past vaccination campaigns, Geita district in Tanzania still faces ongoing rabies transmission and cases. Therefore, the study was conducted to implement an adapted tool for identifying the main factors influencing the increase in rabies transmission and to assess pathways to interventions in the Geita district, Tanzania.

Methods: The study adopted a group model-building, a participatory approach, to map the socio-economic and ecological drivers of rabies transmission.A one-day workshop was held with 20 subnational-level participants from human health, animal health, environment, community development, community leaders and community members in Geita district. Following the Group Model Building methodology, we created a Causal Loop Diagram as a first step to system dynamic model of rabies transmission. We analysed trends with a behaviour-over-time graph, developed a causal loop map, and identified intervention points.

Results: The causal loop diagram identified 25 variables influencing rabies transmission, categorised into economic (7), ecological (2), social (7), and political (9). There were 18 direct contributing factors, six underlying factors, and 67 connections. Free-roaming dogs were identified as the primary driver of rabies, with increases in their population leading to more dog bites. Economic factors, such as agricultural activities and high vaccine cost, exhibited a positive influence on disease spread, while knowledge and awareness, responsible dog management, and improved household income showed an inverse relationship. In Geita, shrubs provided habitat for carnivores such as hyenas and foxes which may come in contact with roaming dogs. Furthermore, population growth and land-use changes have turned displaced wildlife habitat into residential areas. Political leaders and law enforcement have been found to have a positive impact on reducing the spread of rabies. From the mapping, the potential interventions which were highly ranked were community-centred awareness campaigns, enhancing vaccine supply and access and engagement of the community and reverend leaders in behavioural change campaigns

Conclusion: The dynamics of rabies transmission are shaped by various interconnected factors. The results also show that social, economic, and political drivers can play a more significant role in the spread of rabies than ecological factors. Systems mapping, which is founded on transdisciplinarity and meaningful participation, is a useful tool for visualising these connections, interactions and feedback loops, helping to identify key intervention points. Therefore, the study highlights the importance of adopting a systems thinking approach to strengthen effective One Health operationalisation.

1604 – Operationalising gender and equity in One Health AMR surveillance, policy, and practice: lessons from GEAR up consortium

Syeda Tahmina AHMED (1), Ralalicia LIMATO (2), Anne NGUNJIRI (3), Abriti ARYAL (4), Sammy GACHIGUA (3), Webster MAVHU (5), Mavis Pearl KWABLA (6), Kate HAWKINS (7), Katy DAVIS (2), Rosie STEEGE (2)

1: BRAC James P Grant School of Public Health, BRAC University, Bangladesh; 2: Liverpool School of Tropical Medicine, UK; 3: LVCT Health Kenya; 4: HERD international Nepal; 5: Centre for Sexual Health and HIV/AIDS Research, Zimbabwe; 6: University of Health and Allied Sciences, Ghana; 7: Pamoja Communications, UK

Antimicrobial resistance (AMR) is not gender neutral. Beyond biological differences and risk factors, gender and intersecting social inequities shape exposure to infection, patterns of antimicrobial use, and access to healthcare, diagnostics, and treatment. These aspects are important in a One Health context, where human, animal, and environmental health systems interact. Yet gender and equity considerations

remain largely absent from national AMR planning and are rarely integrated into routine surveillance systems.

WHO guidance on addressing gender inequalities in AMR national action plans (NAPs) calls for gender-responsive and equity-informed approaches in development, revision, implementation, and monitoring. Recommended actions include collecting and reporting sex, age, and other disaggregated surveillance data; analysing gender-related inequalities; strengthening health worker capacity; reviewing diagnostic and prescribing practices for bias; and assessing whether AMR policies may unintentionally restrict equitable access to essential antimicrobials.

Through 'Gender and Equity in Antimicrobial Resistance' (GEAR up), a grant from the Fleming Fund, we demonstrate how inequities can be identified and addressed in real-world settings. We showcase grounded examples from the GEAR up consortium, sharing global work to take forward gender and equity approaches including:

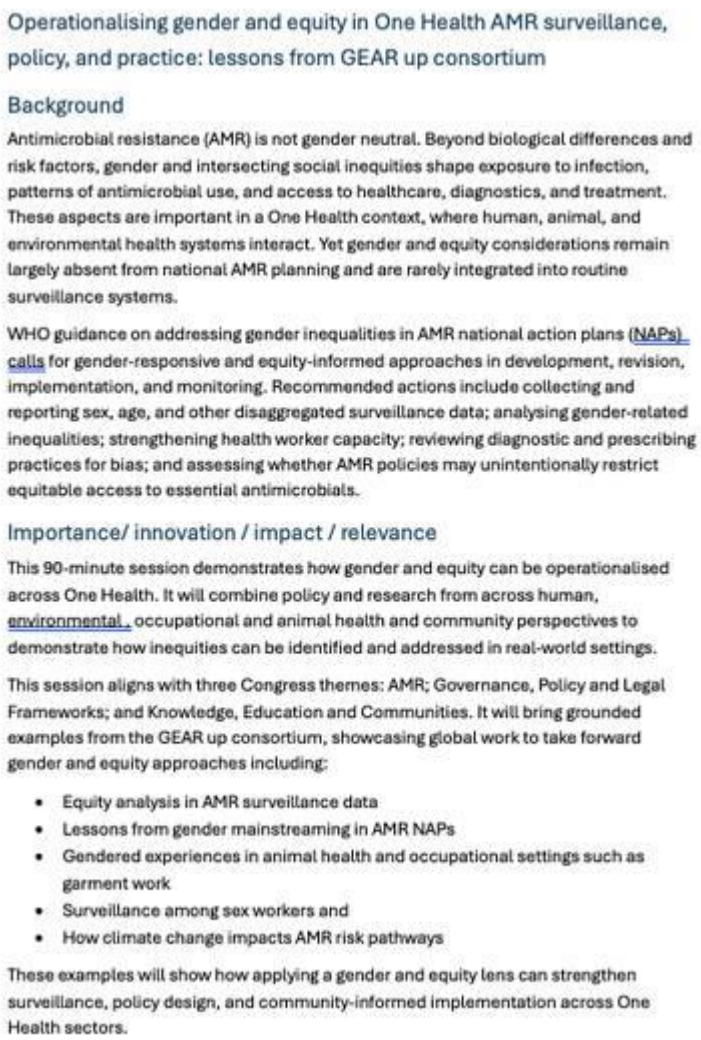
· Equity analysis in AMR surveillance data and inclusion of vulnerable groups in surveillance structures

· Gender mainstreaming in AMR NAPs and policy documents

· Participatory research into the gendered experiences and AMR pathways in animal health and occupational settings

· Creative communications on gender and equity in AMR

These examples will show how applying a gender and equity lens can strengthen surveillance, policy design, and community-informed implementation across One Health sectors.



Operationalising gender and equity in One Health AMR surveillance, policy, and practice: lessons from GEAR up consortium

Background

Antimicrobial resistance (AMR) is not gender neutral. Beyond biological differences and risk factors, gender and intersecting social inequities shape exposure to infection, patterns of antimicrobial use, and access to healthcare, diagnostics, and treatment. These aspects are important in a One Health context, where human, animal, and environmental health systems interact. Yet gender and equity considerations remain largely absent from national AMR planning and are rarely integrated into routine surveillance systems.

WHO guidance on addressing gender inequalities in AMR national action plans (NAPs) calls for gender-responsive and equity-informed approaches in development, revision, implementation, and monitoring. Recommended actions include collecting and reporting sex, age, and other disaggregated surveillance data; analysing gender-related inequalities; strengthening health worker capacity; reviewing diagnostic and prescribing practices for bias; and assessing whether AMR policies may unintentionally restrict equitable access to essential antimicrobials.

Importance/ innovation / impact / relevance

This 90-minute session demonstrates how gender and equity can be operationalised across One Health. It will combine policy and research from across human, environmental , occupational and animal health and community perspectives to demonstrate how inequities can be identified and addressed in real-world settings.

This session aligns with three Congress themes: AMR; Governance, Policy and Legal Frameworks; and Knowledge, Education and Communities. It will bring grounded examples from the GEAR up consortium, showcasing global work to take forward gender and equity approaches including:

- Equity analysis in AMR surveillance data
- Lessons from gender mainstreaming in AMR NAPs
- Gendered experiences in animal health and occupational settings such as garment work
- Surveillance among sex workers and
- How climate change impacts AMR risk pathways

These examples will show how applying a gender and equity lens can strengthen surveillance, policy design, and community-informed implementation across One Health sectors.

Educational outcome

Participants will obtain or gain:

- Understanding of how to apply equity analysis in surveillance, including how sex, age, occupation, and other social stratifiers can be used to identify inequities and inform action
- Insight into how gender and equity can be mainstreamed through AMR NAPs and implementation processes, drawing on country learning and policy experience
- Concrete examples of applying a gender and equity lens in research across One Health, including human, animal, occupational, and environmental health settings

Keywords

AMR; One Health; gender; equity; surveillance; national action plans; occupational health; environmental health; community engagement; animal health; art-based communication

Proposed chairs, speakers, and titles

Each participant will give a-5 minute lightning talk, followed by time for questions and discussion after the human health presentations, and again after the animal and environmental health presentations, with synthesis at the end.

	Name, institution	Presentation title
Chair, discussion facilitator	Rosie Steege *Liverpool School of Tropical Medicine (LSTM)*	
	UHAS	
Speaker	Anne Ngunjiri *LVCT Health*	Gender mainstreaming through AMR NAPs: learning from Uganda
	Abriti Arival *HERD International*	Understanding gender and equity dimensions in the One Health policy environment in Nepal
Ralalicia Limato, Independent/ LSTM?	Ralalicia Limato *LSTM*	How to do an equity analysis of AMR surveillance data?
	Mavis Pearl Kwabla *UHAS*	Examining equity gaps in AMR surveillance data in Ghana
	Webster Mavhu *CeSHHAR*	Neisseria gonorrhoea surveillance among sex workers in Zimbabwe
Webster Mavhu, CeSHHAR	Tahmina Ahmed *BRAC James P Grant School of Public Health*	Exploring occupational AMR risk factors: garment workers in Bangladesh
Tahmina Ahmed, BRAC James P Grant School of Public Health	Katy Davis *World Organisation for Animal Health (WOAH), LSTM*	Equity and AMR in animal health: gaps and opportunities
Sammy Gachigua, LVCT Health	Sammy Gachigua *LVCT Health*	Environmental transmission of AMR: photovoice in Kenya
Clarissa Magdalena, LSTM	Clarissa Magdalena *LSTM*	Diaper waste in Naivasha, Kenya: community-identified environmental risk factors amid climate change

1618 – Integrating environmental surveillance and bird movement to understand avian influenza dynamics in wetlands of central Chile

Soledad RUIZ (1,2), Erik SANDVIG (2,5), Pablo GALDAMES (3), Cristobal OYARZUN (4), Natalia GUZMAN (4), Franco VILLALOBOS (5), Pedro JIMENEZ-BLUHM (4)

1: Escuela de Medicina Veterinaria, Facultad de Recursos Naturales y Medicina Veterinaria, Universidad Santo Tomás, Chile; 2: Centro Bahía Lomas, Facultad de Ciencias, Universidad Santo Tomás, Chile.; 3: Departamento de Medicina Preventiva Animal, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Chile; 4: Escuela de Medicina Veterinaria, Facultad de Ciencias Biológicas, Facultad de Medicina, Facultad de Agronomía e Ingeniería forestal, Pontificia Universidad Católica de Chile, Santiago, Chile; 5: Red de Observadores de Aves y Vida Silvestre de Chile (ROC), Chile

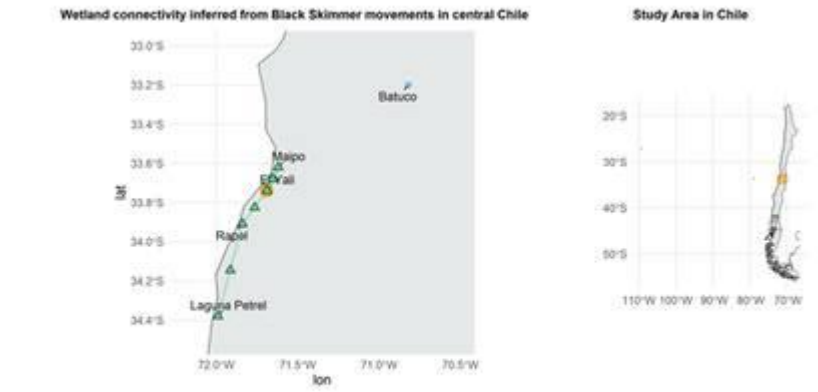
BackgroundWetlands represent key ecological interfaces where wildlife, environmental reservoirs, and pathogens interact. Avian influenza viruses (AIV) circulate naturally in wild waterbirds, particularly in aquatic ecosystems where environmental persistence may facilitate indirect transmission. However, the ecological processes that influence viral circulation and dispersal across wetland networks remain poorly understood in South America. Previous surveillance conducted in Chile has identified the Black Skimmer (*Rynchops niger*) and the Yellow-billed Teal (*Anas flavirostris*) as important AIV reservoirs. Both species perform regional movements within South America, suggesting a potential role in regional viral dissemination. Despite this, the relationship between bird movement, wetland connectivity, and AIV circulation has not been formally evaluated. This question has become particularly relevant in the context of the ongoing regional spread of Highly Pathogenic Avian Influenza H5N1. The aim of this study is to integrate environmental surveillance with GPS-based movement data to detect avian influenza virus circulation in wetland environments and evaluate whether movements of key reservoir species may create ecological connectivity between wetlands that could facilitate viral dispersal.

MethodsThe study is being conducted in two wetlands in central Chile: Río Maipo Wetland and Batuco Wetland. Monitoring began in November 2025 and will continue for three years. During each field visit, fresh environmental fecal samples from wild birds are collected for AIV detection using real-time RT-PCR, and positive samples are subjected to genomic sequencing. In parallel, GPS tracking devices were deployed on Black Skimmers to characterize movement patterns, habitat use, and connectivity among wetlands. Movement analyses include quantification of inter-wetland connectivity, stopover duration, spatial overlap with other bird assemblages, and patterns of habitat use across coastal and inland ecosystems. Future deployments are planned for Yellow-billed Teals to further assess ecological connectivity.

Results Between November 2025 and March 2026, a total of 849 environmental fecal samples were collected, of which 45 tested positive for AIV RNA (overall prevalence: 5.3%; 95% CI: 3.8–6.8), confirming active viral circulation in both wetlands. Sequencing analyses of positive samples are currently underway. Preliminary GPS tracking data indicates frequent movements of Black Skimmers between coastal wetlands, suggesting ecological connectivity across wetland networks that could facilitate pathogen dispersal.

Conclusions

Integrating environmental surveillance with movement ecology provides a framework to identify potential pathways of AIV circulation among wetlands. In the context of the ongoing spread of Highly Pathogenic Avian Influenza H5N1 in South America, understanding connectivity among wild bird populations is critical for improving early detection and strengthening surveillance strategies at the wildlife–environment interface within a One Health framework.



Wetland connectivity and potential movement pathways of Black Skimmers in central Chile. El Yali is highlighted due to the ongoing HPAI H5N1 outbreak.

1628 – Characterization of bush meat and its associated infectious agents via eDNA across a socio-environmental gradient in Ivory Coast and Liberia

Nea Yves NOMA (1,2), Gbohonou Fabrice GNALY (3), Hjalmar KUEL (2), Bi Sery Ernest GONEDELE (5), Jan Frederick GOGARTEN (2), Ivo STEIMANIS (6), Fabian LEENDERTZ (1), Sébastien Calvignac SPENCER (4), Lorenzo LAGOSTINA (1)

1: Helmholtz Institute for One Health, Germany; 2: Senckenberg Institute Muessum for nature Gorlitz, German; 3: Ecole Inter-Ecoles des Sciences Veteriniare Dakar, Senegal; 4: Department of Pathogen Evolution Helmholtz Institute for One Health, Germany; 5: Université Felix Houphouet Boigny /Cote d'Ivoire; 6: University of Marbug

Background

Bushmeat is an important source of animal protein for millions of people across developing countries in most tropical regions. Its consumption is an ancient tradition in West Africa, where it is eaten as a protein source in both rural and urban areas. Despite the availability of other sources of protein in most cities of West Africa, bushmeat continues to be valued due to a number of cultural factors. Unfortunately, bushmeat consumption raises two major concerns: biodiversity loss and the potential for pathogen transmission. Hunting wildlife depletes populations and disrupts ecosystems and creates potential exposure to a broad range of pathogens. Our study aimed to investigate which species are consumed in different socio-ecological niches — from rural habitats and agroforestry landscapes to urban areas in Côte d'Ivoire and Liberia (Figure 1) — and will aim to characterize pathogens associated with this bushmeat in subsequent stages of the project.

Methods

In both regions, bushmeat is consumed in households, but also frequently in restaurants called "maquis" in Ivory Coast and "koboshop" in Liberia. A first field mission in Ivory Coast was performed in 2024, where 109 restaurants were sampled (42 villages, 5 towns, 4 cities). A second field mission in Liberia was conducted in 2025, where 84 restaurants were sampled (32 villages, 12 towns, 3 cities). Samples were collected by swabbing utensils (machetes, knives, cutting boards, kitchen containers), surfaces (table tops, door handles and surfaces, window sills, and refrigerators) and rubbish bins. DNA was extracted and vertebrate metabarcoding was performed on a pool of extracts representing different surfaces from individual restaurants. In addition to the swab samples, bushmeat was directly sampled when the restaurants owners agreed (without compensation); this included swab (oral and rectal) and different organs. Both animal and environmental extracts will be tested for pathogens using PCRs targeting *orthopoxviruses*, *filoviruses* and B*cbva* (sylvatic anthrax), as well as RNA-seq.

Results

We detected an impressive number of wild taxa in the 106 restaurant swab samples from the Ivory Coast that we have already processed, including several species relevant for zoonotic diseases, including giant pouched rat (*Crycetomys emini*) and straw-colored fruit bat (*Eidolon helvum*). So far, of the 82 animals

tested for orthopoxviruses, filoviruses and *Bcbva* were all negative, butpathogen screening work is currently ongoing.

Conclusions

Preliminary results from the metabarcoding of swabbing of restaurant's surfaces in Ivory Coast indicate how eDNA tools can be used to study the consumption of wildlife, including of endangered taxa and taxa that frequently harbor pathogens with a zoonotic potential. This dataset will help to understand where animals are sourced, and if there are significant differences in species consumed in cities, town, and villages.

1647 – Bat-origin coronaviruses continue to represent a substantial emerging disease threat to people & livestock

Peter DASZAK (1), Aleksei CHMURA (1), Anna DURRANCE-BAGALE (1,2), Hume FIELD (1), Nichar GREGORY (1), Tom HUGHES (1,3), Anne LAUDISOIT (1,4), David MORENS (1), Alessandra NAVA (1,5), Paula PRIST (1,6), Jamie REASER (1,7), Gerardo SUZÁN (1,8), Carlos ZAMBRANA-TORRELIO (1)

1: Nature Health Global, Tallman, NY 10982, USA; 2: London School of Hygiene & Tropical Medicine, UK; 3: Conservation Medicine, Malaysia; 4: University of Antwerp, Belgium; 5: Fiocruz Amazônia, Manaus, Amazonas, Brazil; 6: IUCN, Washington DC, USA; 7: Rain Crow Consulting, USA; 8: Universidad Nacional Autónoma de México, Mexico City, Mexico

Background: In the aftermath of the emergence of COVID-19, and in some cases an erosion of national and global preparedness for the next pandemic, it is timely to assess whether bat-origin coronaviruses continue to represent a threat for future emerging diseases.

Methods: This research brings together analyses and case studies from a series of largescale field and lab research programs (PREDICT, NIH CREID and others), including wildlife and human serological and PCR surveillance, spatial analyses of risk, and viral characterization.

Results: We show that 1) there is a high diversity of bat-CoVs present in emerging disease hotspots where these have been sampled; 2) when further characterized, some of these CoVs appear to represent a clear and present risk of human exposure; 3) there is substantial evidence of active spillover pathways from wildlife to people that remain high risk; and 4) where tested, there is evidence of frontline communities being infected by bat-CoVs and other bat viruses. Additionally, the complex interactions among bats, livestock and people represents a threat of CoV spillover to livestock and subsequent amplification to people. Despite these risks, there is a lack of substantial global coordination in dealing with the underlying drivers of zoonotic CoV emergence, including the wildlife trade, land use change/deforestation, and agricultural intensification.

Conclusions: Despite the loss of pandemic preparedness in many countries, the risk of continued CoV spillover from wildlife to livestock and people remains high and is likely rising concomitant with increasing anthropogenic pressure on our planet. We propose an increased focus on working with communities, industries and governmental agencies on the frontline of EID risk, to understand the incentives behind EID drivers, and to develop workable solutions that support economic and cultural

activities, reduce risk of spillover, and preserve biodiversity. These challenges should remain a key focus for One Health globally, in the era of pandemics.

1664 – Early immunomodulatory effects of Trypanosoma cruzi-derived components on canine immune cells

Juliana Inês WEBER (1), Cláudia MORENO (1), Micheli FERLA (1), Marta MONTEIRO (2,3), Vânia VIEIRA (1), Joana PALMA-MARQUES (1), Telmo NUNES (4), Wilson ANTUNES (5), Rui FERREIRA (6), Inês CARDOSO (6), Graça ALEXANDRE-PIRES (2,3), Isabel PEREIRA DA FONSECA (2,3), Armanda RODRIGUES (1), Gabriela SANTOS-GOMES (1)

1: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisboa, Portugal; 2: Centre for Interdisciplinary Research in Animal Health, CIISA, Faculty of Veterinary Medicine, FMV, University of Lisbon; 3: Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Portugal; 4: Microscopy Center, Faculty of Sciences, Campo Grande, 1749-016 Lisboa, Portugal; 5: Instituto Universitário Militar (IUM), Centro de Investigação, Desenvolvimento e Inovação; 6: Banco de Sangue Animal, Porto, Portugal

Background: Chagas disease, caused by the parasite *Trypanosoma cruzi*, is a vector-borne zoonosis of major concern within the One Health framework, as it involves complex interactions among humans, domestic animals, and insect vectors. Dogs play a significant role in the domestic transmission cycle, acting as reservoirs that contribute to parasite persistence and increase the risk of human exposure. Given the absence of effective vaccines or specific treatments for canine infection, a better understanding of host–parasite interactions in dogs is essential to improve integrated disease control strategies. Therefore, studying canine infection is particularly relevant from a One Health perspective, as control interventions targeting animal reservoirs can contribute to reducing transmission at the human–animal–environment interface.

Methods: This study investigated the early immunomodulatory effects of *T. cruzi* components on canine immune cells using an *in vitro* co-culture from peripheral blood of healthy dogs. Peripheral blood mononuclear cells (PBMCs) were differentiated into monocyte-derived macrophages (MDM). MDM were exposed to epimastigotes, parasite antigens (Ag), or *T. cruzi*-derived extracellular vesicles (EVs) during 4h, 24h and 48h. Then, MDM were incubated with lymphocytes during 72h establishing the co-culture. The expression of cell markers to identify cell subpopulations, was analyzed by multiparametric flow cytometry using fluorochrome-conjugated specific antibodies. Gene expression of innate receptors (TLRs) and of cytokines was assessed by semi-quantitative real-time PCR. Scanning Electron Microscopy was applied to capture cellular interactions and morphological changes.

Results: Flow cytometry analysis revealed that stimulation with Ag and EVs induced significant upregulation of MHCI+ cells and modulation of CD3+CD8⁺ lymphocytes after 24h, suggesting activation of cytotoxic immune responses. On the other hand, exposure to parasites was found to expand MHCII+ cells and CD3+CD4+CD25-FoxP3- lymphocyte subset, although these changes were not statistically significant. Gene expression analysis by qPCR further demonstrated that EVs and Ag significantly increased the transcription of innate immune receptors and of pro-inflammatory mediators, including TLR2, NOD1, IL-12, and TNF-α. In addition, scanning electron microscopy showed pronounced morphological alterations in macrophages following exposure to parasites and EVs, consistent with cellular activation and interaction with parasite-derived components.

Conclusions: The *in vitro* co-cultured cell model used in this study allowed for the analysis of the immune response the dog.Overall, these findings provide new insights into the early immune responses triggered by *T. cruzi* in canine cells and highlight potential mechanisms through which parasite-derived molecules modulate host immunity. Understanding these processes in a key reservoir host contributes to the broader comprehension of Chagas disease transmission dynamics and supports the development of integrated control strategies aligned with the One Health approach.

Funding: This work was supported by FCT: 2023.17706.ICDT, GHTM-UID/04413/2025, LA-REAL-LA/P/0117/2020, CIISA-UIDB/00276/2025, and AL4AnimalS-LA/P/0059/2020. Rodrigues A (2022.00499.CEECIND/CP1725/CT0023). PhD studentships: Weber JI (2022.13899.BD), Monteiro M (UI/BD/152819/2022), and Palma-Marques J (2021.05579.BD).

1668 – Genomic Characterisation of Antimicrobial Resistance Across Enterobacterales From Livestock, Wildlife, Food, and Environmental Interfaces of an Integrated Pig–Arable Farm

Stacey DUVENAGE, **Hayley THOMPSON**
NRI, University of Greenwich, United Kingdom

Background

Integrated livestock–crop production systems create interconnected ecological pathways that facilitate the movement of antimicrobial resistance (AMR) between livestock, wildlife, food products, and environmental reservoirs. Understanding how AMR genes disseminate across these interfaces is essential for developing ecosystem-centred surveillance within One Health frameworks.

Methods

Enterobacterales were sampled across multiple compartments of an integrated pig–arable farm, including reservoir and brook water, manure, soil, pig feed, pig faeces, rat faeces, and pork sausage. Phenotypic antimicrobial susceptibility testing was performed, and hybrid whole-genome sequencing (Illumina + Nanopore) was used to characterise antimicrobial resistance genes (ARGs), plasmid content, and phylogenetic relatedness of *Escherichia coli*, *Proteus* spp., and *Serratia fonticola* isolates.

Results

Ten *E. coli* isolates displayed substantial genomic heterogeneity. Core genome phylogeny identified four closely related strains spanning water, manure, and pork sausage, suggesting inter-compartment transmission. ARG profiles varied widely: some isolates encoded *bla*CTX-M-15, *sul1*, *dfrA17*, *aadA5*, and quinolone resistance mutations (*gyrA S83L*, *parC S57T*), while one isolate harboured no ARGs despite possessing the p0111 plasmid. IncF and large conjugative IncH12/IncH12A plasmids were detected across farm niches.

Among eight *Proteus* isolates, seven exhibited multidrug resistance and ESBL phenotypes; two carried chromosomal AmpC. Six encoded *tetC*, and one isolate possessed a broader ARG profile (*cmlA1*, *sul3*, *dfrA1*, *aac(3)-IV*). A downstream-brook isolate contained a Col3M plasmid with *qnrD1*.

Six *S. fonticola* isolates lacked plasmids but consistently encoded *fosA8*, *arnT*, and *SFDC1*. ESBL-associated *bla*FONA variants (-2, -5, -6) were found across water, soil, and pork sausage isolates, alongside the disinfectant-resistance gene *qacG*.

Conclusion

AMR determinants were unevenly distributed across livestock, food, environmental, and wildlife sources, revealing multiple overlapping transmission pathways within the farm ecosystem. The combination of phenotypic and genomic data demonstrates the value of integrated, ecosystem-centred AMR surveillance frameworks that capture cross-niche gene flow beyond clinical settings—critical for One Health-aligned risk mitigation in mixed farming systems.

1676 – Habitat Degradation and Restoration Influence Biodiversity and Zoonotic Pathogen Prevalence in Small Mammals

Baraka MWAMUNDELA (1,2), **Joachim MARIEN** (4,5), **Alfan RIJA** (2), **Apia MASSAWE** (1,2), **Herwig LEIRS** (4), **Lucinda KIRKPATRICK** (3,4)

1: Institute of Pest Management, Sokoine University of Agriculture, Morogoro, Tanzania; 2: Department of Wildlife Management, Sokoine University of Agriculture, Morogoro, Tanzania; 3: School of Environmental and Natural Sciences, Bangor University, Bangor, UK; 4: Evolutionary Ecology Group (EVECO), Universiteit Antwerpen, Antwerp, Belgium; 5: Virus Ecology Unit, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium

Changes in habitat due to land degradation or urbanization can influence the transmission of zoonotic pathogens in small mammals because they alter host density, behavior, and interactions among small mammals. Changes of biodiversity associated with both habitat degradation and restoration will therefore impact the prevalence and transmission of zoonotic pathogens. In order to test this, we conducted a capture mark recapture study in Morogoro, Tanzania, from February 2025 to February 2026, to assess the influence of habitat degradation and restoration on small mammal assemblages and resultant pathogen prevalence and transmission. We compared the diversity and abundance of rodents

and shrews alongside ectoparasite presence and bacterial pathogen prevalence, testing whether alpha diversity influences pathogen prevalence across different ecological contexts. We use polymerase chain reactions (PCR) to detect bacterial pathogens and apply ecological models to test the relationship between pathogen prevalence and diversity across ecosystem contexts. We find that habitat degradation and restoration differ in alpha diversity, with consequences for pathogen prevalence, and that these relationships are not consistent through the year. These results provide valuable insights into the relationship between biodiversity loss, recovery and pathogen prevalence. Understanding the mechanisms linking biodiversity, disease regulation, and human-wildlife interactions will be essential for mitigating future health threats while supporting ecological resilience in Tanzania and beyond.

1685 – Challenges to Implementing a One Health curriculum across campus: Bringing OH Research Gains into Practice

Jennifer WISHNIE (1), Julia JERNBERG (2), Heidi BROWN (3), Bonnie BUNTAIN (1)

1: University of Arizona, College of Veterinary Medicine, United States of America; 2: University of Arizona, College of Medicine, United States of America; 3: University of Arizona, College of Public Health, United States of America

Background. Significant gains have been made to incorporate transdisciplinary One Health (OH) into research, but its integration into practice is lagging. The continued global emergence of OH requires an OH approach that involves both researchers and practitioners, yet curricular stumbling blocks remain in training OH practitioners. Until academic institutions determine how to support inter- and transdisciplinary OH training, TD OH training will be relegated to extracurricular activities. **Methods.** We describe the challenges encountered in developing and implementing a novel TD OH course involving faculty and students from veterinary medicine, human medicine, and public health. The 1-week, full-day, in-person course was structured around published OH competencies and emphasized collaborative, interdisciplinary teamwork, with each day devoted to a different OH topic. **Results.** Reflections from students, partners, and faculty in 2025 echoed published findings from the 2024 course, noting the course's logistical burden but overall success. Semi-structured interviews with practitioners from veterinary medicine, human medicine, and public health conducted during the 2025 course further emphasized the need to incorporate inter- and transdisciplinary OH training into academic curricula to support application in practice. Moreover, discussions with colleagues at other universities reinforced the widespread challenges associated with delivering TDOH training. **Conclusion.** Lessons learned from the design, implementation, and evaluation of this course underscore the need for robust training of One Health practitioners. Addressing persistent logistical and funding challenges to delivering interdisciplinary One Health training in academia is essential to ensure practitioners are equipped to meet emerging One Health threats.

1689 – Wildlife Anthrax in Gonarezhou National Park, Zimbabwe, 2024: Outbreak Characterization and Implications for Disease Surveillance

Bob MANDINYENYA (1), **Jared PALAZZA** (2,3), Stephanie MITCHELL (2,3,4)

1: Gonarezhou National Park, Chiredzi, Zimbabwe; 2: Center for One Health Research, University of Washington, Seattle, United States of America; 3: Department of Environmental Health, University of Washington, Seattle, United States of America; 4: S. Mitchell Consulting, LLC, Sammamish, United States of America

BackgroundAt the human-wildlife-livestock interface in Zimbabwe's southern districts, bioclimatic models have consistently classified the region as marginally suitable for anthrax, yet catastrophic outbreaks in wildlife (2004-2005, 2024) demonstrate that climate variables alone cannot predict disease emergence across this shared landscape. We describe the spatial and temporal patterns of a 31-day anthrax outbreak (August-September 2024) in Gonarezhou National Park that was successfully contained within wildlife populations (n= 227 animals,9 species), predominantly buffalo (61%). A single kudu carcass was confirmed as the first case via blood smear, triggering coordinated surveillance between aerial and ground teams.

Methods

Daily aerial surveillance identified carcass locations, coordinating with ground teams for immediate investigation and containment through burning or chemical treatment to prevent spore dispersal. Following strict biosecurity protocols to safeguard human health, teams compiled GPS coordinates, species identification, carcass age, and daily case counts. Community outreach facilitated livestock vaccination campaigns and ensured affected areas were avoided during the outbreak. Temporal dynamics were assessed using ARIMA modeling. Spatial analyses included kernel density estimation (KDE) with Diggle bandwidth selection, Ripley's K function (99 Monte Carlo simulations), and Knox tests for space-time interaction. Spatial relationships with the Mwenezi River and road-rail infrastructure were assessed using Euclidean distances.

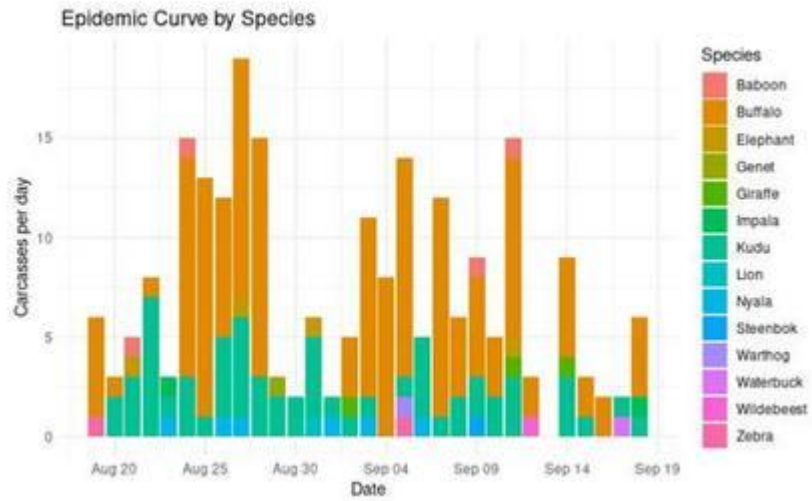
Results

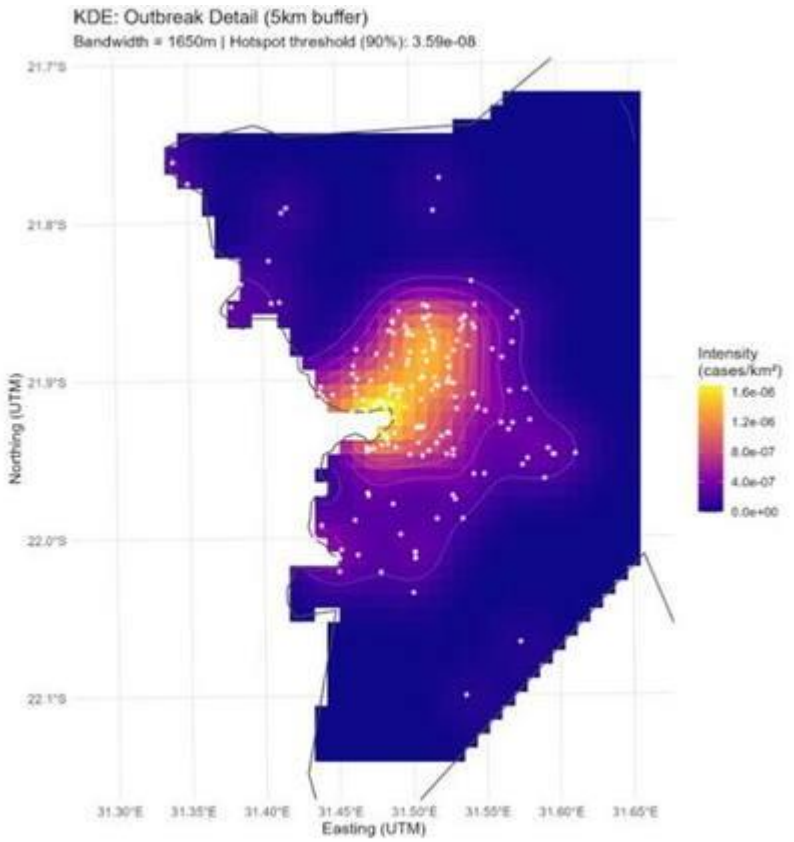
The outbreak exhibited rapid early growth (doubling time: 2.4 days), peaking 8 days after detection. ARIMA modeling selected a (0,0,0) specification, indicating daily cases fluctuated around a constant mean (7.3 cases/day) without temporal autocorrelation, characterizing this as a point-source environmental event rather than sustained transmission. Of 227 carcasses, 179 (79%) occurred within park boundaries and 48 (21%) outside, with extralimital cases significantly closer to the Mwenezi River, suggesting wildlife congregation near water before death. All carcasses occurred south of a road-railway corridor, indicating this infrastructure may function as an ecological boundary. KDE revealed two primary hotspots (peak intensity: 1.6×10^{-6} cases/km^2), indicating localized environmental contamination. Ripley's K function confirmed significant clustering at all scales (3-28km, p0.05). Knox test showed strong space-time interaction at short scales (500m/7-day: Obs/Exp=1.89, p0.05), consistent with sequential exposure to point-source contamination as animals visited common resource sites.

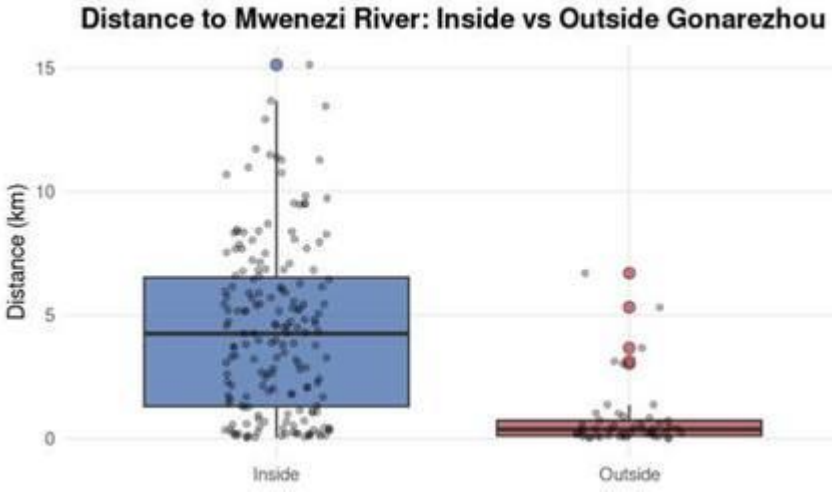
Conclusion

The swift, coordinated aerial surveillance and immediate carcass containment led by Gonarezhou National Park enabled outbreak containment, reducing the opportunity for anthrax to spread to livestock or people in adjacent communities on the park boundary. The combination of rapid doubling time, absent temporal autocorrelation, and focused spatial clustering suggests that the outbreak was driven by climatic activation of soil-borne spores rather than transmission from infected carcasses to healthy animals. Spatial analysis identified two focal hotspots for targeted surveillance. River-adjacent areas outside the park should be prioritized for surveillance during future outbreaks.

Figures and Tables




KDE: Outbreak Detail (5km buffer)
Bandwidth = 1650m | Hotspot threshold (90%): 3.59e-08
21.7°S
21.8°S
21.9°S
22.0°S
22.1°S
Northing (UTM)
31.30°E
31.35°E
31.40°E
31.45°E
31.50°E
31.55°E
31.60°E
31.65°E
Easting (UTM)
Intensity (cases/km²)
1.6e-06
1.2e-06
8.0e-07
4.0e-07
0.0e+00


Distance to Mwenezi River: Inside vs Outside Gonarezhou
Distance (km)
15
10
5
0
Inside
Outside

Poster zone 2

Sardines

1205 – “I used a polecat's tail to treat my legs”: Experiences of podoconiosis patients on access to Water, Sanitation, and Hygiene (WASH) in Butaro, Rwanda

Pacifique UFITINEMA (1), Nina SANDRA NATASHA NGOWI (1), Maria ALBIN QAMBAYOT (1), Janna M SCHURER (1,2)
1: University of Global Health Equity, Rwanda; 2: Cummings School of Veterinary Medicine at Tufts University, North Grafton, USA

Background

Podoconiosis is a highly preventable, non-infectious Neglected Tropical Disease which causes progressive lower limb lymphoedema and chronic disability. The recommended management, collectively referred to as home-based management (HBM), includes daily foot hygiene with soap and clean water, as well as consistent use of protective footwear. The ability to maintain these practices is strongly influenced by access to water, sanitation, and hygiene (WASH). This study aimed to explore podoconiosis patients' access to WASH and to identify barriers and facilitators of HBM.

Methods We conducted a qualitative phenomenological study in the Butaro Sector, Rwanda. A door-to-door screening was first carried out to identify individuals with lower-limb lymphoedema. Those with leg swelling were further assessed and highly probable cases were selected for clinical assessment by a medical doctor. Only individuals confirmed to have podoconiosis were invited for one-on-one in-depth interviews. Interviews were complemented by observation and photographs. Data was transcribed, inductively coded in Dedoose (version 9.0.80), and analyzed through thematic analysis.

Results A total of 26 interviews were conducted across all five cells of Butaro Sector. Poverty and physical inability were major barriers to accessing water and other HBM essentials such as soap. Most participants relied heavily on relatives or neighbors for assistance. However, some of them found a financial solution by selling animal or household waste to meet daily needs. Social stigma further constrained access, as experiences of shame, laughter, and discrimination discouraged participants from fetching water, using common roads, or purchasing hygiene items in local markets. Moreover, participants demonstrated little or no knowledge about podoconiosis. Many attributed the disease to witchcraft, blood contamination, or God’s will, and these beliefs influenced their treatment choices which included visiting traditional healers, self-treatment, or health centers.

Conclusion

These findings demonstrated the need for a podoconiosis care model that goes beyond routine clinical care to address the broader challenges patients face. Such a model should combine podoconiosis care with patient education to address misconceptions and stigma, alongside practical support to improve access to WASH and HBM essentials. Embedding this model within local health service delivery systems offers a practical pathway toward stronger and more sustainable podoconiosis care. These findings also informed the establishment of a podoconiosis clinic at Butaro Health Center, which currently serves 60 patients from Butaro and the neighboring Rusarabuye Sector. Through bi-weekly group sessions, the clinic strengthens HBM by providing essential supplies, delivering education on podoconiosis prevention and care, and promoting safer livelihood activities to support long-term self-reliance.

1211 – First 16S rRNA metabarcoding survey of blood-borne zoonotic bacteria in wild armadillos from the Brazilian Pantanal

Marília LIMA DA CONCEIÇÃO (1), **Danilo KLUYBER** (1,2,3), Mayara CAIAFFA (4), Ana Carolina MONTEIRINHO LOBO (5), Arnaud Léonard Jean DESBIEZ (4), Idris MHAIDI (1), Baptiste VERGNES (1), Expedito José DE ALBUQUERQUE LUNA (2), **Julio BENAVIDES** (1)
1: MIVEGEC, Montpellier University, CNRS, IRD, Montpellier, France; 2: Faculdade de Medicina, Universidade de São Paulo (USP), São Paulo, Brazil; 3: Naples Zoo at Caribbean Gardens, Florida, USA; 4: Instituto de Conservação de Animais Silvestres (ICAS), São Paulo, Brazil; 5: Universidade do Estado de São Paulo (Unesp), Botucatu, Brazil

Background: Armadillos are key players in environmental microbial diversity through their nomadic habits and interactions with biological diversity during burrowing across different communities and ecosystems. They are also known as reservoirs or hosts for certain infectious diseases. This study aims to identify pathogens present in the blood of the giant armadillo (*Priodontes maximus*) and the six-banded armadillo (*Euphractus sexcinctus*) in the Brazilian Pantanal.

Methods: Eighteen free-living armadillos were manually captured and anesthetized following the protocol described by Kluyber et al. (2020)1 for the collection of 20 blood samples at the Baía das Pedras ranch and neighboring farms, covering approximately 450 km, between 2019 and 2024. DNA was extracted from 200 µL of each blood sample and 16S rRNA gene metabarcoding was performed targeting the V3–V4 region to investigate bacterial diversity. Sequencing was performed on the Illumina NovaSeq platform, generating overlapping reads covering the ~460 bp V3–V4 fragment. Raw paired-end reads were demultiplexed, quality-filtered, and analysed using BMKGENE's standard pipeline.

Results: 16S rRNA metabarcoding revealed a low-biomass bacterial profile dominated by environmentally ubiquitous genera commonly associated with contamination. Nonetheless, vector-associated and zoonotically relevant genera were detected, including *Coxiella* (A18: 0.62%; A19: 0.02%), *Mycoplasma*, the most prevalent and abundant genus (18/20 samples; 14 above the 0.1% threshold for confident detection, with markedly high abundances in A03: 78.5%, A11: 61.8%, and A15: 74.5%), and *Mycobacterium* (9/20 samples; 5 above 0.1%; range: 0.24 - 2.28%).

Conclusions: The detection of vector-associated bacterial genera, such as *Coxiella* in armadillos, is ecologically plausible, reflecting host-vector-microbe interactions that occur in the wild and reinforcing the role of armadillos as potential reservoirs or epidemiological sentinels in Neotropical ecosystems2. *Mycoplasma* is known to establish infection in the bloodstream of various mammalian species3, including armadillos4. Here, its detection across both species and the high relative abundances observed in several individuals suggest active hemotropic infection and widespread *Mycoplasma* circulation within the Pantanal ecosystem, independent of host species. Furthermore, the detection of *Mycobacterium* is highlighted since armadillos are known carriers of *Mycobacterium leprae* and are therefore of zoonotic importance5.

This work was supported by the Expos'UM France 2030 project 'Zamba', the ICAS, Fundo Mobilidade Santander, Fundo Brasileiro para a Biodiversidade - Funbio e Wildlife Conservation Network.

1217 – Serious Games as One Health tools for commmunity awareness, education and advocacy

Isabel TOSTES (1), Alexandre CARON (2), Anne CONAN (3), Cécile SQUARZONI (4), Mathieu BOURGAREL (5), Antoine LURY (6), Charlotte MAQUET (7), **Florence AYRAL** (8), Christophe LE PAGE (9)

1: Earth Innovation Institute, Cuiabá, Brazil; 2: CIRAD ASTRE – ILRI, ILRI, Nairobi, Kenya; 3: CIRAD ASTRE, Harare, Zimbabwe; 4: CIRAD ASTRE, Reunion Island, France; 5: CIRAD ASTRE - UEM, Maputo, Mozambique; 6: CIRAD ASTRE, Montpellier, France; 7: CIRAD ASTRE, Montpellier, France; 8: VetAgro Sup, Lyon 1 University, RS2GP, Marcy L'Etoile, France; 9: CIRAD SENS, Montpellier, France

Background: The One Health (OH) approach has gained significant recognition in research and policy arenas, and emphasizes the need for greater integration across disciplines, institutions, and sectors. As a result, there is growing interest in participatory tools that facilitate dialogue, experimentation, and collective reflection among stakeholders involved in complex health–environment systems. Among these approaches, serious games (SGs) have emerged as a promising tool for enabling interactions among stakeholders.

Although definitions may vary in the literature, SGs are designed for purposes beyond entertainment, such as learning or decision-making. SGs allow participants to interact with simplified representations of complex systems, enabling them to test strategies, experience the consequences of decisions, and explore trade-offs in a safe, controlled environment. Therefore, SGs may contribute to system thinking, collective learning processes and foster dialogue among actors who typically do not interact in traditional policy or research settings.

Methods: This study presents a literature review examining the application of serious games in OH and related fields. Searches were performed in major scientific databases (e.g., Scopus, Web of Science, PubMed, and Google Scholar). The review explores the types of games used, their objectives, the contexts in which they are applied, and the outcomes reported in the literature, including learning processes,

awareness raising, advocacy, and the promotion of core OH values and practices. The study also draws from our respective experiences in designing and using SGs for OH applications.

Results: SGs have been applied in several domains of public health, including disease prevention, health education, and policy training. However, their application within the specific context of OH remains relatively recent. Existing studies often focus on educational or awareness-raising objectives, and relatively few explore how SGs can support intersectoral collaboration, collective action, or governance processes for complex health–environment challenges, such as zoonotic diseases or pollution. Different SGs can be designed for a vast range of stakeholders, from local communities and citizens to students, professional staff and policy makers. SG can be used to raise awareness about basic OH concepts (local communites, citizen, primary & secondary schools). Others can be used to sensitize technical staff involved in OH institutionalizaiton and operationalisation (academics, government technical staff). SGs can also be used to promote more system thinking and collective action amongst various stakeholders, promoting interdisciplinarity and/or intersectorality; notably at policy makers' level (e.g., municpality or ministerial levls). Examples will be provided for each category.

Conclusions: By synthesizing the current evidence, this work highlight opportunities and limitations of SGs as tools to support communication, capacity building, participatory and collective action in the OH field.

1226 – Biodiversity as a Sentinel: Assessing how pathogen-agnostic monitoring using environmental DNA (eDNA) could contribute to pandemic preparedness

Anne E. RITTSCHER-FOGG (1), Peter REININK (1), Inge M. WOUTERS (1), Leonard SCHUELE (3), Bas OUDE MUNNINK (3), Johannes N. WIEGERS (4), Ni Made Ayudita A. L. WEDAYANTI (1), Mia COUPARD (1), Marion KOOPMANS (3), Alex BOSSERS (1,2), Lidwien A.M. SMIT (1)

1: Population Health Sciences - Institute for Risk Assessment Sciences, Utrecht University, Utrecht, The Netherlands; 2: Wageningen Bioveterinary Research, Wageningen University and Research, Lelystad, The Netherlands; 3: Department of Viroscience, Erasmus MC University Medical Center, Rotterdam, Netherlands; 4: Ecology & Biodiversity group, Department of Biology, Utrecht University, Utrecht, The Netherlands

Background: Land use change is disrupting historical patterns of disease spillover between wild and farmed animals.Many existing surveillance systems employ targeted surveillance for known pathogens, making them less agile in new situations. In contrast, pathogen-agnostic surveillance target drivers of disease, such as the presence of certain host species, and can therefore provide early signals about potential spillover risks. Recently, analysis of environmental DNA (eDNA) from air has emerged as a promising tool for the analysis of animal communities. With this study, we aimed to assess airborne eDNA collection in and around a livestock farm to assess the method’s suitability as a pathogen-agnostic surveillance tool through monitoring host species.

Methods: Air samples (n=12) were collected in May 2025 for two one-week periods, at a farm and two nearby nature estates (Figure 1). At the farm, samples were collected both indoors in the air intake and outdoors. The nature estates had one or two sampling locations.

Airborne dust was collected using a pump which drew air through a Teflon filter contained in a Harvard impactor. Total nucleic acids were extracted from the filters employing the LGC extraction kit and subsequently used for metabarcoding and metagenomic sequencing to identify the vertebrate, viral, bacterial, and fungal communities. Additionally, we compared these findings to three complementary methods; camera trapping, bioacoustics monitoring, and collection of insects for invertebrate derived DNA classification (iDNA).

Results: Based on the Bray-Curtis dissimilarity matrix, the compositon of the bacterial, fungal and vertebrate communities showed distinct clustering based on the collection site. Fungal communities also displayed temporal clustering. The viral communities displayed no pattern based on location or sampling period.

Fifty-three vertebrate taxa were present in the air samples, with the greatest diversity found at the farm. The air samples found all but two of the species found by the camera traps, and an additional six species not seen in the images. The bioacoustics analysis detected 34 families of birds while only 14 of these families were also found using eDNA.Finally, DNA from eight vertebrate families was recovered from the surfaces of the collected insects.

Conclusions: Airborne eDNA analysis provided a complete picture of the bacterial, fungal, vertebrate and viral communities present at each site. This establishes the tool's potential for both pathogen-agnostic host monitoring, as well as for targeted surveillance. Additionally, airborne eDNA performed well in comparison to the camera traps, while the bioacoustics showed the value of combining multiple methods. More research is needed into the ecology of eDNA before it can be a stand-alone tool, however its capability for detecting all aspects of the living environment with an accessible and cost-effective sample, could make it a powerful part of our pandemic preparedness toolkit.

1237 – Advancing Global One Health Intelligence: Strengthening Early Warning through the GLEWS+ Tripartite Collaboration

Gisela GIOIA (1), Elisa PALAMARA (1), Dubravka SELENIC MINET (2), Paolo TIZZANI (3), Pavel NEGINSKY (1), Eduardo MACHADO (1), Ismaila SECK (1), Madhur DHINGRA (1)

1: Food and agriculture organization for the United Nations (FAO), Italy; 2: World Health Organization of the United Nations (WHO), Switzerland; 3: World Organisation for Animal Health (WOAH), France

Background: Emerging and re-emerging health threats at the human–animal–ecosystem interface continues to pose significant risks to global health security.Increasing interconnectedness, environmental change, intensification of livestock systems, and global mobility require strengthened mechanisms for early detection, coordinated risk assessment, and joint response. Integrating One Health intelligence across human, animal, and environmental health sectors is critical for enabling timely detection and rapid response to emerging zoonotic threats before they escalate into widespread outbreaks. The Global Early Warning System for health threats and emerging risks at the human–animal–ecosystem interface (GLEWS+), jointly implemented by the Food and Agriculture Organization of the United Nations (FAO), the World Health Organization (WHO), and the World Organisation for Animal Health (WOAH), represents a flagship One Health intelligence mechanism supporting global situational awareness and coordinated action across sectors.

Methods: GLEWS+ integrates indicator-based and event-based surveillance information from multiple sources, including official reporting systems, open-source epidemic intelligence platforms, and partner networks. Through the Tripartite coordination mechanism, FAO, WHO, and WOAH jointly monitor signals, verify health events, conduct risk assessments, and share information with Member States and partners. The platform for confidential information exchange has been recently modernized to enhance data integration, analytical workflows, and timely information exchange. In addition, a newly launched public-facing website ensures that validated health events and One Health resources are accessible to the broader community, improving transparency and supporting informed decision-making.

Results: The modernization of GLEWS+ internal communication and the launch of a public-facing website strengthens the sensitivity and timeliness of early warning through integration of epidemic

intelligence streams, including the Epidemic Intelligence from Open Sources (EIOS) initiative developed by the WHO Hub for Pandemic and Epidemic Intelligence. The system enhances joint situational awareness across the human–animal–ecosystem interface and supports coordinated risk assessment and communication among the Tripartite. GLEWS+ contributed to monitoring and joint risk assessments of major zoonotic and transboundary threats such as highly pathogenic avian influenza, Rift Valley fever, anthrax, and other health hazards. The new public website also expands access for the public, improving transparency, engagement and utilization of global One Health intelligence .

Conclusions: GLEWS+ exemplifies the operational value of institutionalized collaboration between FAO, WHO, and WOAH in strengthening global early warning under a One Health framework. The modernization of the platform and the launch of the public-facing website an important step toward more transparent, integrated, and data-driven global intelligence systems. Sustained investment in digital interoperability, cross-sectoral collaboration, and epidemic One Health intelligence will be essential to further strengthen preparedness and coordinated responses to emerging health threats worldwide.

1249 – KNOWLEDGE, ATTITUDE, AND PRACTICE OF VETERINARY OFFICERS REGARDING ANTIBIOTIC USE AND RESISTANCE IN LIVESTOCK FARMING IN VIETNAM

Hai NGO (1), Kim DANG (1), Thai PHAM (2), Duc TRAN (3), Rogier VAN DOORN (1), **Sonia LEWYCKA** (1)

1: Oxford University Clinical Research Unit, Hanoi, Vietnam; 2: National Institute for Hygiene and Epidemiology, Hanoi, Vietnam; 3: Sub-Department of Animal Health, Nam Dinh, Vietnam

Background: Antibiotic use in agriculture is a major driver of antimicrobial resistance (AMR). Previous studies indicate that animal health officers significantly influence farmer's decisions regarding antibiotic use in livestock farming.We aimed to explore the knowledge, attitude and routine practices (KAP) of community-level veterinary officers regarding antibiotic use in animal health, and to identify factors associated with their recommendations.

Methods: A KAP survey was conducted among veterinary officers (81% male) from 64 communes in Nam Dinh Province, Vietnam. Descriptive analysis, Wilcoxon signed-rank test and logistic regression were used to analyse the data. We also conducted focus group discussions with veterinary officers from 7 of the communes. Discussions were transcribed and analysed thematically.

Results: Of the 64 participants,97% participants held a college degree in veterinary medicine, with an average of 23 years of experience (SD=14 years) and mostly treated animal diseases on small-scale farms (89%). Limited access to diagnostic services means that veterinary officers relied on physical examinations and experience for diagnosis and treatment. Despite being trained recently in AMR (55%) or animal health regulations (85%), participants demonstrated poor knowledge of animal infectious diseases (mean score: 1.8/7, SD=0.8), antibiotic treatment (mean score: 1.7/12, SD=0.5) and relevant regulations (mean score: 0.9/5, SD=0.6), but they reported moderate confidence in AMR relevant issues (mean score 4.1/7, SD=1.0). One-third refrained from prescribing antibiotics for prophylaxis, while 88% advised farmers to stop antibiotics use before selling animals. Overall, veterinary officers trained in either animal health regulations (W = 296, p = 0.01) or AMR knowledge (W = 331.5, p = 0.02) showed significantly better confidence in addressing antibiotic relevant issues (W = 296, p = 0.01). Counterintuitively, veterinary officers who had more frequent discussions about AMR with farmers had 2.83 higher odds of recommending antibiotics for prophylaxis.Interviews revealed veterinary officers prioritised disease prevention to reduce the risk of outbreaks. This included vaccination and biosecurity, but may also explain the advice on prophylactic antibiotic use to reduce infection risks. Though some veterinary officers preferred to promote non-pharmaceutical disease prevention methods. Veterinary officers suspected that antibiotics were often present in animal feeds without farmers knowing and needed tighter regulation. They were also concerned that use of river water for farming may transmit pathogens.

Conclusions: Veterinary officers have close relationships with the farmers in their communities, and a desire to provide advice. Having limited knowledge about antibiotics and AMR-relevant issues means that advice may focus on farm productivity and reducing outbreaks sometimes at the expense of antimicrobial stewardship. Holistic intervention packages for both veterinary officers and farmers are urgently needed to improve antibiotic use and combat AMR in the livestock sector.

1251 – Seroprevalence of Toxoplasma gondii infections in pigs and associated risk factors in smallholder farms in peri-urban Nairobi County, Kenya.

Cherotich TANGUS (1), Bruno ENAGNON LOKONON (2,8), Ndichu MAINGI (1), Chege NGANGA (1), Karanja NJUGUNA (1), Kariuki NJAANAKE (3), Mercy AKINYI (4), AAndrée Prisca NDJOUG NDOUR (5), Esther KIMARO (6), Gloria Ivy MENSAH (7), Kennedy KWASI ADDO (7), Bassirou BONFOH (8)

1: Department of Veterinary Pathology, Microbiology and Parasitology, Faculty of Veterinary Medicine, University of Nairobi, Kenya; 2: University of Abomey-Calavi, Abomey-Calavi Bénin, Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan Côte d'Ivoire; 3: Department of Medical Microbiology, University of Nairobi, Nairobi, Kenya; 4: Kenya Institute of Primate Research, Nairobi, Kenya; 5: École Inter-États des Sciences et Médecine Vétérinaires de Dakar,Sénégal; 6: Nelson Mandela African Institution of Science and Technology, Arusha, Tanzania; 7: Noguchi Memorial Institute for Medical Research, University of Ghana, Legon, Accra, Ghana.; 8: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan Côte d'Ivoire

Background: Toxoplasmosis, caused by *Toxoplasma gondii*, is a neglected zoonosis with pigs serving as intermediate hosts and a source of human infection through consumption of undercooked pork meat. Despite the growth of peri-urban pig farming and the established zoonotic risk of *T. gondii*, data on *T. gondii* infections in pigs, risk factors, and transmission to humans are limited in Kenya. This study investigated the seroprevalence of T. *gondii* in pigs and analysed multi-level risk factors within peri-urban smallholder systems in Kenya

Methods: A cross-sectional study was conducted from April to July 2025 in 3 selected peri-urban sub-counties of Nairobi. Blood samples were collected from 240 pigs below 2 months old in 40 randomly selected smallholder farms. Interview-based data were obtained from farmers using semi-structured questionnaires and included knowledge of toxoplasmosis, farm, and household practices. Observation-based data were recorded during farm visits and included animal and farm characteristics. Serum samples were analyzed for anti-*T. gondii* antibodies using an indirect ELISA. Data were analyzed using descriptive statistics and logistic regression to assess associations between seroprevalence and potential risk factors.

Results: Overall seroprevalence of *T. gondii* in pigs was 44.6%. At the animal level, grower pigs showed lower odds of seropositivity than adult pigs (AOR = 0.49; 95% CI: 0.26–0.91; $p \leq 0.02$). At the farm level, pigs that never had access to clean potable water had higher odds of infection (AOR = 2.74; 95% CI: 1.24–6.25; $p \leq 0.014$). Most farms operated a semi-intensive informal system (75%), with temporary pens (77.5%), unhygienic feed storage (70.0%), and poor waste management and sanitation (72.5%). Free-roaming cats were observed on all farms, increasing the risk of environmental contact with pig feed and manure

Farmer knowledge of toxoplasmosis was low (22.5%, $p \leq 0.001$), with risky practices such as feeding cats with raw meat (90%), use of untreated water (65%), absence of protective clothing (100%), and limited biosecurity measures (65%).

Conclusion: High seroprevalence of *T. gondii* in pigs showed a high exposure risk to humans. Low farmer knowledge, risky practices, and the presence of cats likely maintain *T. gondii* transmission and increase chances for human exposure. To effectively reduce porcine infection and zoonotic risk, risk characterization will guide farmer-led interventions integrating hygiene, education, and incentives.

Fig. 1: Graphical abstract: **Seroprevalence of *Toxoplasma gondii* infections in pigs and associated risk factors in smallholder farms in peri-urban Nairobi County, Kenya.**

Main Variable	Categories	Response	Frequency (%)	p-value
Knowledge of Toxoplasmosis	Heard of toxoplasmosis	Yes	9 (22.5)	0.001*
		No	31 (77.5)	
	Toxoplasmosis affects humans	Yes	7 (17.5)	<0.001*
		No	33 (82.5)	
	Pig infected with Toxoplasma	Yes	10 (25.0)	0.002*
		No	30 (75.0)	
Behavioural factors (Food consumption practices)	Eat undercooked meat	Yes	0 (0.0)	<0.001*
		No	40 (100)	
	Eat raw vegetables	Yes	10 (25.0)	0.002*
		No	30 (75.0)	
	Boil milk	Yes	26 (65.0)	0.058
		No	14 (35.0)	
	Eat pork	Yes	38 (95.0)	<0.001*
		No	2 (5.0)	
Household hygiene practices	Wash fruits/vegetables	Yes	27 (67.5)	0.027*
		No	13 (32.5)	
	Treat water before use	Yes	14 (35.0)	0.058
		No	26 (65.0)	
	Wear gloves when gardening	Yes	0 (0.0)	0.001*
		No	40 (100)	
Farm management practices	Clean housing	Yes	11 (27.5)	0.004
		No	29 (72.5)	
	Adequate waste management	Yes	2 (5.0)	<0.001
		No	38 (95.0)	
	Moderate hygiene	Yes	13 (32.5)	0.027
		No	27 (67.5)	
	Inadequate hygiene	Yes	26 (65.0)	0.058
		No	14 (35.0)	
	Commercial feed	Yes	12 (30.0)	0.011
		No	28 (70.0)	
	Kitchen waste feed	Yes	29 (72.5)	0.004
		No	11 (27.5)	
	Dirty feed storage	Yes	27 (67.5)	0.027*
		No	12 (30.0)	
Animal–environment exposure	Cat presence	Yes	40 (100)	<0.001
		No	0 (0.0)	
	Cat kept indoors	Yes	0 (0.0)	<0.001
		No	40 (100)	
	Cat roaming	Yes	40 (100)	<0.001

Table 1. Knowledge, behavioural factors, household and farm practices related to *Toxoplasma gondii* among pig farmers (n = 40)

Variable	Category	N	No. Positive (%)	AOR	95% CI	P-value
Pigs age	Adult	74	38 (51.4)	Ref	–	–
	Finisher	72	37 (51.4)	1.00	0.52–1.92	0.99
	Grower	94	32 (34.0)	0.49	0.26–0.91	0.02*
Farming System	Intensive	26	9 (34.6)	Ref	–	–
	Semi-intensive	214	98 (45.8)	1.60	0.70–3.90	0.28
Type of Housing	Permanent	7	0 (0)	Ref	–	
	Semi-permanent	45	21 (46.7)	–	–	0.98
	Temporary	188	86 (45.7)	–	–	
Waste Management	Adequate	10	2 (20.0)	Ref	–	–
	Inadequate	174	80 (46.0)	3.40	0.82–22.99	0.12
	Moderate	56	25 (44.6)	3.23	0.73–22.87	0.16
Access to Clean Water	Always	59	23 (39.0)	Ref	–	–
	Sometimes	33	19 (57.6)	2.12	0.90–5.13	0.088
	Rarely	104	37 (35.6)	0.86	0.45–1.68	0.66
	Never	44	28 (63.6)	2.74	1.24–6.25	0.014*
Rodent-Proof Housing	Yes	4	0 (0)	Ref	–	–
	No	236	107 (45.3)	–	–	0.98
Cats in the neighborhood	yes	240	107 (44.6)	–	–	–
Cat access to pigs housing	yes	240	107 (44.6)	–	–	–
Feed Type	Commercial Feed	52	18 (34.6)	Ref	–	–
	Butcher Waste	14	8 (57.1)	2.52	0.75–8.75	0.13
	Kitchen Waste	174	81 (46.6)	1.65	0.87–3.19	0.12
Feed Storage	Moderate Storage	72	29 (40.3)	Ref	–	–
	Dirty Storage	168	78 (46.4)	1.29	0.74–2.28	0.38

Table 2. Animal and Farm-Level Risk Factors Associated with *Toxoplasma gondii* Seropositivity in Pigs (n = 240)

1254 – From the grassroots up: Redefining public health surveillance in Nigeria through Community Action Networks

Eniola CADMUS (1,2), Mathias BISONG (3), Funmilayo OLALEYE (4), Samuel OWOICHO (3), Adeyemi JOLAOSO (5), Adegboyega OBADUA (6), Adegboyega FAMOKUN (7), Terese ORUM (8), Ephraim NWANGA (8), Victor AKINSEYE (10), Emmanuel AWOSANYA (11), Hezekiah ADESOKAN (11), Rashid ANSUMANA (9), **Simeon CADMUS** (4,10,11)

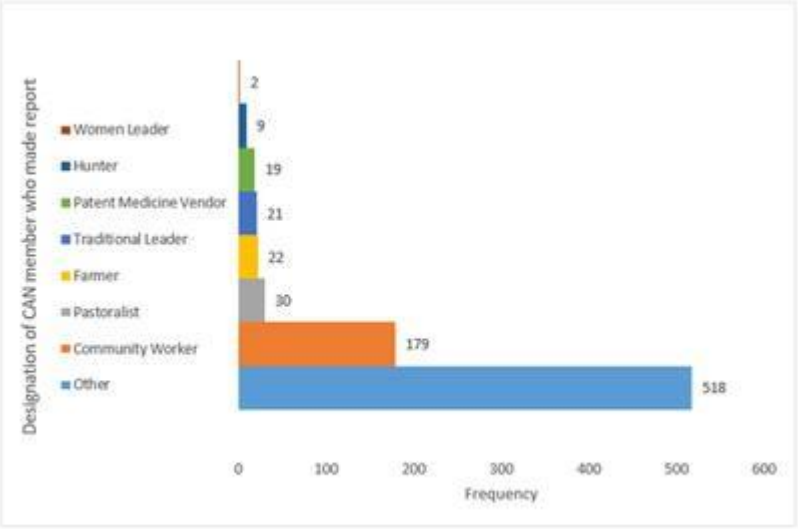
1: Department of Community Medicine, College of Medicine, University of Ibadan; 2: Chief Tony Anenih Geriatric Centre, University College Hospital, Ibadan; 3: Federal Ministry of Agriculture, Abuja, Nigeria; 4: Damien Foundation Centre for Genomics and Global Health, University of Ibadan, Nigeria; 5: Department of Veterinary Services, Ogun State Ministry of Agriculture; 6: Department of Veterinary Services, Ministry of Agriculture, Akure, Ondo State, Nigeria; 7: Department of Epidemiology and Disease Control, Ondo State Ministry of Health; 8: Ministry of Agriculture and Natural Resources, Ebonyi State, Nigeria; 9: Njala University, Bo, Sierra Leone; 10: Nigerian Institute of Medical Research, Yaba, Lagos; 11: Department of Veterinary Public Health & Preventive Medicine, University of Ibadan, Nigeria

Background Nigeria's persistent burden of communicable diseases continues to expose significant gaps in early detection and response, particularly at the community level, where formal surveillance systems often miss early warning signals. Public health surveillance is essential for timely evidence gathering and effective control of infectious and zoonotic diseases. Given that many emerging infections originate from animals, a multidisciplinary One Health approach is critical. The Community Action Network (CAN) was developed under the West Africa One Health (WAOH) project as a transformative, community-led surveillance model. CAN mobilises trained community members as frontline health informants to bridge the gap between underserved populations and the formal health system.

Methods The WAOH project was implemented across five Nigerian states, targeting high-risk Local Government Areas (LGAs) for priority zoonotic and epidemic-prone diseases such as Lassa fever, Mpox, COVID-19, and Ebola. Project sites were selected through disease risk analysis, with stakeholder engagement at national, state, and community levels ensuring strong multisectoral collaboration. CAN is a key component of the project, composed of 12–15 residents per site, trained in symptomatic surveillance, case definitions, risk communication, and digital reporting. WhatsApp and other mobile tools were used to enable real-time participatory surveillance, especially in remote settings.

Results Eighty-six (86) CAN members were trained with a mean age of 40.3 ± 9.6 years. Most (60.5%) resided in rural areas, 39 (45.4%) were female, and 83.7% had lived in their communities for over five years. Additionally, 79.1% were married, and 72.1% had a tertiary education. Between January 20, 2023, and March 31, 2025, a total of 800 health events were reported across five states, covering 8 LGAs. The human health sector accounted for 674 (84.2%) events, while environmental and animal health contributed to 62 (7.8%) and 64 (8%) of reports, respectively. Edo State reported the highest number of events (490; 61.3%), followed by Ebonyi (173; 21.7%) and Ogun (114; 14.3%). District State Notification Officers submitted most reports (69.9%). Reported events included human and animal diseases, unexplained deaths, and environmental hazards.

Conclusion The CAN model has significantly strengthened community-level surveillance in Nigeria by improving early detection, promoting gender inclusion, and fostering community trust. It demonstrates the effectiveness of leveraging local human resources and mobile technology to enhance participatory surveillance. This paper advocates for the policy integration of CAN as a scalable, cost-effective model aligned with Nigeria's health security and One Health goals.



*Others include: Traditional healers, birth attendants, teachers, community informants, artisans, and retailers

Variable		Frequency n	Percent (%)
Health event			
Environmental Health		62	7.8
Animal Health		64	8.0
Human health		674	84.2
State (LGA)			
Ogun			
i.	Abeokuta South	98	12.3
ii.	Ipokia	16	2.0
Edo			
i.	Esan West	78	9.8
ii.	Etsako West	412	51.5
Oyo			
i.	Iwajowa	10	1.3
Ebonyi			
i.	Izzi	135	16.9
ii.	Ezza	38	4.8
Ondo			
i.	Owo	13	1.6

1261 – Bridging the Science–Policy gap with a Scalable Decision Support Tool: Country-Level Applications for Rift Valley Fever and Avian Influenza

Claudia PITTIGLIO, Ismaila SECK, Fredrick KIVARIA, Xavier ROCHE, Alessandra FALCUCCI, Giuseppina CINARDI, Gianluca FRANCESCHINI, Karl MORTEO, Charles BEBAY, Madhur DHINGRA, **Gisela GIOIA**
Food and Agriculture Organization of the United Nations (FAO), Italy

Background:

Despite advances in disease risk modelling, remote sensing, and big-data analytics, translating scientific outputs into actionable policy remains a challenge. Veterinary authorities often struggle to interpret complex predictive models and integrate them into preparedness and response planning. Bridging this science–policy gap requires operational frameworks that translate analytical outputs into clear, country-level decision support for evidence-based interventions. To address this need, the Food and Agriculture Organization of the United Nations (FAO) developed a scalable Decision Support Tool (DST) framework and web-based platform—initially for Rift Valley fever (RVF DST) and later adapted for avian influenza (AI DST)—to strengthen risk monitoring, early warnings, and national capacity for evidence-based decision-making.

Methods: The DST integrates multi-source data—including epidemiological, satellite-derived climatic and environmental indicators, animal mobility, and livestock data—into dynamic risk maps and dashboards tailored to national contexts. The FAO approach combines stakeholder consultation, iterative calibration and customization, and targeted training for national veterinary services and One Health partners. Modelling outputs are validated through participatory processes, with risk layers translated into simplified categories and interactive dashboards to strengthen surveillance, vaccination and early actions. The DST operates through a dual-access model: a publicly available global platform for situational awareness and customized country-level tools with restricted access for analysis of confidential national data by authorized users.

Results: The RVF DST has been developed and operationalized since 2019, when it was piloted in three African countries. A public version covering the African continent was launched in November 2025 to support real-time risk monitoring and alerts. Country-level implementations have since progressed at different stages across 11 countries: Tanzania, Kenya, Uganda, Mozambique, Rwanda, Madagascar, Senegal, Mali, Mauritania, The Gambia, and Tunisia.. In Eastern Africa, the RVF DST enabled anticipatory risk intelligence informing FAO/IGAD joint alerts and triggering preparedness ahead of outbreak detection. By translating forecast signals into operational triggers, it shifted decisions from reactive case confirmation to forecast-informed risk escalation

The AI DST was developed in 2023 in Africa and has since expanded globally. It incorporates wild bird ecology, poultry density, and movement dynamics to support targeted surveillance and prevention strategies. National workshops in Ghana and Guinea validated preliminary hotspots for avian influenza spillover and identified additional high-risk interfaces not previously recognized. Participatory validation improved contextual accuracy, while training and iterative customization strengthened local capacity and adoption.

Conclusions:

The DST bridges the science–policy gap by translating complex analytics into user-friendly operational tools. RVF and AI experiences demonstrate that embedding advanced modelling within a participatory, user-centred framework enhances veterinary services, cross-sectoral coordination, and risk-based disease management under a One Health approach. The framework is scalable and adaptable to other priority diseases, supporting both global situational awareness and country-level decision-making.

1266 – Eco-epidemiological modelling of Pteropus lylei in Cambodia predicts regular seasonal coronavirus shedding in bats

Cherie YU (1,2,3), Thavry HOEM (4), Tey Putita OU (4), Veasna DUONG (4), Julien CAPPELLE (1,3), **David PLEYDELL** (2,1,3)

1: CIRAD, UMR ASTRE, F-34398 Montpellier, France; 2: INRAE, UMR ASTRE, F-34398 Montpellier, France; 3: ASTRE, CIRAD, INRAE, Univ Montpellier, Montpellier, France; 4: Virology Unit, Institut Pasteur du Cambodge, Pasteur Network, Phnom Penh, Cambodia

Introduction

Bat-borne zoonoses pose an ongoing threat to human health. Understanding the mechanisms behind the transmission, maintenance, and spillover of these pathogens is crucial for effective surveillance and control. Evidence suggests that many bat–coronavirus systems exhibit predictable seasonal viral shedding. However, other bat–virus systems, with similar reproductive phenology, exhibit more complex dynamics. Understanding why some bat-virus systems yield regular seasonal outbreaks whilst others generate more complex dynamics has direct implications for anticipating when spillover risk to humans and domestic animals is highest. This study explores the seasonality of coronavirus shedding in Lyle's flying fox (*Pteropus lylei*) - a fruit bat species of particular One Health relevance given that its roosts and foraging sites frequently interface with human settlements, livestock, and agricultural land across Southeast Asia.

Methods

Four age-structured, seasonally forced mechanistic models of coronavirus dynamics were developed, incorporating seasonal birth pulses, maturation, and the waning of both maternal and acquired immunity. Models were calibrated to longitudinal ecological and epidemiological data from a *P. lylei* colony in Kandal Province, Cambodia (2014–2016), consisting of age-structured capture data and coronavirus PCR data from rectal swabs. Model selection was used to identify the optimal model, whose predictive performance was tested against independent *P. lylei* data from Thailand. Markov chain Monte Carlo was used to explore regions of parameter space yielding complex or chaotic infection dynamics. Random forests were used to explore which parameters, or parameter combinations, most strongly influenced the periodicity of coronavirus shedding.

Results

Model selection identified that a MSIRS (maternally acquired immunity, susceptible, infected, recovered, susceptible) model provided the best predictive performance. This model reliably predicted the timing of peak coronavirus circulation in neighbouring Thailand. Results indicate that bat reproductive phenology together with coronavirus-specific transmission and immunity parameters are sufficient to generate regular annual peaks in viral shedding. More complex, non-annual dynamics were only detected in parameter regions outside the posterior and prior distributions of the best-supported model. The random forest analysis revealed that the basic reproductive ratio (R0) and the rates of recovery, maternal immunity loss, and transmission, exerted the strongest influence on the complexity of infection dynamics.

Conclusions

These results suggest that predictable annual cycles of coronavirus shedding arise naturally in *P. lylei*. This implies that surveillance could be transformed from a resource-intensive year-round effort into a targeted, timely intervention. Our framework exemplifies how integrating wildlife ecology, epidemiological modelling, and field data can facilitate anticipatory, cross-sectoral zoonotic risk management at the human-animal-environment interface. The findings enable veterinary and public health agencies to synchronise sampling, biosecurity measures, and community outreach with predicted shedding peaks, within Cambodia and the wider Mekong region.

1269 – Five species feces: Metagenomic virome analysis of feces of five northern European bat species

Ella SIPPOLA (1), Elena SGARABOTTO (1), Mert ERDIN (1), Thomas LILLEY (1), Viktor OLANDER (1), Teemu SMURA (1), Kati SUOMINEN (1), Tarja SIRONEN (1), Eda ALTAN (1), Melissa MEIERHOFER (1,2)

1: University of Helsinki, Finland; 2: University of Cincinnati, Ohio, USA

Background

Bats are a species-rich group offering a multitude of ecosystem services, and they share a long history of co-existence with humans, often roosting in anthropogenic structures. In addition, bats have a unique immune system allowing them to withstand infections that in other organisms can cause more severe pathology. Together, these characteristics make bats an important study organism from the One Health perspective. In the last decade, high-throughput sequencing and metagenomic virome analyses have advanced research on bat-associated viruses, however studies still remain limited in Northern Europe.

Methods

We conducted a RNA virome analysis on 15 individual bat fecal samples collected in Finland and Latvia. These bats belong to five species known to roost in anthropogenic structures in Northern Europe – *Eptesicus nilssoni*, *Myotis brandtii*,*Myotis mystacinus*, *Pipistrellus nathusii* and *Plecotus auritus*. Sequences were assigned to 33 families using theLazypipe de novo assembly NGS pipeline for virus discovery. We further analyzed the phylogenetic relationships of a subset of these viral families with known zoonotic potential or of which our sequences represented novel findings.

Results

The results revealed sequences belonging to several viral families known to infect mammals, including *Circoviridae, Coronaviridae, Hepeviridae, Parvoviridae, Picornaviridae,* and *Polyomaviridae*. Among these, the highest number of sequences corresponded to the *Parvoviridae* family, which was detected in all collected fecal samples. Following *Parvoviridae*, sequences belonging to the *Picornaviridae* family were detected in seven samples, revealing a high diversity of sequencing belonging to this family. In addition, sequences clustering with MERS-Like coronaviruses (Merbecovirus) were identified in one sample, and a putative novel virus was detected with high distance to any known viral families except *Hepeviridae* was detected in another sample. Furthermore, one sample contained sequences associated with a *Polyomavirus*. In addition to mammalian viruses, a large number of sequences corresponding to insect-associated viruses were detected.

Conclusions: This study characterizes bat fecal viromes and expands our knowledge of bat-associated viruses, particularly in northern Europe, where studies remain limited. Novel sequences discovered in this study contribute to our understanding of viral diversity, also within viral families with known zoonotic potential.

1271 – An unwanted Christmas gift: detection of West Nile Virus in mosquitoes in December

Maria Liliana DI PASQUALE, Francesco LA RUSSA, Eugenia OLIVERI, Sara Mariolina VILLARI, Pietro RIOLO, Francesca GUCCIARDI, Marzio COMETA, Germano CASTELLI, Federica BRUNO, Francesca DI GAUDIO, Fabrizio VITALE

Istituto Zooprofilattico Sperimentale della Sicilia "A. Mirri", Italy

Climate change is increasingly recognised as one of the main factors driving changes in the ecology and epidemiology of vector-borne diseases. Rising temperatures, milder winters and changes in seasonal patterns can affect vector survival, pathogen reproduction and development, potentially prolonging transmission seasons and altering geographical distribution.

Within the One Health framework, understanding these climate-driven changes requires integrated surveillance of vectors, wildlife, humans, and the environment.

West Nile virus (WNV), a mosquito-borne virus that maintains an enzootic cycle between birds and mosquitoes, is one of the most important emerging arboviruses in Europe. In Italy, national and regional surveillance plans monitor WNV circulation during the vector activity season, typically focusing on late spring to autumn when mosquito abundance is highest. However, climatic anomalies and milder winter temperatures may allow vectors to remain active longer than expected, potentially allowing the virus to circulate outside the traditionally monitored period.As established by the current National Surveillance Plan in Italy (National Arbovirus Plan, PNA 2020-2025), mosquito samples collected in southern Italy in December 2025 were analysed, even though the official surveillance season had already ended. The mosquito pools were treated and tested for the presence of arboviruses using molecular diagnostic methods and were found to be positive, highlighting a potential change in seasonal transmission dynamics.

These findings suggest that WNV circulation may persist longer in the year than previously assumed. Milder winter conditions, which are becoming more frequent in the Mediterranean region, may favour prolonged mosquito survival and maintenance of the virus within vector populations. Such climate-related ecological changes could reduce the predictability of transmission seasons and challenge current surveillance systems.

From a One Health perspective, the off-season detection of WNV in mosquito vectors highlights the importance of adaptive, climate-sensitive surveillance strategies. Continuous or extended monitoring of vector populations may be necessary to better capture changes in arbovirus circulation patterns. Furthermore, the integration of entomological, ecological, and climatic data could improve early warning systems and risk assessment models.Our observations contribute to the growing evidence that climate change may influence the temporal dynamics of vector-borne diseases in Europe. Strengthening interdisciplinary surveillance and integrating environmental indicators into public health strategies will be essential to anticipate emerging risks and protect human, animal and ecosystem health.

1281 – Global and Regional Drivers of Malaria Transmission and Elimination: An Integrated Analysis of Ecological, Financial and Policy Dimensions

Chenyu WANG (1,2), Caitlin BUTALA (1), Sue WELBURN (1,2)

1: University of Edinburgh, United Kingdom; 2: Zhejiang University – University of Edinburgh Institute (ZJE), Haining, China

Malaria remains one of the most significant global public health challenges. Despite substantial progress in malaria control since 2000, transmission persists in many regions. In 2024, an estimated 282 million malaria cases and 610,000 deaths were reported worldwide, with the majority occurring in sub-Saharan Africa. Malaria persistence is influenced by a combination of ecological and socio-economic factors, including climatic conditions favourable for mosquito breeding, widespread poverty, and limited access to healthcare infrastructure.

This research examines the spatial heterogeneity of global malaria transmission, identifies key drivers of malaria persistence, and evaluates strategies that support elimination. Using malaria incidence data from the World Health Organization alongside environmental indicators and vector distribution datasets, the study analyses global transmission patterns in 2024. Descriptive statistics, geographic information system (GIS) spatial mapping, and trend analysis are used to examine geographic variation in malaria burden. The results highlight strong regional contrasts, particularly between high-burden countries in sub-Saharan Africa and regions approaching elimination. The analysis further explores how ecological factors, including climate variation and dominant vector species, interact with socio-economic determinants such as healthcare infrastructure and population vulnerability.

A detailed case study of Jingdong County in Yunnan Province, China, illustrates how local interventions can achieve malaria elimination. Using unpublished surveillance records, demographic data, and entomological reports, the study evaluates the impact of China's “1-3-7” surveillance strategy, which requires case reporting within one day, investigation within three days, and response within seven days. These measures were supported by vector control interventions, including insecticide-treated nets and targeted spraying, as well as community engagement and cross-sector collaboration. Jingdong has maintained zero indigenous malaria cases for over a decade.

The study also examines malaria financing patterns in 37 African endemic countries between 2015 and 2024. Using WHO Global Malaria Reports and additional datasets including G-FINDER, IATI, and Devex, the analysis identifies substantial funding gaps and disparities in per-capita investment. Many high-burden countries remain heavily dependent on external assistance.

Overall, the findings highlight the importance of integrating ecological, socio-economic, and health system perspectives in malaria control. Sustainable financing, context-specific interventions, and cross-sector collaboration are essential to accelerate progress towards malaria elimination.

1288 – Integrated One Health Digital Platform for Transboundary Infectious Disease Outbreak Management

Dinesh MONDAL (9), Prakash GHOSH (1), Rea Maja KOBIALKA (1), Kostas DELAKOURIDIS (2), Leonidas KAZATZOPOULOS (2), Lotta Henni TRUYEN (1), Arianna CERUTI (1), Sara SAVIC (4), Luisa BARZON (3), Tamaš PETROVIC (4), Nazif ELALDI (5), Zati VATANSEVER (6), Manfred WEIDMANN (1), Julius Boniface OKUNI (7), Oumar FAYE (8), Martin PFEFFER (1), Uwe TRUYEN (1), Richard PAUL (10), **Ahmed ABD EL WAHED** (1)

1: Institute for Animal Hygiene and Veterinary Public Health, Leipzig, Germany; 2: UNIVERSITA DEGLI STUDI DI PADOVA, Department of Molecular Medicine (DMM), Padova, Italy; 3: UNIVERSITA DEGLI STUDI DI PADOVA, Department of Molecular Medicine (DMM), Padova, Italy; 4: SCIENTIFIC VETERINARY INSTITUTE NOVI SAD, NOVI SAD, Serbia; 5: SIVAS CUMHURIYET UNIVERSITESI, SIVAS, Turkiye; 6: KAFKAS UNIVERSITESI, KARS, Turkiye; 7: MAKERERE UNIVERSITY, KAMPALA, Uganda; 8: INSTITUT PASTEUR DE DAKAR, DAKAR, Senegal; 9: International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh; 10: Institut Pasteur Paris

Background: Increased global mobility, climate change, and environmental alterations have contributed to the rapid spread of zoonotic infectious diseases. Rapid identification of the causative agent during an outbreak is key to the timely implementation of effective control measures. The PREPARE-TID initiative has successfully developed and validated a comprehensive, end-to-end pipeline to enhance global capacity for the rapid detection, surveillance, and response to transboundary infectious diseases.

Methods: The project developed a digital One Health platform that integrates anonymized patient data resulting from diverse diagnostic methods directly in the field. The project is funded by the EU horizon program. By including samples from humans, animals, vectors (ticks, mosquitoes), and the environment, the system supports a comprehensive One Health approach to disease surveillance. This digital ecosystem combines a mobile application for field data collection with a web-based dashboard and features a pathogen traceability framework to map epidemiological links between humans, animals, and the environment.

Results: The platform's key features include 90-second real-time data entry, rapid data syncing, and syndromic data organization, which collectively reduce the time incurred by manual paper-based data entry by 85%. The integrated pipeline's capabilities were demonstrated in a series of real-world emergency deployments. The mobile application is on trial in Bangladesh and France.

Conclusions: Visualizing all results on a dashboard depicting an interactive map enhances situational awareness, enabling health authorities and researchers to monitor outbreaks and identify patterns. Real-time data accessibility allows experts to track disease transmission and implement timely interventions. This interconnected system ensures data-driven decision-making, revolutionizing global outbreak surveillance through faster detection and improved coordination of response efforts across borders.

1302 – National surveillance of non-typhoidal Salmonella in Vietnamese chickens reveals high but declining multidrug resistance and the emergence of serovars of public health significance

Ramon MALUPING (1), Thu Thuy NGUYEN (2), Thi Hue LE (2), Thi Phuong Loan NGUYEN (2), Thi Hue PHAN (2), Thi Kim Chung NGUYEN (2), Thi Trang PHAM (2), Thomas CHISNALL (1), Alistair DAVIES (1), Jazmin CONWAY (1), Juan CARRIQUE-MAS (3), Minh Hong NGUYEN (3), Pawin PADUNGTOD (3), Roderick CARD (1), Van Tuat CHU (2)

1: UK FAO Reference Centre for AMR, Animal and Plant Health Agency (APHA), Weybridge, United Kingdom; 2: Department of Animal Health and Production (DAHP), Hanoi, Vietnam; 3: Food and Agriculture Organization of the United Nations (FAO), Hanoi, Vietnam

Background:

Non-typhoidal *Salmonella* (NTS) is a leading cause of foodborne gastroenteritis worldwide, and poultry products are a major source of human infection. In Vietnam, previous studies have reported high levels of NTS contamination in poultry, but most investigations have been limited in scale and sampling representativeness. Furthermore, antimicrobial use in poultry production is extensive, raising concerns about the emergence and spread of antimicrobial resistance (AMR). This study aimed to characterise the diversity of NTS serovars circulating in Vietnamese chickens and to describe the phenotypic and genotypic AMR profiles of isolates collected through national surveillance between 2017 and 2023.

Methods:

A total of 498 NTS samples were collected through the Vietnamese national surveillance programme (2017–2023) from chicken cloacal swabs obtained at wet markets and slaughterhouses across multiple provinces. Of the 489 isolates recovered, 200 were randomly selected for further testing. These included antimicrobial susceptibility testing using broth microdilution (Sensititre™ EUVSEC3 plates) to determine

minimum inhibitory concentrations for 15 antimicrobials, with resistance interpreted using EUCAST epidemiological cut-off values. Isolates resistant to third-generation cephalosporins were further investigated using EUVSEC2 plates. Whole-genome sequencing was conducted to determine serovars, sequence types (ST), AMR genes (ARGs), and plasmid incompatibility types. Temporal trends in resistance were assessed using Cochran–Armitage trend tests and stratified analyses comparing early and late surveillance periods (August 2022–November 2023).

Results:

Thirty serovars and 46 sequence types were identified. Seven serovars accounted for 71.5% of isolates: *S.* Infantis (n=53; all ST32), *S.* Agona (ST13), *S.* Kentucky (ST198, ST314), *S.* Newport (ST46, ST4157), *S.* Corvallis (ST1541), *S.* Albany (ST292, ST3633), and *S.* London (ST155). Multidrug resistance (MDR) was observed in 72% of isolates, with the highest prevalence in *S.* Infantis (96.2%). Resistance to highest-priority critically important antimicrobials was common, including ciprofloxacin (77%) and nalidixic acid (76%), largely associated with *qnrS* and *gyrA* mutations. Resistance to third-generation cephalosporins was also substantial (cefotaxime 38%, ceftazidime 33.5%), mainly linked to *bla*CTX-M-65, *bla*CTX-M-14, and *bla*CTX-M-27 genes. Colistin resistance was low (4%) and mediated by *mcr-1* or *mcr-3*. No resistance was detected to amikacin or meropenem. Whole-genome analysis identified 66 ARGs and 33 plasmid incompatibility types, with strong concordance between phenotypic and genotypic resistance. Temporal analyses indicated significant reductions in MDR and resistance to four antimicrobials in the later surveillance period.

Conclusions:

This national surveillance study demonstrates substantial serovar diversity and high levels of MDR among chicken-origin NTS in Vietnam, particularly involving *S.* Infantis ST32. Although resistance to several antimicrobials has declined over time, resistance to critically important antimicrobials remains high. These findings provide an important national benchmark for monitoring NTS serovar distribution and AMR trends in poultry in Vietnam and will support future comparisons with human isolates to better understand the role of poultry in the burden of salmonellosis.

1308 – Building empirical virus-host networks from global to local contexts: a case study on mammal viruses in The Gambia

Jose Gabriel NINO BARREAT (1), David REDDING (1), Senzor CONSORTIUM (1,2,3,4)

1: Natural History Museum, London, United Kingdom; 2: Robert Koch Institut, Germany; 3: London School of Hygiene and Tropical Medicine, United Kingdom; 4: Institut de recherche pour le développement, France

Background

Mammals are the primary source of viruses of zoonotic concern. However, the circulation of viruses in wild species of mammals in natural ecosystems, and at the interfaces with humans and domestic animals is only incompletely known. In fact, surveys generally target a single or a few virus species and samples remain heavily skewed towards humans, domestic and peridomestic mammals, while many wild species remain overlooked. Metaviromic surveys of wild mammal species have the potential to bridge this gap, but still require a framework of prior knowledge on which to place their findings. We present a framework for synthesising the current knowledge of virus and mammal host associations in a region of interest, focusing on The Gambia as a case study. The framework integrates sources of global and local knowledge, making the synthesis highly relevant for scientists conducting surveys on virus ecology in the region, as well as for local veterinary and public health stakeholders.

Methods

We used two approaches to infer empirical networks for communities of viruses and their mammalian hosts in The Gambia: searching for virus-host associations reported globally for all terrestrial mammals present in the country (potential interaction network), and a systematic search of the primary literature for viruses described in the country together with their hosts (observed/sampled interaction network). First, we compiled a list of mammal species present in The Gambia by integrating species occurrence records from the Global Biodiversity Information Facility, the Mammal Diversity Database and Wikipedia. We then screened the NCBI Virus,Virus-Host and VIRION databases to retrieve all virus records at a global

level associated with the mammal species identified. For the second approach, research papers were systematically searched following the PRISMA-S guidelines to identify reports of viruses affecting mammals in The Gambia.

Results

The two empirical networks were constructed, visualised and compared in terms of topology and structural features such as size, composition, degree distributions, connectance, centrality and modularity metrics. We identified key differences in the empirical networks built by the global and local approaches. Graph Neural Networks (GNNs) were applied to the empirical network structure to investigate their potential in predicting unsampled virus-host associations for mammals in The Gambia.

Conclusions

By combining information of virus-host associations in publicly accessible databases at a global scale, with primary literature at a local level, it was possible to build informative empirical networks of observed associations between viruses and mammals in The Gambia. This provides a framework on which to contextualise findings of metagenomic and targeted virus surveys in The Gambia, and also to inform the priorisation of future sampling efforts.

1321 – Food for thought: The role of One Health in keeping what we eat safe

Jorge PINTO FERREIRA (1), **Celia MANAIA** (2), **Lawrence GOODRIDGE** (3), **Alejandra LATORRE** (4), **Maura DI MARTINO** (1), **Fong/Tammy WONG** (5), **Jeffrey LEJEUNE** (1)

1: Food and Agriculture Organization of the United Nations (FAO), Italy; 2: Universidade Catolica Portuguesa, Portugal; 3: University of Guelph, Canada; 4: Universidad de Concepcion, Chile; 5: 636 Hospitality/Rainbow Chinese Restaurant, USA

Through the act of eating, we intentionally expose ourselves to components from the environment (foods of plant origin, water) and animals (meats, seafoods, eggs, milk, honey). Thus, food, although seldomly explicitly stated, sits at the nexus of the human–animal–plant–environment interface. The interactions and complexities of agrifood systems involved in food production and processing may affect the health of animals, plants, and result in environmental degradation. Reciprocally, the food production environment, the health of animals and the contamination of plants with zoonotic pathogens and chemical contaminants may impact food safety. This intimate interconnectivity within agrifood systems means a One Health approach is critical to addressing food safety. And food safety is critical to promoting One Health.

With a global burden of foodborne illnesses exceeding 2 billion cases annually, food safety remains a globally relevant challenge affecting everyone, requiring collaboration, coordination, and communication across ministries, sectors, and disciplines, thereby making it a topic of interest for scientists, regulators, policymakers, and practitioners alike. This session will highlight the interconnectedness of various social, biological, and environmental thematic elements and provide real-world examples of how One Health principles and approaches are being leveraged to understand and address food insecurity and global health caused by unsafe food. Discussion on food inherently engages diverse ministries, academic, non-governmental organizations and private stakeholder partners and opens door for policy-relevant discussions. The proposed speakers (below) in this session represent a gender balanced and inclusive slate of experts from multiple geographical regions, career stages and sectors that will tackle an often unappreciated, yet critically important, aspect of one health—food safety.

1327 – Operationalizing environmental health systems surveillance through the integration of an environmental module in an established open-source digital surveillance platform

Emeline JANIGAN, Pilar HERNANDEZ

SORMAS Foundation, Germany

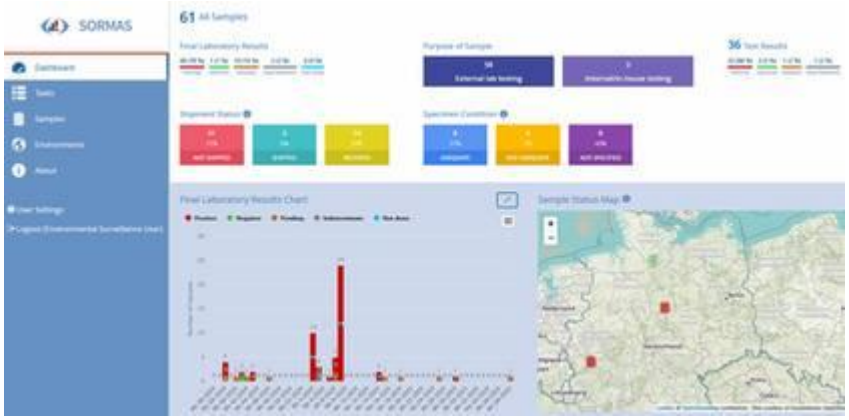
Background: Environmental health systems surveillance requires interoperable, integrated digital infrastructures to support the monitoring of environmental hazards and population health impacts. This work describes the design and development of an environmental surveillance module within the digital

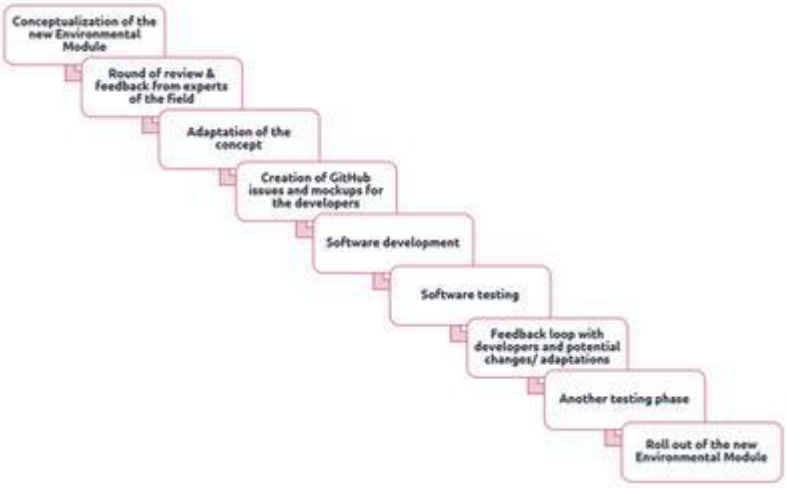
Surveillance Outbreak Response Management and Analysis System (SORMAS). SORMAS is an open-source system that enables routine disease surveillance, early detection, and outbreak management. It facilitates multidirectional data exchange among users and supports over 40 infectious diseases and is used in multiple countries across five continents. The integration of this module facilitates data collection and processing of environmental samples, analysis, and human data as a first step into a full one health approach.

Methods: The module was designed and developed following an iterative, user-centered approach, with public health experts informing requirements, usability, and system integration. In Phase I, the initial concept was developed and refined through expert consultation and feedback. This concept was then integrated in Phase II, initiating another feedback loop. Once the concept was finalized, features were programmed and completed in a preliminary version. This initial version was then tested, and feedback was collected from future users and experts, which was incorporated into a subsequent development cycle. The first version of the module is complete and deployed for live operation. We are currently gathering feedback on usability and other requirements for further expansion.

Results: The environmental surveillance module is an extension of the existing SORMAS architecture, leveraging its case-based surveillance framework and interoperability capabilities. It enables documentation of environmental exposures, periods, categories, and contextual data. It allows users to enter and analyze environmental samples such as water, soil or rock, air, biota, and vectors. The location of these samples is recorded on a map, enabling real-time analysis and early detection of increased occurrences in specific areas. For example, if a body of water is contaminated with cholera, users can track cases, water samples, local events and event participants on the map and use this information to support decision-making. The integration of the environmental module expands SORMAS from a human-focused surveillance tool to integrate human and environmental health surveillance in one system. This offers a baseline for public health investigation strategies, enabling consistent documentation, and assessment of environmental risks factors. An interoperable design allows alignment with existing workflows while maintaining flexibility for future data sources and indicators.

Conclusion: The addition of an environmental module to SORMAS demonstrates how existing systems with public health relevant data can be used and extended to support environmental health systems surveillance. Embedding environmental data within an established disease surveillance infrastructure enhances early detection, risk assessment, and evidence-based decision-making. This implementation illustrates a scalable approach for strengthening environmental health surveillance capacities in routine and incident-driven contexts.





1333 – Applying Systems Thinking in One Health: Mapping Community Engagement in the HEAL Socio-Ecological System

Agathe J. VERHULST (1), Simon R. RÜEGG (2), Siobhan MOR (3,4), Lian THOMAS (3,5)

1: Veterinary Public Health Institute, University of Bern, Switzerland; 2: Section of Epidemiology, University of Zurich, Switzerland; 3: International Livestock Research Institute, Nairobi, Kenya; 4: Institute of Infection, Veterinary & Ecological Sciences, University of Liverpool, United Kingdom; 5: Division of Global Agriculture and Food Systems, University of Edinburgh, United Kingdom

Background: Health outcomes emerge from the dynamic interplay between human, animal, and environmental systems. The One Health approach calls for transdisciplinary collaboration, the inclusion of diverse knowledge systems, and the ability to navigate systemic complexity. While community engagement is increasingly recognised as essential for effective One Health implementation, practical examples illustrating how community voices influence system dynamics remain limited. This study explores how Systems Thinking can be applied to map and understand the role of community engagement within complex socio-ecological systems.

Methods: Using the Kenya subsystem of the HEAL (One Health for Humans, Environment, Animals and Livelihoods) project as a case study, this research applied a qualitative Systems Thinking approach. Secondary data analysis was combined with eleven semi-structured interviews with stakeholders involved in the HEAL system. Systems mapping tools, including Rich Pictures and Causal Loop Diagrams, were used to visualise stakeholder relationships, feedback loops, and systemic dynamics shaping community engagement.

Results: The analysis identified a multi-level governance system linking community actors, service delivery platforms, and institutional stakeholders. Three integrative platforms—the Multi-Stakeholder Innovation Platforms (MSIPs), One Health Units (OHUs), and One Health Task Forces (OHTFs)—emerged as

key connectors between local communities and higher-level governance structures. Systems mapping revealed reinforcing feedback loops linking systemic trust, advocacy, governance uptake of the health delivery model, and community-based monitoring. Together they shape the uptake and sustainability of integrated One Health services in pastoralist contexts. Community engagement through MSIPs strengthened local ownership and the contextual relevance of interventions but remained sensitive to power dynamics and institutional support.

Conclusions: Applying Systems Thinking provides a valuable lens for visualising and navigating complexity within One Health initiatives, making interdependencies and leverage points visible. This case study illustrates how community engagement mechanisms can strengthen the responsiveness and sustainability of integrated health services in pastoralist socio-ecological systems. The approach provides a practical example of how Systems Thinking can contribute to more inclusive and context-sensitive One Health implementation.

Figure 1: Rich Picture of the HEAL Socio-Ecological System (SES), visualizing stakeholder interactions and system dynamics, based on secondary data and developed using Adobe Fresco (Multi-layered file)

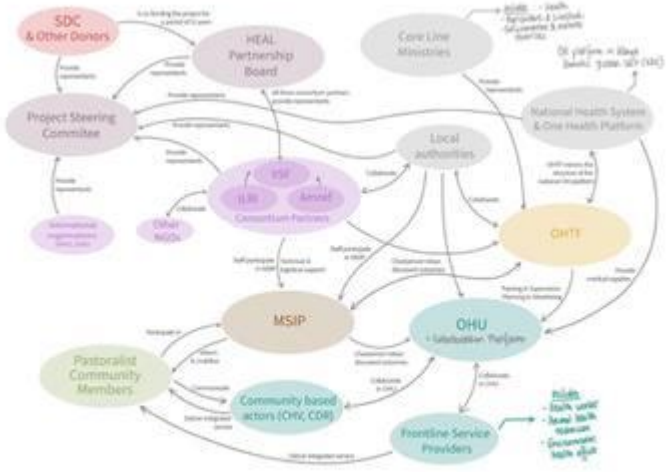


Figure 2: Stakeholder groups cited in Mor et al. (2024) mapped according to their interconnections within the HEAL system, following the method proposed by Elias et al. (2001). Arrows represent institutional linkages and collaboration pathways connecting community actors with One Health governance and service delivery structures.

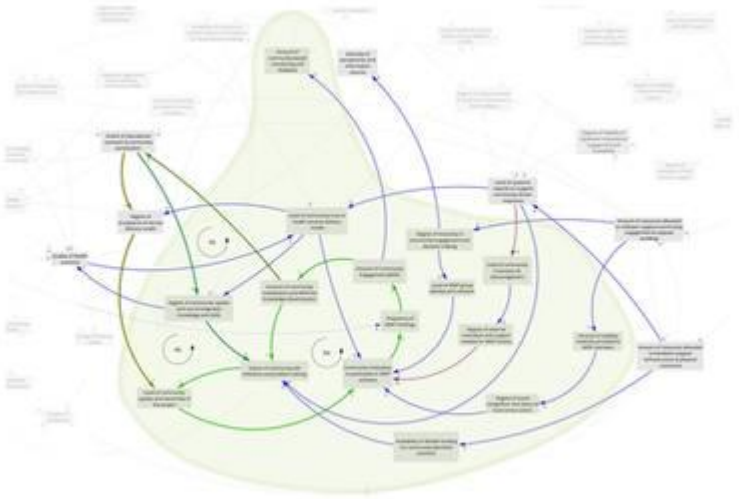


Figure 3: Zoomed-in view of the HEAL Causal Loop Diagram, highlighting feedback pathways linking community engagement, knowledge dissemination, and the uptake and ownership of integrated One Health services.

1337 – Applying Social Entrepreneurship for One Health and Climate Education: A Retrospective Analysis of Pre- and Post-Course Evaluation Data for a One Health and Global Food Security Course

Brianna PARSONS (1,2), Brittany WATSON (1)

1: University of Pennsylvania, School of Veterinary Medicine, Philadelphia, United States of America; 2: FAIR Farms Gambia, www.fairfarmsgambia.com, Busura, The Gambia

Background: One Health is a concept of interconnectivity between human, animal, and environmental health, as well as an approach to creating stronger health systems and outcomes for all. Teaching One Health as an approach is difficult pedagogically as it requires both acquisition of new knowledge and the application of that knowledge (the One Health approach) to be effective. Several core competencies have defined essential skills and behaviors to support One Health education (Frankson et al. 2016; Togami et al. 2018; Larsen 2021; Laing et al. 2023), but more work is needed to fully operationalize the field (Zinsstag et al. 2023; Winkler et al. 2025). Social entrepreneurship is a systems-thinking approach praised for creating social change by developing new business models that blend financial revenue with social impacts (Montgomery et al. 2012; Gupta et al. 2020; Kickul et al. 2022). This approach can help provide an application-based paradigm to increase systems thinking in One Health education.

Methods: We evaluate how careful integration of social entrepreneurship into the One Health and Global Food Security course supported students' learning through a retrospective analysis of participant-matched pre- and post-course surveys from undergraduate, graduate and professional students enrolled in the course in years 2024 (n=11) and 2025 (n=9). Several Likert-scale questions ask student participants to self-assess knowledge across key topics, rank importance of these topics to global health, rank classroom activities impact on learning, and remark on likeliness to engage in future activities related to the course and social entrepreneurship. Descriptive statistics and Wilcoxon Signed Rank tests are performed to understand student learning outcomes from this One Health course.

Results: Students' self-assessed knowledge of six key topics (food systems, sustainability, social entrepreneurship, one health, global food security, impact assessment) increased significantly (p.001) through participation in the course, as shown in **Table 1**. Students' understanding of social entrepreneurship increased, as evaluated by significant improvements (p.001) to rubric-graded definitions of the term pre- and post-course. Students rated several aspects of applied social entrepreneurship (pitch presentation, case study project) as highly impactful to their learning. Additionally, students were likely to use social entrepreneurship in their future and to recommend social entrepreneurship as a tool for climate action.

Conclusions: Taken together, these results suggest social entrepreneurship course content can support One Health education. As the One Health field contemplates strategies for operationalization, social

entrepreneurship can be a relevant systems-thinking approach. Further research can explore efficacy of additional One Health curriculums and approaches for integrating social entrepreneurship, to understand most effective pedagogies for practical instruction of these concepts. This course is one of several One Health courses run through Penn Vet School as part of an emerging One Campus One Health certificate program, open to undergraduate, graduate and professional students.

Table 1: Descriptive Statistics for Pre- and Post Course Self-Assessed Knowledge Scores when asked "How would you quantify your knowledge for the following topics from 1 (none at all) to 5 (a great deal)"

Combined 2024 - 2025	Pre/ Post	N	Mean	Median	Std. Dev.	Min.	Max.	P Value	Effect size (r)
Food Systems	Pre	20	2.60	2.5	1.095	1	5	<.001*	0.75
	Post	20	3.95	4.0	.686	3	5		
Sustainability	Pre	20	2.60	3.0	.598	2	4	<.001*	0.85
	Post	20	4.0	4.0	.649	3	5		
Social	Pre	20	1.9	2.0	.788	1	3	<.001*	0.86
Entrepreneurship	Post	20	3.80	4.0	.696	2	5		
One Health	Pre	20	3.15	3.0	1.04	1	5	<.001*	0.80
	Post	20	4.50	5.0	.607	3	5		
Global Food	Pre	20	2.35	2.0	.745	1	4	<.001*	0.87
Security	Post	20	4.20	4.0	.696	3	5		
Impact	Pre	20	1.8	2.0	.834	1	4	<.001*	0.89
Assessment	Post	20	3.95	4.0	.887	2	5		

1344 – Invasive mosquitoes at the Gate: surveillance of exotic species in sicilian Points of Entry (PoE)

Francesco LA RUSSA, Maria Liliana DI PASQUALE, Eugenia OLIVERI, Sara Mariolina VILLARI, Pietro RIOLO, Marzio COMETA, Silvia SCIBETTA, Stefano REALE, Fabrizio VITALE, Francesca DI GAUDIO

Istituto Zooprofilattico Sperimentale della Sicilia "A. Mirri", Italy

Globalization, intensified trade, and increasing international mobility have significantly enhanced the risk of introduction and spread of invasive vectors and vector-borne pathogens. Ports, airports, and other Points of Entry (PoE) represent critical interfaces where human activity, goods movement, and ecological processes intersect. Within a One Health framework, entomological surveillance at PoE plays a crucial role in preventing the establishment and dissemination of invasive mosquito species and the pathogens they may carry, particularly in the context of climate change and environmental transformation.

Climate warming and changing ecological conditions are expanding the suitable habitats for many vector species, increasing the probability that introduced mosquitoes may survive, establish local populations, and contribute to the transmission of arboviruses. In Mediterranean regions, where climatic conditions already favor mosquito proliferation, early detection of invasive vectors is essential to mitigate potential public health risks. As part of a structured entomological monitoring program, mosquito surveillance activities were conducted at selected Points of Entry in Southern Italy. The surveillance strategy included systematic sampling using ovitraps and adult mosquito traps positioned in strategic locations within port and airport areas characterized by intense international traffic and the movement of goods. Sampling was designed to detect both native mosquito populations and potential introductions of invasive species associated with transport routes.

Collected specimens were morphologically identified and, when necessary, confirmed through molecular approaches to ensure accurate species determination. Particular attention was given to species recognized as competent vectors of arboviruses affecting human and animal health. The surveillance system aimed to provide early detection of exotic species and to support rapid response measures if introductions were identified.

The results of this monitoring activity confirmed the presence of several mosquito species already established in the region and highlighted the continued vulnerability of Points of Entry as gateways for vector introduction. The findings emphasize the importance of maintaining continuous and structured entomological surveillance in high-risk locations where environmental suitability, international trade,

and human mobility converge. Within the One Health perspective, surveillance at Points of Entry represents not only a biosecurity measure but also an essential component of climate-adaptive health systems. Integrating entomological monitoring with environmental data, climate indicators, and epidemiological surveillance can enhance early warning capacities and support evidence-based risk assessment. Strengthening surveillance infrastructures at Points of Entry is increasingly important as climate change reshapes vector ecology and extends the potential range of mosquito species capable of transmitting pathogens. Proactive monitoring and coordinated responses between public health, veterinary, and environmental sectors are therefore essential to protect human, animal, and ecosystem health in an interconnected and rapidly changing world.

1349 – A multisectoral One Health analysis of climate change impacts, vulnerabilities, and adaptation in Rwanda

Dr Maria Albin QAMBAYOT, Prof Rex WONG, Prof Phaedra HENLEY
University of Global Health Equity, Rwanda

Background; Climate change and its effects on human, animal, and environmental health are closely intertwined, making it a critical One Health concern mostly in low-resource settings where communities rely heavily on climate-sensitive livelihoods and have limited adaptive capacity. However, evidence from frontline professionals who directly observe these impacts across sectors remains limited. This study examined the multifaceted evindece on vulnerabilities, impacts and adaptation of climate change through a One Health lens, from the perspectives of frontline health professionals in Rwanda.

Methods; Using an exploratory design, 97 in-depth interviews were conducted with frontline health professionals, including community health workers, medical practitioners, veterinary officers, and environmental officers, in five districts identified as highly vulnerable to climate change. The findings from this phase were also intended to inform the development of a monitoring and evaluation framework capable of supporting future real-time assessment of climate-related health impacts. Data were collected through in-depth interviews (IDIs) using a semi-structured interview guide. Interviews were conducted with key frontline professionals from the three One Health domains, including community health workers, nurses, doctors, veterinary officers, and environmental health officers. Participants were purposively sampled based on their professional roles and their likely experience with climate-sensitive health, animal health, and environmental health issues within their communities. Data was analyzed using thematic analysis and the results were presented as emerging themes and subthemes.

Results; Findings indicate that shifting weather patterns contribute to rising respiratory illnesses, skin conditions, and delayed wound healing in humans, while extreme events like floods and landslides exacerbate injuries and mental health challenges. Altered rainfall and drought patterns intensify waterborne diseases, food insecurity, and malnutrition, particularly among children, straining already burdened health systems. For animal health, climate change drives outbreaks of diseases such as Rift Valley Fever and tick-borne illnesses, alongside livestock mortality, reduced productivity, and economic losses. Environmental health is compromised through land degradation, soil erosion, and water contamination, threatening agricultural productivity and water security. Community vulnerabilities included demographic factors like age, gender, and occupation, with children, the elderly, and certain workers being disproportionately affected. Geographic and economic constraints further exacerbate exposure to health risks and limit preventive measures. Adaptation strategies identified include the promotion of climate-resilient crops, soil conservation, water storage improvements, and stricter environmental regulations. However, challenges such as resistance to behavioral change, urbanization, and competing priorities hinder sustainable adaptation.

Conclusion; The study underscores the necessity of integrated, multisectoral approaches that address ecological, social, and economic dimensions to enhance community resilience. Coordinated efforts across sectors are essential to mitigate vulnerabilities and strengthen adaptive capacities in regions affected by climate change.

1353 – Community evidence for the incremental benefit of integrated One Health Unit service delivery in pastoral areas of Ethiopia and Kenya

Gezahegn ALEMAYEHU (1), Zelalem TERFA (1), Buke WAKO (2), **Siobhan MOR** (3)

1: International Livestiock Research Institute, Ethiopia; 2: International Livestiock Research Institute, Kenya; 3: University of Liverpool, UK & International Livestiock Research Institute, Kenya

Background:

Pastoral communities in the arid and semi-arid lands of the Horn of Africa face disproportionate barriers to accessing human, animal, and environmental health services. The HEAL project introduced One Health Units (OHUs) in remote pastoral areas of Ethiopia and Kenya to improve service delivery to these areas. This study evaluated community awareness, utilisation, and perceptions of the OHU model, identifying attributes, challenges, and pathways toward sustainability.

Methods:

A qualitative study was conducted across five HEAL sites: Borana (Oromia), Dawa and Filtu woredas (Somali region) in Ethiopia, and North Horr (Marsabit) and Merti (Isiolo) in Kenya. Data were collected through 23 Key Informant Interviews and 12 gender-segregated Focus Group Discussions with pastoral community members and multisectoral stakeholders. Semi-structured guides incorporated participatory techniques (proportional piling, pairwise ranking). Qualitative data were analysed thematically; participatory data were aggregated across sites and gender groups.

Results:

Awareness of the One Health Unit approached 100% in all sites. Participants reported that before OHU introduction, human and animal health services were fragmented, inaccessible, and uncoordinated; animal health relied largely on self-treatment with market-purchased drugs and sporadic vaccination campaigns. Following introduction of the OHUs, utilisation of services increased substantially, including medical consultations, antenatal and postnatal care, child immunisation, nutrition screening, and livestock treatment. Environmental and rangeland health had the lowest utilisation, though WASH practices, water handling, waste management, and rangeland stewardship improved.

Participants reported improved health-seeking behaviours including earlier care-seeking for maternal and child health, shifts from traditional to formal services, and improved antimicrobial stewardship including observing withdrawal periods before consuming milk; these were associated with perceived improvements in livestock productivity, maternal and child health outcomes, and household nutrition. Communities attributed these changes to the integrated OHU model rather than individual sectoral services, ranking One Health integration and accessibility as the most valued attributes. Highest-priority services included One Health awareness, antenatal care, and AMR awareness; animal vaccination and family planning were lower priorities. Persistent challenges included mobility, remoteness, supply shortages, cultural practices, and donor dependency. Sustainability pathways included community willingness to contribute financially, revolving drug funds and community insurance schemes (Ethiopia), emerging county government ownership (Kenya), and MSIP-based local governance across both settings.

Conclusions:

These findings indicate that OHUs substantially increased utilisation of human and animal health services in pastoral settings where access was previously minimal and were associated with perceived improvements in health-seeking behaviour, livestock productivity, and household livelihoods. Community valuation was high and cost-sharing mechanisms were emerging, though affordability constraints and donor dependency remain unresolved. Pastoral mobility, supply shortages, and workforce limitations constrained service coverage despite increased demand. Economic studies evaluating the costs of the OHU model are ongoing and will be critical to informing longer-term health systems integration.

Figure 1: Proportion of the community that is aware of One Health Unit (OHU) services across human health, animal health, and rangeland sectors, as estimated by participants using proportional piling during FGDs.

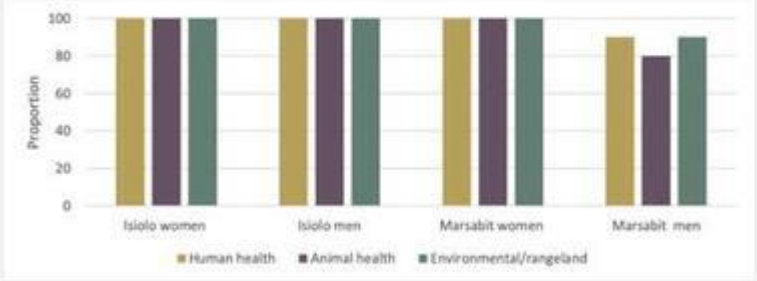
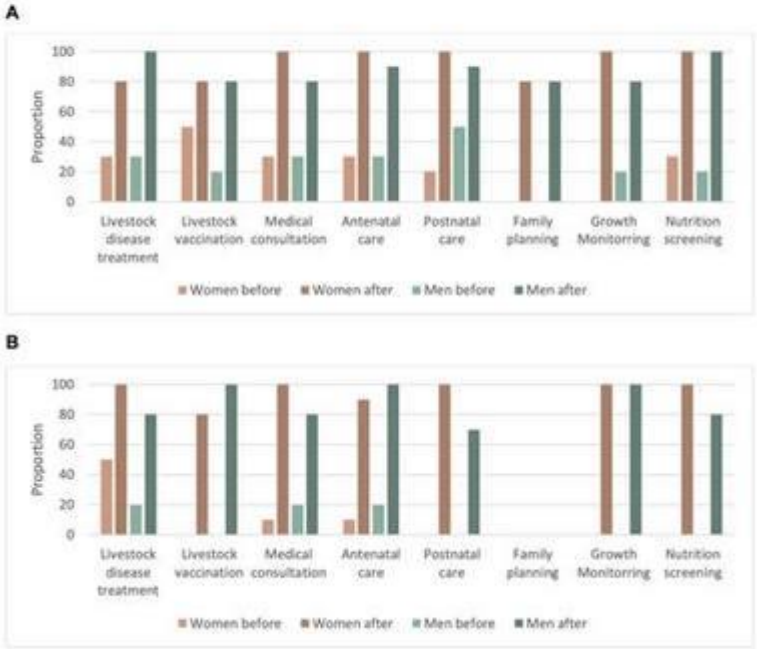


Figure 2: Estimated proportion of the community utilizing OHU services before and after establishment of the community-based OHUs in (A) Isiolo and (B) Marsabit. Values represent community estimates generated through proportional piling during FGDs.



1357 – Restoring nature's health: Investigating the effects of ecosystem restoration on zoonotic disease risk.

Cato VANGENECHTEN (1,2), Pauline VAN LEEUWEN (1,3), Claude MANDE (1,4), Steve NGOY (4), Pascal BAELO (4), Ali-Hassan TWAHA (4), Corneille KAHANDI (4), Madeleine ALIMASI (4), Joel KANGO (4), Moïse Bipoo AKAWA (4), Tine COOREMAN (1,2), Emilie GOOSSENS (2,5,6), Herwig LEIRS (1), Sophie GRYSEELS (1,7), Vincent SLUYDTS (1), Guy-Crispin GEMBU (4), Lucinda KIRKPATRICK (8), Joachim MARIËN (2)

1: The Evolutionary Ecology Group, Department of Biology, University of Antwerp, Antwerp, Belgium; 2: The Virus Ecology Unit, Department of Biomedical Sciences, The Institute of Tropical Medicine, Antwerp, Belgium; 3: Laboratory of Conservation Genetics, Faculty of Sciences, Université de Liège, Liège, Belgium; 4: Centre de Surveillance de la Biodiversité (CSB), Université de Kisangani, Kisangani, The Democratic Republic of Congo; 5: Research Group Zoology: Biodiversity & Toxicology, Centre for Environmental Sciences, Hasselt University, Diepenbeek, Belgium; 6: Department of Biology, Royal Museum for Central Africa, Tervuren, Belgium; 7: The Taxonomy and Phylogeny Unit, Institute of Natural Sciences, Brussels, Belgium; 8: School of Environmental and Natural Sciences, Bangor University, Bangor, United Kingdom

Background: Emerging infectious diseases pose a significant threat to global public health. Among the factors contributing to the increase of emerging infectious diseases today, ecosystem degradation stands out as a prominent driver, exerting both direct and indirect influences on disease dynamics. While it is commonly assumed that simply reversing ecosystem degradation will restore disease regulation mechanisms, such a presumption may oversimplify the complex responses that are involved. Within the RESTOREID project, we aim to investigate how ecosystem restoration influences zoonotic disease risk, focusing on small mammal host and microparasite diversity.

Methods: Here, we report on a case study with samples collected across fifteen sampling sites along a restoration gradient in the Yangambi Biosphere Reserve (Democratic Republic of the Congo), representing four stages of restoration (i.e. 5 years old, 15-20 years old, 70-80 years old, and >150 years old). Using integrated field approaches—including small mammal trapping, invertebrate-derived DNA (iDNA), environmental-derived DNA (eDNA), and passive acoustic monitoring—we will assess how host diversity changes over time since restoration. In parallel, PCR-based screening will target RNA viruses commonly associated with African small mammals (*Flaviviridae*, *Paramyxoviridae*, *Filoviridae*, and *Arenaviridae*) to examine links between host diversity and viral dynamics.

Results: A total of 486 terrestrial small mammals (rodents and shrews), 388 bats, and 810 carrion flies were collected. In addition, 20 vegetation swabs and approximately 2000 acoustic recordings per site were obtained. Analyses of iDNA demonstrate that carrion flies enable the detection of small mammal DNA across the restoration gradient, revealing differences in host diversity among sites, with older secondary forests supporting higher diversity than other sampled locations. Additionally, viral screening indicates circulation of RNA viruses within small mammal communities, with variation among host taxa. Ongoing work will further investigate how patterns of viral diversity and prevalence relate to host biodiversity and time since ecosystem restoration.

Conclusions: By linking changes in wildlife communities with pathogen dynamics, this study provides initial insights into how ecosystem restoration may reshape zoonotic disease risk. Our findings highlight the importance of integrating biodiversity monitoring and pathogen surveillance within a One Health framework for landscape restoration.

1365 – Implementating One Health for rabies control in Cameroon- The Rabies Control and Elimination (RACE) program

Rodrigue Simonet POUEME NAMEGNI (1), **Katherine WORSLEY-TONKS** (2), **Elisabeth DIBONGUE** (7), **Sebastien DJIENOUASSI** (8), **Alvine AMAVOTA** (7), **Linda ESSO** (6), **Inès EMAH MANDA:** (6), **Jean-Marc FEUSSOM** (10), **Marie Paulette DEYA-YANG** (10), **Monique LECHENNE** (4,5), **Magloire Eleonore TCHAMBA** (10), **Stephanie MAUTI** (4,5), **Serge Eugene MPOUAM** (9), **Richard NJOUOM** (3), **Perrine PARIZE** (2), **Gregorio TORRES** (9), **Conrad NTOH NKUO** (7), **Ambroise GARGA GONNE** (10), **Jakob ZINSSTAG** (4,5), **Mathurin Cyrille TEJIOKEM** (1), **Hervé BOURHY** (2)

1: Epidemiology and Public Health Service, Centre Pasteur du Cameroun, Yaoundé, Cameroon; 2: Institut Pasteur, Université Paris Cité, Lyssavirus Epidemiology and Neuropathology Unit, Paris, France; 3: Virology Department, Centre Pasteur du Cameroun, Yaoundé, Cameroon.; 4: Swiss Tropical and Public Health Institute, Allschwil, Switzerland.; 5: University of Basel, Basel, Switzerland; 6: Direction de le lutte contre les maladies, les épidémies et les pandémies (DLMEP), MINSANTE, Yaounde, Cameroon; 7: Programme National de Prévention et de Lutte contre les Zoonoses Emergentes et Ré-émergentes (PNPLZER), plateforme Une Seule Santé au Cameroun; 8: Cellule des Enquêtes et des Statistiques MINEPIA, Yaounde, Cameroon; 9: World Organisation for Animal Health (WOAH); 10: Direction des Services Vétérinaires (DSV), Yaounde MINEPIA

Background

Rabies remains a major global public health problem and is endemic in several countries in Africa and Asia. It is the first priority zoonosis in Cameroon following a multisectoral One Health approach. That is why, in line with the Global Strategic Plan to End Human Deaths from Dog-Mediated Rabies by 2030, developed by the Tripartite organizations (WHO, WOAH, FAO) in 2018, Cameroon developed an integrated national strategic plan for rabies elimination.

Methods

To support the implementation of this strategy, the Rabies Control and Elimination (RACE) program was launched in Cameroon with financial support by BMZ through the World Organisation for Animal Health (WOAH). Implemented over a five-year period using the “One Health” approach, the program aims to strengthen surveillance, mass vaccination of dogs, and management of human exposure to rabies. In

order to evaluate its implementation, activities were carried out in two pilot regions (Centre and Far North), covering nine departments.

Results

After three years of implementation, activities co-developed with stakeholders have strengthened community-based surveillance through the involvement of Community Health Workers from both the animal and human health sectors in reporting rabies alert signals. The decentralization of rapid diagnostic tests across the nine pilot departments enabled the detection of 70.27% (26/37) of confirmed canine rabies cases between 2024 and 2025 by trained veterinary personnel. Increased awareness and training of medical staff on sample collection and shipment to laboratories improved human rabies surveillance, going from zero human samples submitted in the previous five years to 23 suspected samples in 2025, including six confirmed cases. To mitigate the lack of data on the dog population size, a cross-sectional survey conducted in 2023 estimated the canine population in the Central and Far North regions at 421,505, corresponding to a human-to-dog ratio of 15/1. Following multiple awareness campaigns in schools and among 2,500 administrative authorities, community leaders, and religious leaders in the pilot departments, three mass vaccination campaigns were conducted, resulting in the vaccination of 264,198 animals, including 226,886 dogs. A significant increase in the vaccination coverage rate of dogs at the household level was observed, rising from 52% in 2023 to more than 80% in 2025.The innovation of these mass vaccinations was the complete digitalization of vaccination activities, enabling real-time monitoring through the national tool CAHIS (Cameroon Animal Health Information System). Prophylaxis accessibility and availability in rural areas for populations exposed to the rabies virus have been improved by the operationalization of three rabies vaccination centers in the Far North region.

Conclusion

The lessons learnt through the RACE program are helping inform the transition towards sustainability and national ownership. Scaling-up these activities across the country will be essential to achieve the goal of zero human deaths from dog-transmitted rabies by 2030.

1369 – Assessment of bacteriological water quality and perception of health risks associated with the use of Funa River water in Kinshasa: an integrated One Health approach

Blaise MBIALA VODIASILUA (1,2), Liévins NTUMBA MAMONEKENE (4), Victor NDADI NKUEMBE (1), Esther KIMARO GWAE (3), Diafuka SAILA NGITA (1)

1: Faculty of Veterinary Medecine, Université de Kinshasa, Kinshasa, Congo, Democratic Republic of the; 2: Institut One Health pour l'Afrique, Université de Kinshasa, Kinshasa, Congo, Democratic Republic of the; 3: Central Veterinary Laboratory, Kinshasa, Congo, Democratic Republic of the; 4: Nelson Mandela African Institution of Science and Technology, Arusha, Tanzania

Introduction:

Quality water scarcity is a global challenge,necessitating water reuse in agriculture and industry, particularly in urban areas . This multifaceted issue requires a multisectoral approach. In many African cities, waterborne diseases remain a major concern where access to safe drinking water and sanitation is limited. In Kinshasa, riverside communities rely on surface water for domestic and economic activities, potentially exposing them to enteric pathogens. The Funa River, flowing through densely populated areas, receives substantial loads of faecal and environmental waste. This study assessed Enterobacteria risk and user perception regarding Funa River water using a Quantitative Microbial Risk Assessment (QMRA) and sociological surveys to inform public health interventions.

Materials and methods:

A descriptive cross-sectional study wasconducted in the Funa River valley in Kinshasa, DRC. We analyzed 96 water samples from six strategic sites during dry and rainy seasons. We isolated *E. coli*, *Salmonella* spp., *Klebsiella* spp., *Proteus* spp., *Providencia*spp., and *Pseudomonas* spp. using standard culture methods on MacConkey, SS agar, EMB, and TBX media. The study included a spatial characterization of the human–animal–environment interface using a Geographic Information System (GIS) and visual observation.). We surveyed 150 individuals using the river for household needs, gardening, sand gathering, and vehicle washing. Analysis focused on socio-demographic characteristics, exposure contexts, hazard knowledge, and risk behaviors. We estimated the annual infection risk for *E. coli* and

Salmonella sp. using a beta-Poisson dose–response model with Monte Carlo simulations. Scenarios included bathing, irrigation, and washing utensils or vehicles. Statistical analyses were performed using R software.

Results:

Findings revealed critical, persistent faecal contamination. *E. coli* was detected in 100% of samples (mean: 249.65 CFU/mL) with no significant seasonal variation, indicating chronic pollution. Other bacteria showed lower sporadic prevalence: *Klebsiella* sp. (11.46%), *Providencia* sp. (2.08%), *Proteus* sp. (2.08%), *Salmonella* sp. (1.04%), and *Pseudomonas* sp. (1.04%). Quantitative Microbial Risk Assessment results indicated that exposed populations face an annual *E. coli* infection probability approaching 100% under certain scenarios, with a 25% probability of illness. The survey showed that while 86% of users recognized health risks, over 50% continued to dispose of waste including human excreta directly into the river. This highlights how socio-economic constraints and lack of infrastructure drive environmental behaviors.

Conclusions:

The Funa River is severely contaminated with microorganisms, predominantly E. coli, exposing riverside populations to a high health risk. Despite recognition of the danger, observed behaviours contribute to the persistence of pollution. These results highlight the need to strengthen microbiological monitoring, improve sanitation and adopt integrated interventions adapted to the local context.

1373 – Integrating Gender and Equity into AMR Research: Findings from Six-Countries

Sarah VON HUMBOLDT-SCOTLAND (1), Cèlia VENTURA I GABARRO (1), Victoria SAINT2 (2), **Erica WESTWOOD** (1)

1: International Centre for Antimicrobial Resistance Solutions (ICARS); 2: Department of Population Medicine and Health Services Research (AG2), School of Public Health, Bielefeld University

Background

Antimicrobial resistance (AMR) research has historically focused on biomedical perspectives, despite AMR being a One Health challenge shaped by social, economic, and contextual factors (Lynch et al., 2024; Robbiati et al. 2025). Consequently, there are limited examples where gender and equity (GE) considerations have been integrated into the research cycle. To address this, the International Centre for Antimicrobial Resistance Solutions (ICARS) is providing financial and technical support to six AMR research projects to pilot the *Practical Pathways for Integrating Gender and Equity in AMR Research* framework. It provides a stepwise approach and adaptable entry points for integrating GE across research design, implementation and analysis (Lynch et al. 2023). The objective was to examine how the framework could be operationalised within ongoing AMR research and to identify lessons from an iterative, context-specific implementation process.

Methods

Six ongoing AMR research projects in Ghana, Lao PDR, Malaysia, Pakistan, Thailand and Zimbabwe piloted the framework across animal health (poultry, swine, aquaculture) and human health sectors (surgical, health clinic and pharmacy settings). Countries and projects were purposively selected to ensure representation across sectors, geographical contexts, and AMR research challenges. Each project integrated GE considerations into existing study designs through structured technical support, interdisciplinary collaboration with social scientists and cross-project capacity-strengthening activities. Implementation and learning were advanced through regular project meetings, quarterly cross-project meetings with experts, country progress reports and structured workshops.

Results

Across the six projects, integrating GE considerations led to methodological refinements across the research cycle. During problem framing, teams identified context-specific entry points and relevant equity factors (e.g., age, education, migration status, employment conditions). In study design, projects adapted data collection tools, refined recruitment strategies ensuring broader representation, incorporated community co-design, and developed GE-related indicators. During implementation, targeted training strengthened awareness among research teams, data collectors, research participants and facilitators. Data collection approaches were adapted ensuring flexible timing and accessible locations, for example enabling participation of women with their children after work. Analytical approaches were expanded through integration of GE variables in quantitative analyses and development of qualitative coding frameworks. The teams received training on equitable dissemination strategies.

Conclusion

Applying the Practical Pathways framework showed that GE considerations can be integrated into AMR research through incremental methodological adaptations, strengthening recognition and response to GE dimensions throughout the research process. The framework provided a flexible methodology adaptable to different settings and different AMR intervention challenges in human and animal health sectors. Developing coherent GE indicators remains challenging across diverse projects, and dedicated technical expertise requires resources that should be considered during project design. Nevertheless, these findings highlight that a structured approach coupled with dedicated funding and technical support can facilitate integrating GE aspects into AMR interventions, making them more effective and sustainable.

1376 – One Health surveillance for emerging orthobunyaviruses in South Africa, suggest a under estimated threat to human and animal health

Matshepo RAKAKI (2), Adriano MENDES (2), Paul J. WICHGERS SCHREUR (3), Martin H. GROSCHUP (4), Markus KELLER (4), Nicolette Marie DU PLESSIS (5), Maryke DE VILLIERS (6), Theunis AVENANT (5), June WILLIAMS (7), **Marietjie VENTER** (1)

1: Emerging Viral Threats, One Health Surveillance and Vaccines (EViTOH), Infectious Disease and Oncology Research Institute (IDORI),University of the Witwatersrand, South Africa; 2: Centre for Emerging Arbo and Respiratory Virus Research (CEARV), Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, South AfricaUniversity of Pretoria, South Africa; 3: Wageningen Bioveterinary Research, Houtribweg 39, 8221 RA Lelystad, The Netherlands; 4: Institute of Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institut, Greifswald, Insel Riems, Germany; 5: Department of Paediatrics, Kalafong Provincial Tertiary Hospital, University of Pretoria, South Africa; 6: Department of Internal Medicine, Kalafong Provincial Tertiary Hospital, University of Pretoria, South Africa; 7: Department Paraclinical Science, section Pathology, Faculty of Veterinary Science, University of Pretoria.

Background: Orthobunyaviruses (family *Peribunyaviridae*) have increasingly emerged in recent years, causing outbreaks in humans and animals across expanding geographic regions. Schmallenberg virus was first associated with abortions and congenital defects in European ruminants in 2011, while Oropouche virus has spread widely across South America since 2024. In Africa, several orthobunyaviruses circulate but remain largely undetected, leaving their public health significance uncertain. Shunivirus (SHUV), first identified in Nigeria in the 1960s, has been repeatedly detected in neurological disease in horses, wildlife, and livestock in South Africa since 2009 through One Health arbovirus surveillance, and has been implicated in human neurological illness, including congenital abnormalities in an infant in Gauteng in 2018. SHUV emergence in Israel in 2012, where it caused congenital and neurological disease in cattle and sheep, suggests further geographic expansion potential. SHUV has been detected in *Culicoides* midges and multiple mosquito genera. In 2024, Shamonda virus was identified for the first time in South Africa in an aborted goat foetus. Genome sequencing of SHUV-positive horses and *Culicoides* pools revealed

reassortant Shuni–Shamonda viruses and other orthobunyaviruses, including Schmallenberg virus, highlighting the risk of novel variant emergence.

Methods: To assess SHUV incidence in humans and horses presenting with febrile or neurological illness, we developed and validated IgM and IgG ELISAs for both species using baculovirus-expressed SHUV glycoproteins. Active surveillance from 2019–2022 included human cases with unexplained fever or neurological symptoms from sentinel sites in Gauteng and Mpumalanga, and horses with acute febrile or neurological disease from multiple provinces. Samples were screened using orthobunyavirus-specific real-time RT-PCR and SHUV IgM ELISA, with confirmation by virus neutralisation tests (VNTs). Healthy human controls were assessed using IgG ELISA and VNTs.

Results: Among horses, 11/245 (4.89%) were positive by PCR or IgM ELISA, and 17/245 (6.94%) were IgG positive. While most positive cases were from the Western Cape and Gauteng, the highest infection odds were in the North West, Northern Cape, and Mpumalanga. The equine case fatality rate was 40%, neurological signs occurred in 70% of cases, and abortion was reported in one mare. In humans, 14/225 (6.22%) febrile or neurological cases were PCR- or IgM/VNT-positive; 60% presented with seizures and 40% with meningitis, affecting both children and adults. Among healthy controls, 9/112 (8%) were IgG positive. Sequencing showed human and equine isolates clustering with historical South African and Israeli strains.

Conclusion: SHUV is an under-recognised cause of febrile and neurological illness in humans and horses in South Africa. Detection in infants, birth defects, and abortions in multiple livestock species suggests maternal transmission and warrants investigation in congenital disorders. Its broad vector range and emergence of reassortant viruses underscore the need for strengthened One Health surveillance to detect and monitor orthobunyavirus threats.

1380 – Catalyzing One Health adoption across sectors, disciplines and countries of the OneHealthSecure Network

Claudia ROBBIATI

Italian National Institute of Health (Istituto Superiore di Sanità), Italy, Italy

Background

OneHealthSecure is a three-year project (2024-2027) funded by the European Union which targets disruptions at the human–animal–environment interface such as vector-borne diseases, by promoting One Health (OH) implementation in 23 countries of the Balkan, Black Sea, Middle East, North Africa, and Sahel regions. It engages 120 national reference laboratories, institutions and experts from public health, veterinary services, human and animal virology, medical entomology and environmental sciences. OneHealthSecure capitalizes on the unique OH Network established during the MediLabSecure Project (2014-2024).

To strengthen collaboration across sectors, disciplines and countries, OneHealthSecure established a team of 10 OH Catalysts selected among experienced OH experts within the Network willing to amplify (catalyze) the adoption of multisectoral and multidisciplinary avenues to strengthen OH systems. The OH Catalysts act as connectors and facilitators, promoting awareness, advocacy, knowledge exchange, and collaborative approaches. Through interactive workshops, mentorship activities, and peer-learning initiatives, they help identify practical ways to operationalize OH approaches across different contexts.

Importance / innovation / impact / relevance

OneHealthSecure introduces an innovative OH catalysts model to enhance OH implementation across diverse epidemiological and policy contexts by exploring and promoting approaches to catalyze OH collaboration and communication. This will also support operational research outcomes about improving OH adoption and policy development, considering current national and regional needs for OH implementation.

The aim of this session is to present the OneHealthSecure Project and Network, and the OH catalysts model within OneHealthSecure in amplifying OH action, and levers for catalysing the OH approach across the OneHealthSecure Network and beyond.

Educational outcome

The WOHC26 is the ideal platform to share knowledge about OH advocacy practice to influence the OH community of experts and policymakers. The experience gained within OneHealthSecure spans sectors, disciplines, stakeholders and countries and could address a vast audience that may benefit from the approaches promoted within the OneHealthSecure Project.

Participants will gain practical insights into mechanisms that can strengthen OH collaboration, learn from the experience of the OH Catalysts model, and explore how similar approaches could be adapted to support OH implementation in other regions and contexts.

Proposed talk titles and speakers and chairs

This session will engage experts from different sectors, disciplines, and countries from the OneHealthSecure Project.

Proposed chair: Flavia Riccardo, Italian National Institute of Health (Istituto Superiore di Sanità), Italy

Speakers:

Claudia Robbiati, Italian National Institute of Health (Istituto Superiore di Sanità), Italy: The OneHealthSecure Project and Network 10'

Rusmir Goletic, Institute for Health and Food Safety Zenica, Bosnia and Herzegovina & Balkan One Health Network: The OH catalysts model within the OneHealthSecure Project 10'

Lusine Paronyan, World Health Organization, Country Office Armenia: Leverage points and insights for OH catalyzing activities across the OneHealthSecure Project and beyond 10'

Questions & Answers 10'

1389 – Closing the Genomic Gap: Characterizing African Bat Coronaviruses to Strengthen One Health Surveillance and Zoonotic Risk Assessment

Rochelle RADEMAN (1), Marike GELDENHUYS (1), Ariel ENDLICH-FRAZIER (2), Arkadeb BHUINYA (3,4), Michael Colin LETKO (2), Arinjay BANERJEE (3,4,5,6,7), **Wanda MARKOTTER** (1,8)

1: Centre for Viral Zoonoses, Department of Medical Virology, University of Pretoria, Pretoria, 0001, South Africa; 2: Laboratory of Functional Viromics, Paul G. Allen School for Global Health, Washington State University, Pullman, Washington, United States of America; 3: Vaccine and Infectious Diseases Organization (VIDO), University of Saskatchewan, Saskatoon, SK S7N 5E3, Canada; 4: Department of Veterinary Microbiology, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, SK S7N 5E3, Canada; 5: Department of Biology, University of Waterloo, Waterloo, ON N2L 3G3, Canada; 6: Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC V6T 1Z3, Canada; 7: Department of Laboratory Medicine and Pathobiology, Temerty Faculty of Medicine, University of Toronto, Toronto, Ontario, Canada; 8: Future Africa Platform, University of Pretoria, Pretoria, Gauteng, South Africa

Background

Horseshoe bats (Rhinolophus spp.) are recognized as the natural reservoir for a large diversity of sarbecoviruses with zoonotic potential and were previously implicated in the SARS outbreak and the SARS-CoV-2 pandemic. While Asia's extensive surveillance has generated hundreds of sarbecovirus genomes from rhinolophid bats, African datasets remain extremely limited, representing only a small fraction of the global genomic record. Despite the high diversity of Rhinolophus in Africa, only a limited number of species and roosting sites have been sampled. This disparity constrains regional zoonotic risk assessments, our understanding of virus evolution, and the development of early warning systems within the African One Health surveillance networks.

Methods

To address this gap, coding-complete sarbecovirus genomes and spike gene sequences were recovered from Rhinolophus bats detected during surveillance activities in South Africa and Rwanda, using multiple sequencing approaches for low-concentration samples. Genomic diversity and recombination patterns were assessed using Simplot++ and RDP5, while phylogenetic analysis characterized circulating viral variants. Functional assays were performed to evaluate ACE2 receptor usage and interferon antagonism by viral accessory proteins.

Results

Ten coding complete sarbecovirus genomes and 38 spike gene sequences were recovered. The South African lineage shared high nucleotide identity (94.7%) with sarbecoviruses from Zimbabwe, suggesting regional circulation across southern Africa. Recombination events between South African and East African sarbecoviruses were detected, particularly within the spike gene and accessory regions. Phylogenetic analysis showed strong phylogeographic clustering and highlighted two variants circulating within the Rhinolophus population. The receptor-binding domain of the spike gene showed both unique and conserved residue substitutions within the South African lineage; however, most variations were associated with low binding affinity to human ACE2 receptors. Viral entry assays confirmed that the South African lineage could not use canonical human ACE2 receptors, unlike a bat sarbecovirus from Rwanda sequenced in this study. Functional assays further showed that accessory proteins, particularly ORF6, could suppress Type I interferon responses.

Conclusion

These findings expand the currently limited genomic dataset of African sarbecoviruses and demonstrate the importance and functionality of genomic and spike gene sequence data. The study also highlights critical gaps in regional surveillance, particularly along the East African escarpment, where several Rhinolophus species overlap. The limited availability of genome and spike gene sequences, incomplete host species identification, and insufficient sequence metadata hamper accurate analyses of evolutionary relationships and transmission dynamics within bat host populations. Strengthening transdisciplinary One Health surveillance of wildlife reservoirs across Africa is essential to detect mutations and recombination events that may alter host range, identify ecological drivers and host behaviours associated with viral excretion, and characterize human-animal-environment interfaces that may facilitate spillover. This will improve early detection, zoonotic risk assessment, and strengthen pandemic preparedness on a regional and global scale.

1397 – Expanding risk of West Nile virus in Italy

Lara MARCOLIN (1), Antonino BELLA (2), Martina DEL MANSO (2), Ilaria DORIGATTI (3), Patrizio PEZZOTTI (2), Piero POLETTI (4), Flavia RICCARDO (2), Moreno DI MARCO (1)

1: Dept. of Biology and Biotechnologies "Charles Darwin", Sapienza University of Rome, Viale dell'Università 32, I-00185 Rome, Italy; 2: Department of Infectious Diseases, Istituto Superiore di Sanità, Rome, Italy; 3: MRC Centre for Global Infectious Disease Analysis, School of Public Health, Imperial College London, London, UK; 4: Center for Health Emergencies, Bruno Kessler Foundation, Trento, Italy

Background: West Nile virus (WNV) poses an increasing public health burden in Italy, which consistently reports the highest number of human neuroinvasive disease cases in Europe. Predicting the risk of human infection from mosquito bites is a persistent challenge due to the complex zoonotic cycle of the pathogen which includes many avian hosts. To plan effective surveillance and mitigation, several ecological factors driving WNV host and vector distributions must be considered, alongside climatic and environmental variables that favour viral transmission. But these applications have been limited so far.

Methods: The study utilized a machine learning framework to predict WNV risk across Italian municipalities. The methodology integrated environmental, socio-economic, and macroecological data to characterize the virus's recent expansion. To ensure robustness, the modelling framework was validated using both spatial and temporal cross-validation techniques to evaluate its ability to discriminate between areas with and without human WNV cases.

Results: The findings successfully captured the virus's decadal spatio-temporal dynamics, specifically its progressive expansion beyond the endemic core of the Po Valley. Notably, the model identified that environmental suitability often precedes clinical detection, flagging high-risk areas along the Adriatic coast and southern Italy before human cases were officially recorded. Minimum temperature was identified as the primary risk driver, followed by the specific year and human population density.

Conclusions: Embedding detailed ecological analysis into WNV risk modelling significantly improves the understanding of viral expansion dynamics. The study demonstrates that such a framework can effectively predict emerging risk zones, providing a critical tool for risk mapping, informing surveillance efforts, and guiding targeted public health interventions in Italy.

1400 – ISAVET program strengthens frontline Veterinary Epidemiology capacity in Ethiopia through structured in-Service training

Getachew Gari JIMOLU
FAO Ethiopia

Background National Need and Readiness Assessment was carried out in Ethiopia in 2019 and identified major technical gaps among frontline animal health personnel, particularly in surveillance, outbreak response, and applied epidemiology. Approximately 80% of frontline animal health workers demonstrated moderate to high skill deficits, highlighting the need for structured and continuous professional development. In response, the Ministry of Agriculture introduced the In-Service Applied Veterinary Epidemiology Training (ISAVET) program to enhance the competencies of field veterinarians and para-professionals. This study assesses ISAVET's impact following its expansion under the Emergency Prevention and Preparedness for Animal Health (EPPR) Project funded by the Pandemic Fund.

Methods ISAVET consists of one month of classroom instruction followed by three months of mentored field practice. The curriculum covers surveillance, outbreak investigation, zoonotic diseases, food safety, and data management. Trainees conducted field studies in district veterinary clinics, collected data using standardized tools, and presented findings through written and oral reports. A post-training assessment was conducted six months after completion (April 2023) in 10 districts across Oromia, South Ethiopia, and Sidama Regions. Data were collected through structured interviews with 10 ISAVET trainees and two supervisors, focusing on skill application, data quality, and outbreak response improvements.

Results Prior to the EPPR project, 74 (11 females) frontline staff from 74 districts had been trained through USAID support. With additional funding from the Pandemic Fund, the program expanded to train 160 more professionals (16 female), increasing coverage from 74 to 234 districts and growing academic partnerships from one to six universities.

Post-training assessment showed measurable improvements in epidemiological competencies. Trainees reported enhanced ability to analyze and interpret surveillance data, produce graphical and tabular summaries, and submit timely reports to district offices. Outbreak detection and response capacity improved substantially with more effective disease control measures. ISAVET graduates collectively produced three peer-reviewed publications, submitted an additional three manuscripts, and four trainees received career promotions attributable to improved technical proficiency. Supervisors confirmed improved completeness and quality of disease reporting at district level.

Conclusion The ISAVET program significantly strengthened Ethiopia's frontline veterinary epidemiology workforce by improving data analysis, surveillance reporting, and outbreak response. Expansion supported by the Pandemic Fund enabled broader geographic reach and institutional collaboration, addressing critical capacity gaps identified at national level. The program demonstrates a scalable model for sustainable workforce development aligned with One Health priorities and national animal health system strengthen.

1408 – High Prevalence of Sheep-Adapted Cryptosporidium xiaoi and Salmonella enterica subsp. diarizonae 61:k:1.5,(7) in Finnish Sheep: Molecular and Genomic Insights

Essi ROININEN (1), Rauni KIVISTÖ (1), Tarja POHJANVIRTA (2), Tarja PITKÄNEN (1,3)
1: University of Helsinki; 2: Finnish Food Authority; 3: Finnish Institute for Health and Welfare

Backround: Sheep are reservoirs for several zoonotic pathogens, including *Salmonella* spp., and *Cryptosporidium* spp. which can cause intestinal infections in animals and humans. *Salmonella* serovars Typhimurium and Enteritidis are major causes of human gastroenteritis in Europe. The zoonotic relevance of these pathogens differs between species and genotypes, yet in Finland the data on the prevalence and genomic diversity of these two pathogens in sheep remain limited. This study aimed to determine the prevalence and genomic diversity of *Salmonella* and *Cryptosporidium* spp. in slaughtered sheep in Finland, and their potential relevance to human infections.

Methods: In 2023, a total of 187 samples were collected for *Salmonella* spp. analyses and 188 samples for *Cryptosporidium* spp. analyses from three slaughterhouses across Finland. Faecal samples were collected

from the rectum and/or large intestine of sheep or from pens. *Salmonella* spp. were analysed using culture-based methods, followed by whole-genome sequencing, MLST typing, and antimicrobial-resistance profiling and pan-genome wide association study (Pan-GWAS). For pan-GWAS analysis whole-genome sequences (n=78) of *Salmonella enterica* subsp. *diarizonae* 61:k:1,5,(7) human isolates were downloaded from EnteroBase. *Cryptosporidium* spp. was detected and identified using nested PCR targeting a partial fragment of the 18S rRNA gene.

Results: The only *Salmonella* serovar detected was *S. enterica* subsp. *diarizonae* 61:k:1,5,(7) (20%). Pan-GWAS showed that Finnish sheep isolates lacked gene clusters associated with adhesion, colonization and competitive gut survival that were present in 12 human *S. diarizonae* O61 isolates from France, UK and Germany, indicating reduced virulence potential and supporting a low zoonotic potential. All isolates carried the aminoglycoside resistance gene *aac(6')-Iaa* and the *parC* T57S mutation, and this serotype is known to be host-adapted to sheep. *Cryptosporidium* spp. was detected in 48% of the samples, with *C. xiaoi* as the dominant species (44%), and zoonotic *C. ubiquitum* presentat 4.2%, while *C. parvum,* commonly associated with human infections, was not observed. Although the prevalence of both *Salmonella* and *Cryptosporidium* was high, the dominant species represented host-adapted lineages with minimal zoonotic relevance.

Conclusions: The pathogens detected were dominated by host-adapted species and subtypes such as *Salmonella enterica* subsp. *diarizonae* O61 and *Cryptosporidium xiaoi*, suggesting a low likelihood of sheep being a major source of human infections in Finland. Pan-GWAS showed that all Finnish sheep *S. diarizonae* O61 isolates lacked multiple gene clusters associated with adhesion-, colonization- and gut survival, that were present in human isolates. This further suggests limited zoonotic potential for Finnish sheep *S. diarizonae* O61 isolates. To further investigate this, comparative analyses of virulence factors, metabolic pathways and pseudogenes are underway to further examine additional functional differences between sheep and human *S. diarizonae* O61 isolates.

1414 – Molecular epidemiology of pathogens associated with scours in Western Canada.

Aayush POUDEL, M. Faizal ABDUL-CAREEM, Johnathan CANTON, Karin ORSEL, Frank VAN DER MEER
Faculty of Veterinary Medicine, University of Calgary, Canada

Background: Neonatal calf diarrhea (NCD) remains a major challenge globally. This multifactorial disease's pathogenic causes often involve infections with multiple enteric pathogens. Some of these pathogens are zoonotic, while others possess zoonotic potential. Hence, beyond the economic impact on the cattle industry, NCD associated pathogens pose an occupational risk to producers and veterinarians. However, many cases remain underreported or are managed at the farm level. Since control of NCD heavily relies on preventive measures such as vaccination and therefore characterizing the molecular epidemiology of these agents is essential to understand if vaccination can be expected to induce sufficient protection against circulating strains of NCD pathogens.

Methods: Fecal sample from scouring dairy calves were collected through convenience sampling across Western Canada. Samples were first screened for pathogens of interest, which includes zoonotic pathogens like *Cryptosporidium*, enterotoxigenic *Escherichia coli (ETEC)* and *Salmonella* spp, where positive samples are further processed for strain typing. Sanger sequencing will be performed on PCR products obtained targeting VP4 and VP7 for bovine rotavirus (BRV), spike protein for bovine coronavirus (BCoV) and K99 pilus gene for *ETEC*. Multiplex PCR targeting different toxin producing genes will be run to strain type *Clostridium perfringens*. For parasites, SSU rRNA for *Cryptosporidium* will be PCR-amplified, indexed, pooled, and sequenced on Illumina MiSeq.

Results: To date (March 2026), we have received 33 fecal samples, with pathogens detected at the following frequencies: BRV (23/33), BCoV (9/33), *E. coli* (4/33*), Clostridium perfringens* (15/33), *Cryptosporidium* (16/33), and *Giardia* (7/33). Notably a zoonotic Salmonella, a notifiable pathogen in Canada, was identified in two samples during screening. Ongoing strain typing is expected to elucidate the prevalence of pre-existing as well as emerging strains of pathogens of public health interest. Additionally, Information on circulating strains will be used to evaluate their antigenic similarity with commercially available pre-partum vaccines against NCD, which is currently based on historical data.

Conclusion: Preliminary results highlight a high occurrence of BRV and *Cryptosporidium* in scouring calves across Western Canada. Through identifying specific circulating genotypes and toxin profiles, this study

aims to get producers and veterinarians a better information to develop targeted prevention strategies for NCD, thereby reducing the zoonotic risk to producers and veterinarians.

1422 – Tribeč virus detected in ticks and fieldfares in Finland

Maija T. SUVANTO (1,2), **Katariina KAANSALO** (1,2), Pinja NENONEN (2), Roope NYKÄNEN (1), Sanna SAINMAA (3), Anne J. JÄÄSKELÄINEN (4), Jasmin KINNUNEN (1), Phuoc T. TRUONG NGUYEN (1), Viktor OLANDER (1,2), Jani SORMUNEN (5), Eero VESTERINEN (5), Hanna VAUHKONEN (1), Paula M. KINNUNEN (2,7), Tarja SIRONEN (1,2), Teemu SMURA (1), Olli VAPALAHTI (1,2,4), Ruut JOENSUU (1,2,6), Eili HUHTAMO (1,2), Essi M. KORHONEN (1,2)

1: Department of Virology, Faculty of Medicine, University of Helsinki, Finland; 2: Department of Veterinary Biosciences, Faculty of Veterinary Medicine, University of Helsinki, Finland; 3: Korkeasaari Zoo, Wildlife hospital, Helsinki, Finland; 4: HUS Diagnostic Centre, Clinical Microbiology, Helsinki University Hospital and University of Helsinki, Finland; 5: Department of Biology, Faculty of Science, University of Turku, Finland; 6: Department of Geosciences and Geography, Faculty of Science, University of Helsinki, Finland; 7: Companion Animal Business Unit, Nordic Cluster, MSD Animal Health, Espoo, Finland

Background: While studying brain tissues of deceased wild birds using a metagenomic approach, we detected fragments of genomic sequence belonging to Tribeč virus (TRBV). TRBV is a tick-borne zoonotic orbivirus (Sedoreoviridae family, Orbivirus genus) endemic to Central and Eastern Europe. Although evidence of human TRBV infection remains limited, TRBV and related tick-borne orbiviruses have been associated with febrile and neurological disease in humans [1]. In Finland, serological findings from cattle in the 1970s [2] suggested previous TRBV circulation, but no further evidence has been available. This study aimed to characterize the detected TRBV strain, develop molecular methods for its detection, and investigate the prevalence of TRBV in ticks collected from wild birds and dogs, and in wild birds from Southern Finland.

Methods: Brain tissues collected from deceased wild birds in the Korkeasaari Zoo Wildlife hospital were used for NGS and virome analysis in a small subset of samples. A TRBV-positive brain sample was used to isolate the virus in cell culture, and the recovered strain was sequenced for phylogenetic analyses. A specific one-step RT-qPCR assay targeting the TRBV T2 genome segment was developed for targeted screening. The assay was used to screen ticks collected from wild birds and dogs, as well as bird brain samples. Further sequencing of RT-qPCR–positive samples is ongoing.

Results: TRBV RNA was detected in multiple tick and bird brain samples from southern Finland. High-throughput sequencing led to the detection of a TRBV sequence in a fieldfare (Turdus pilaris) and a total of two fieldfares were positive for TRBV in brain tissues (n=2/236). Positive findings included also Ixodes ricinus ticks (n=2/16) collected from a dog in the Turku region and ticks removed from wild birds (n=3/272), including fieldfare (Turdus pilaris), common blackbird (Turdus merula), and European greenfinch (Chloris chloris). Virus isolation was conducted to first positive bird brain sample, and sequence analyses confirmed TRBV identity. Phylogenetic comparison demonstrated genetic similarity to previously described East European TRBV strains.

Conclusions: This study provides molecular evidence of TRBV in ticks and wild birds in Southern Finland. Detection of viral RNA in both vectors and avian hosts supports the existence of local transmission cycles and suggests a role for migratory birds to virus dispersal. In the context of expanding tick populations, TRBV may represent a neglected arbovirus with emergence potential in the Nordic region. Ongoing studies aim to further characterize viral diversity and distribution in ticks, and to assess exposure in humans, other mammals, and birds. Further studies would be needed for uncovering the distribution, natural circulation, and possible public health significance of TRBV in Northern Europe.

[1] Hubálek Z & Rudolf I. Parasitol Res. 2012;111(1):9–36.

[2] Saikku P & Brummer-Korvenkontio M. Med Biol. 1975;53(5):317–320.

1427 – One Health and Agricultural Workers

Jeff BENDER (1), Amy LIEBMAN (2), Casper BENDIXSEN (3), Devon CHARLIER (1), Bruce ALEXANDER (1)

1: University of Minnesota, School of Public Health United States of America; 2: Migrant Clinicians Network; 3: National Farm Medicine Center

Background: The mission of the Upper Midwest Agricultural Health and Safety Center (UMASH) is to improve the health and safety of agricultural workers, owner-operators, and communities in the Upper Midwest of the United States. We pursue this mission guided by One Health principles utilizing a multidisciplinary cross-sector approach that engages public health, veterinary medicine, health care, and agriculture in the academic, public, and private arenas. Here we present three initiatives demonstrating successful One Health approaches to agricultural worker health and safety.

Methods: We outline three initiatives supporting this One Health effort: livestock production safety training, needlestick prevention, and zoonotic disease prevention. A multidisciplinary team engaged stakeholders to identify needs and develop culturally appropriate tools and resources. Evaluation staff reviewed and assessed the output and impact of developed resources including the network of users and the broader application and use of these tools.

Results: *Safety Training*: The *Seguridad en las Lecherías* curriculum, a bilingual (Spanish and English), five-module worker training curriculum based on the community health worker model, was successfully implemented and evaluated in Minnesota, South Dakota and Wisconsin to promote safety on dairy farms in the rural Upper Midwest. The *Seguridad* curriculum was used to train over 1000 immigrant workers from nearly 100 participating dairies, resulting in an increase in safety knowledge. Producers also shared positive feedback, highlighting impressive improvements in safety culture, behavior changes, and a reduction in incidents on their farms.

Needlestick Prevention: Swine industry representatives requested the development of educational materials to address needlestick injuries on swine operations. This included a review of the literature, engagement with the industry, and review of pharmaceuticals used in the swine production. The materials emphasized increasing awareness and incorporation of human, animal and environmental factors for prevention. The materials, including videos, posters, and webinars, were broadly disseminated and utilized by the industry for worker education.

Zoonotic Disease Prevention: Recent outbreaks and sporadic cases of zoonotic diseases documented at our state health department were identified in farm families, workers, and on the farm visitors, often through agritourism events. Outreach and educational materials were assembled to address this issue from a One Health perspective engaging health professionals, veterinarians, and event organizers. Varied educational materials were assembled and widely distributed and shared to the agricultural community and agritourism event organizers.

Conclusions: We provided resources to support a broad team approach to health and safety on livestock operations. These efforts are culturally responsive to address the needs of a foreign-born workforce. Resources included bilingual needlestick prevention, animal handling, zoonotic disease prevention, and checklists/audit tools (http://umash.umn.edu/). A safer working environment not only supports workers but also has benefits for animal welfare, environmental impacts, and economic sustainability by reducing injury-related costs.

1430 – Mapping Thematic Areas to Inform Climate-Health Indicator Development for Integrated One Health Surveillance in South Africa: A Cross-Institutional Document Analysis

Elizabeth LEONARD (1), Mbhekiseni KHUMALO (2), Bono NEMUKULA (2), Phyllis CHITUKU (1), Wayne RAMKRISHNA (2)

1: Clinton Health Access Initiative, South Africa; 2: South African National Department of Health

Background:

South Africa faces a complex and intersecting set of health challenges shaped by climate change, including vector-borne diseases, food insecurity, extreme weather events, and a growing burden of non-communicable diseases. Strengthening One Health (OH) surveillance in this context requires the identification and embedding of contextually relevant climate-health indicators into existing national surveillance systems. A critical first step toward indicator development is establishing a thematic framework that reflects both the global evidence base and the South African landscape. This study aimed to map and harmonise surveillance-relevant thematic areas across leading international and continental frameworks to provide a structured foundation for climate-health indicator identification in South Africa.

Methods

A structured desktop review and document analysis was conducted using key policy, strategic, and scientific documents from six sources: Africa CDC, the World Health Organization (WHO), the African Union (AU), the One Health Joint Plan of Action (OH-JPA), the Intergovernmental Panel on Climate Change (IPCC), and The Lancet Countdown Series. Documents were selected for their relevance to climate-sensitive health risks, and One Health surveillance. Thematic domains were systematically extracted through iterative cross-referencing of surveillance-relevant content across all six sources. Themes were assessed for convergence and divergence across human, animal, environmental, and climate health dimensions, with reference to the South African context.

Results:

Ten integrated One Health surveillance thematic areas were identified: (1) Vector-Borne & Zoonotic Diseases; (2) Food & Nutrition Insecurity; (3) Airborne Diseases; (4) Heatwaves & Extreme Temperatures; (5) Waterborne Diseases; (6) Mental & Occupational Health; (7) Extreme Weather Events; (8) Antimicrobial Resistance (AMR); (9) Non-Communicable Diseases (NCDs); and (10) Ecosystem Health. Convergence was strongest for vector-borne and zoonotic diseases and food and nutrition insecurity, which appeared across all six sources. Airborne diseases and mental and occupational health were absent from three or more frameworks. NCDs appeared exclusively in WHO documentation, and ecosystem health only in the AU and OH-JPA. AMR featured in Africa CDC, the AU, and OH-JPA but was absent from climate-focused sources. These gaps point to fragmentation at the human-animal-climate interface that surveillance indicator development will need to address.

Conclusion:

This ten-domain thematic framework provides a structured, evidence-informed foundation for the identification of climate-health indicators to be embedded into South Africa's One Health surveillance systems. By surfacing convergences and gaps across six major institutional frameworks, the analysis identifies priority thematic areas requiring indicator development. The framework supports objectives to strengthen integrated surveillance, formalise cross-sectoral data sharing, and develop early warning systems for climate-sensitive health risks.

1434 – Analysis of Puumala Virus and Ljungan Virus Co-infected Wild Bank Voles Reveals Histopathological Differences

Cienna BUCKNER (1), Jussi HEPOJOKI (1,2), Eva KALLIO (3), Anja KIPAR (2,4), Tapio MAPPES (3), Tomas STRANDIN (1)

1: Department of Virology, University of Helsinki, Finland; 2: Institute of Veterinary Pathology, Vetsuisse Faculty, University of Zurich, Switzerland; 3: Department of Biological and Environmental Science, University of Jyväskylä, Finland; 4: Department of Basic Veterinary Sciences, Faculty of Veterinary Medicine, University of Helsinki, Finland

Background: Rodents comprise approximately 40% of mammalian species and play a key role in global ecosystems as well as acting as a natural reservoir for multiple zoonotic pathogens. Bank voles (*Clethrionomys glareolus)* are widespread across Europe and are the natural host of the most prevalent European *Orthohantavirus*, Puumala virus (PUUV). In voles, PUUV establishes life-long infections that, while often considered asymptomatic, decrease overwinter survival rates. Additionally, voles persistently shed the virus in their excrement and transmission to humans is most commonly through inhalation of these excreta. In humans, PUUV infections often remain subclinical but can cause disease ranging from mild to fatal. Furthermore, PUUV in humans has been identified as a risk factor for the development of B-cell lymphomas, but it is unknown if this association is also found in voles. Bank voles are also the primary natural host of Ljungan virus (LV). While LV is considered zoonotic and seroprevalence has been established in both humans and voles, zoonotic potential and modes of transmission remain uncertain. In both voles and humans, LV has been implicated to play a role in development of Type 1 diabetes. Because the role of bank vole as natural reservoirs of human pathogens and bank vole population dynamics is translated into human infection epidemiology, it is important to understand how infection and co-infection impacts the health of voles.

Methods: 160 wild-caught, bank voles were housed in laboratory for 1 year. We analyzed longitudinal blood samples for PUUV and LV seropositivity. At terminal sampling, RNA was extracted from lung tissue and quantitative PCR performed for PUUV and LV. Samples of the lungs, spleen, mesenteric lymph nodes, liver, kidneys, pancreas, adrenal glands, gastrointestinal tract, and salivary glands were processed for histological assessment.

Results: We determined the seroprevalence and seroconversion for PUUV, LV, and coinfections and assessed viral transmission rates in captivity. While PUUV seropositivity did not impact overall body size, it did significantly correlate with splenomegaly and increased cellularity of the red pulp. The most prevalent histopathological changes were related to endoparasitosis. Finally, lesions were analyzed for the presence of PUUV antigen to investigate if PUUV is a risk factor for malignancy development.

Conclusions: This work provides timely insight into how infection and co-infection can impact the overall health of voles. Transmission rates of viruses while in captivity is of interest with the growing use of bank voles as a wild-rodent model. While previous work has investigated coinfection of voles with PUUV and endoparasites, our work broadens that understanding to include endoparasite infections in the context of PUUV-LV coinfection. These results provide the first assessment of the potential risk for PUUV-associated malignancies in bank voles.

1437 – Coronaviruses circulating in synanthropic bat populations in Kenya

Nina SUOMALAINEN (1), Isabella DEANGLIS (2), Reilly JACKSON (2,3), Joseph OGOLA (4), Lauri KAREINEN (1), Veronica LEHTINEN (1), Paul WEBALA (5), Tamika LUNN (6), Kristian FORBES (2), Eda ALTAN (1), Tarja SIRONEN (1)

1: University of Helsinki, Finland; 2: University of Arkansas; 3: Arizona Game and Fish Department; 4: University of Nairobi; 5: Maasai Mara University; 6: University of Georgia

Background: Coronaviruses are prime examples of emerging zoonotic pathogens, with bats and rodents recognized as their primary reservoirs. Although hundreds of diverse coronavirus strains circulate in bat populations, only a limited number have crossed the species barrier to infect humans or livestock, sometimes causing major outbreaks. Identifying the viral traits and ecological drivers that enable such spillover events remains a critical scientific challenge. This study aims to identify coronaviruses with a high potential for cross-species transmission and to investigate environmental and biological factors that may influence spillover risk in synanthropic bat populations in Kenya.

Methods: Since 2016, our collaborative research team has conducted long-term surveillance of bats and their associated viruses in Kenya. Between 2022 and 2024, almost 2000 bat fecal samples were collected from insectivorous bat populations and screened for coronaviruses using pan-coronavirus PCR methods. Positive samples are currently undergoing molecular characterization, and ecological data are being analyzed to assess factors potentially associated with viral prevalence and transmission.

Results: Preliminary screening results indicated a prevalence of approximately 19% Alphacoronavirus among the sampled insectivorous bat populations. The phylogenetic analysis has shown that the two co-roosting species, Angolan free-tailed bat (Mops condylurus) and little free-tailed bat (Mops pumilus) host an Alphacoronavirus belonging to the subgenus Decacovirus, whereas the heart-nosed bat (Cardioderma cor) appears to host a similar but separately clustering Decacovirus. Ongoing molecular analyses aim to characterize the detected viral strains further and to evaluate their genetic diversity and potential relevance for cross-species transmission.

Conclusions: These findings contribute to a better understanding of coronavirus diversity in Kenyan bat populations. Continued molecular and ecological analyses will help evaluate the zoonotic potential of these viruses and support efforts to anticipate and mitigate future coronavirus spillover events.

1448 – Hybrid surveillance and Bayesian modelling to estimate brucellosis incidence in a livestock-keeping population in northern Tanzania

Avery L. HOLMES (1), William A. DE GLANVILLE (1), Victor KATITI (2,3), Ângelo J. F. MENDES (1), Rebecca F. BODENHAM (1), AbdulHamid S. LUKAMBAGIRE (4), Blandina T. MMBAGA (2,3,5), Matthew P. RUBACH (5,6,7), John A. CRUMP (3,5,6,8), Sarah CLEAVELAND (1), Mafalda VIANA (1), Jo E. B. HALLIDAY (1)

1: School of Biodiversity, One Health and Veterinary Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, UK; 2: Kilimanjaro Clinical Research Institute, Good Samaritan Foundation, Moshi, United Republic of Tanzania; 3: Kilimanjaro Christian Medical University College, Tumaini University, Moshi, Tanzania; 4: Sokoine University of Agriculture, Morogoro, Tanzania; 5: Duke Global Health Institute, Duke University, Durham, NC, USA; 6: Division of Infectious Diseases and International Health, Duke University Medical Center, Durham, US; 7: Programme in Emerging Infectious

Diseases, Duke-National University of Singapore, Singapore; 8: Centre for International Health, Dunedin School of Medicine, University of Otago, Dunedin, New Zealand

Background: Brucellosis is a globally distributed and widely under-diagnosed zoonotic bacterial disease that causes infertility and abortion in livestock and potentially debilitating febrile illness in humans. Global human brucellosis incidence estimates are sparse and vary widely between and within countries. Most estimates range from 50 to 100 cases per 100,000 people per year, although some estimates reach as much as a few hundred per 100,000 per year. Estimating brucellosis incidence in low-resource settings is complicated by inaccurate diagnostics and lack of health facility access for many people in rural communities, making the disease impact largely unknown in many endemic contexts.

Methods: To estimate brucellosis incidence in a pastoralist population in northern Tanzania, we developed a Bayesian model that integrates diagnostic test results from individuals sampled through sentinel hospital surveillance, test sensitivity and specificity, and data from a healthcare utilisation survey. We then investigated the sensitivity of incidence estimates to changes in methodology by simplifying the models and using a range of alternative measures for healthcare utilisation.

Results: We show that this pastoralist population in northern Tanzania experienced a high incidence of brucellosis, with estimates of 248.8 illnesses per 100,000 people per year (highest posterior density interval [HPDI]: 109.4 - 398.6) for the total population, 134.9 (HPDI: 14.7 - 288.1) for adults only (aged >15 years), and 429.9 (HPDI: 201.0 - 672.0) for children only (aged ≤15 years). These results are among the highest reported in the world to date. Model variations that did not account for imperfect healthcare utilisation generated substantially lower incidence estimates, indicating the crucial importance of accounting for low levels of healthcare utilisation to avoid under-estimation of disease incidence in this and similar settings.

Conclusions: This study illustrates that brucellosis is a more substantial public health problem in northern Tanzania than current evidence and data suggest. These findings indicate that increased access to and utilisation of effective testing and treatment would likely improve brucellosis case detection and management in this setting. Ultimately, implementing human brucellosis prevention strategies, including livestock vaccination, would likely improve the health of many people living in at-risk rural communities.

1452 – Knowledge gaps and research needs on the implementation of a One Health approach

Elisa MARTELLO (1), Laura TOMASSONE (2), Howard NEEDHAM (3), Ha Hoang NGUYEN (4), Emma WILSON (1), Catrin EVANS (1), Andreas DROULIAS (5), Ioanna LAGOU (5), Grace BROUGH (1), Constantine VARDAVAS (5), Federico GOBBI (6,7), Jo LEONARDI-BEE (1)

1: University of Nottingham, United Kingdom; 2: University of Turin, Italy; 3: European Centre for Disease Prevention and Control (ECDC), Sweden; 4: Amsterdam Universal Medical Center (UMC), The Netherlands; 5: University of Athens, Greece; 6: IRCCS Ospedale Sacro-Cuore Don Calabria, Italy; 7: University of Brescia, Italy

Introduction: One Health (OH) is an integrated approach recognising the interdependencies between the health of humans, animals, plants, and the environment. By promoting holistic strategies across sectors, OH research can address complex and emerging health challenges. However, the design and implementation of OH initiatives remain constrained by conceptual, methodological, and operational barriers.

Methods: A scoping review was conducted to map the research gaps and needs impacting the delivery of an OH approach to address current and emerging health threats to the EU/EEA. Medline, EMBASE and the Cochrane Library were searched (2014 to February 2025) to identify published evidence syntheses on this topic. Screening and data charting were performed independently by two reviewers. Identified gaps were allocated into 5 primary categories: knowledge gaps, conceptual gaps, methodological gaps, data gaps, and practical gaps. Independent topic themes were then identified within each category to provide a more detailed breakdown of the research gaps identified using an inductive approach.

Results: A total of77 evidence synthesis reviews were included. 65% were systematic reviews, 31% scoping reviews, 3% umbrella reviews, and 1% mapping reviews. Most reviews focused on antimicrobial resistance (30%) or infectious diseases (38%). A total of 524 research gaps were identified. Knowledge gaps were reported in 74% reviews focused on contextual challenges, economic resources, environment, intervention, surveillance and monitoring, terminology and definitions, transmission dynamics and epidemiology, and understudied hosts and pathogens. Topic themes in the “Conceptual gaps” category

(70%) focused on conduct and reporting quality, contextualised challenges, inclusive and contextualised partnerships, infrastructure and resource constraints, interdisciplinary approach, operationalisation of OH, policy and regulatory deficit, and system-level integration and coordination. Methodological gaps (59%) themes related to conduct and reporting quality, contextual challenges, data driven tools, diagnostics, intervention, and surveillance and monitoring. Data gaps (42%) themes reflected limitation in data availability, environmental data, surveillance and monitoring. Practical gaps (43%) themes included communication and scientific dissemination, contextual challenges, inclusive and contextualised partnerships, infrastructure and resource constraints, intervention, policy and regulatory deficits, surveillance and monitoring, training and capacity building.

Key challenges include limited data and study availability, particularly in environmental health, and insufficient interdisciplinary integration. Inconsistent definitions and underdeveloped methodological approaches further limit the generation of standardised evidence and its translation into policy and practice. Economic evaluations, diagnostic and treatment innovation, and standardised frameworks receive limited attention. Weak stakeholder engagement, cross-sectoral collaboration and funding constraints continue to hinder surveillance, capacity building, and integrated action.

Conclusion: This scoping review identifies persistent barriers to the effective implementation of OH initiatives across the EU/EEA. Although the volume of OH literature has increased, this review shows that several critical areas across wide-ranging categories and themes remain underexplored and where further research investment could improve integrated responses to emerging health threats.

1456 – Strengthening Leadership in One Health: A Structured Mentorship Program for Students and Early-Career Professionals

Hellen Wambui KARIUKI (1), Lilian Wangechi WAIBOCI (2), Kim Laura WEISZHAR (3), **Phaedra HENLEY** (4), Heidi AUERSWALD (5), Andrea Sylvia WINKLER (3,6)

1: Department of Microbiology, University of Nairobi, Kenya; 2: Department of Biochemistry, University of Nairobi, Kenya; waiboci@uonbi.ac.ke; 3: Department of Neurology, TUM University Hospital and Center for Global Health, TUM School of Medicine and Health, Technical University of Munich, Ismaninger Straße 22, 81675 München, Germany; 4: Center for One Health, University of Global Health Equity, Butaro, Rwanda; 5: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise Giuseppe Caporale; Teramo, Italy; 6: Department of Community Medicine and Global Health, Institute of Health and Society, Faculty of Medicine, University of Oslo, Oslo, Norway

IntroductionThe Women for One Health Network (WfOH) is an interconnected community of One Health (OH) professionals committed to advancing the participation of women and underserved groups in OH research, policy, and practice, thereby promoting equity, diversity, and inclusion. Through community consultations and member engagement, the WfOH network identified a gap in structured mentorship to support professional development and strengthen leadership in OH. In response, the WfOH Secretariat designed and implemented a mentorship program targeting post-secondary students and early-career professionals across OH disciplines. The program aims to strengthen mentees' knowledge, skills, and professional growth in OH practice while contributing to the development of the next generation of OH leaders.

MethodsThe WfOH Secretariat developed the mentorship program through a consultative, phased process incorporating stakeholder input and community feedback. A draft framework was presented to the WfOH community and refined. Supporting materials were developed, including program guidelines, mentorship agreements, application forms, and a sexual exploitation, abuse, and harassment policy. The program was hosted on the WfOH website to ensure secure access, confidentiality, and data protection. The launch was communicated through the website and community meetings. Applications were open to mentors and mentees of any gender, OH discipline, or geographic region and submitted through an online portal.

The Secretariat reviewed applications and matched mentors and mentees using agreed criteria including discipline, career goals, geographic location, and mentee preference for mentors from the WfOH expert database. Matched pairs were introduced through on line meetings, guided through program documents, and provided written consent to participate. Mentorship agreements defined goals, roles, and expectations, and mentorship engagements were designed to last one year.

Program monitoring included quarterly follow-ups by a designated Secretariat member to assess progress toward agreed goals and responsibilities. An online tracking system is under development. Success was assessed through completion of mentorship cycles, reported skills development, and career advancement among mentees.

ResultsA structured online mentorship program with an application, review, and approval system was developed and launched in March 2025. Within one year, 72 mentees, 20 mentors had registered, and 26 mentor–mentee pairs established, with some mentors supporting two mentees. In addition to the registered mentors, seven experts from the WfOH expert database were engaged to provide mentorship. Further analysis is underway to assess participant characteristics, mentorship experiences, and additional program outcomes.

ConclusionThe WfOH Network successfully developed and implemented a globally accessible mentorship program, establishing 26 mentor–mentee partnerships within its first year. By providing a structured and goal-oriented mentorship framework, the program promotes inclusive capacity building and supports career development for diverse professionals and emerging leaders. The initiative also offers a scalable model for mentorship that can contribute to strengthening the One Health workforce and leadership.

1465 – Expanding Geographical Front of a Pandemic-Potential Pathogen: A Spatio-Temporal Analysis of Nipah Virus Infection in Bangladesh, 2001-2025

Sharmin SULTANA (1), Mintu CHOWDHURY (1), Maruf Ahmed BHUIYAN (1), Wasik Rahman AQUIB (2), Sadia SULTANA (1), Mohammed Ziaur RAHMAN (2), Ahmed Nawsher ALAM (1), Joel M MONTGOMERY (3), Syed Moinuddin SATTER (2), Tahmina SHIRIN (1)

1: Institute of Epidemiology, Disease Control & Research, Bangladesh, People's Republic of; 2: icddr,b, Dhaka-1212, Bangladesh.; 3: Viral Special Pathogens Branch, Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA 30333, USA

Background:

Nipah virus (NiV) is a highly virulent pandemic potential zoonotic virus. The first recorded outbreak occurred in 1998-1999 in Malaysia and Singapore and subsequently it emerged in Bangladesh and India in 2001. Since then, it has gained a strong foothold with almost annual outbreaks in Bangladesh and occasional sporadic cases in neighboring India. Most cases in Bangladesh linked to drinking raw date palm sap contaminated with *Pteropus* fruit bats saliva or body fluids in winter season. Given its high fatality and pandemic potential, understanding the long-term spatiotemporal trend is a public health priority. To gain insights into the geographic spread 25 years of surveillance data is analyzed.

Methods:

We conducted a descriptive analysis of national human Nipah surveillance data from January 1, 2001 to December 31, 2025. The surveillance is conducted by Institute of Epidemiology, Disease Control and Research (IEDCR), in collaboration with icddr,b with technical support from US CDC and Coalition for Epidemic Preparedness Innovations (CEPI). Data were collected from findings from national outbreak response between 2001-2005 and routine systematic surveillance from 2006 onward. NiV cases were laboratory confirmed by ELISA during the early period of surveillance subsequently RT-qPCR was added for detection from throat swab and serum since 2017. The 25-year time period (2001-2025) is divided into five distinct time frames to evaluate the temporal expansion . Total number of cases, deaths and the case fatality rate (CFR) were also calculated for each distinct period to understand the epidemiological shifts.

Results:

Across the 25-year span, Bangladesh recorded a total of 347 Nipah cases, resulting in 249 deaths (CFR 72%). Geographically, NiV progressively expanded outward from the initial northwest-central “Nipah belt”. Starting from 11 affected districts (2001-2005), the virus has spread to 35 districts spanning across 6 divisions. The most dramatic geographic spread occurred between 2011 and 2015, adding 15 new districts. However, most cases are still reported from the initial affected districts(2001-2005), with sporadic infrequent cases from newly affected districts including coastal and island districts (e.g., Jhalakathi, Bhola). Notably, the fatality reached its peak at 78% in the most recent period (2021-2025). Moreover in the last 3 years fatality is 100% (2023-2025).

Conclusions:

Over the past quarter-century NiV has shown a gradual and progressive outward expansion including the coastal region, rendering the traditional “Nipah belt” concept obsolete. This expansion, coupled with persistently high fatality, significantly escalates the risk posed by this deadly virus which might indicate a viral adaptation to new demographic and ecological niche. These findings underscore the importance for scale up the surveillance in newly affected areas in “One Health” approach. In addition, in-depth research to find out the human animal interface areas, Community awareness and community engagement on risk behavior to prevent future spillover.

Table 1. NiV Cases, Deaths, and CFR with new districts from 2001 to 2025

Time Period	Cases	Deaths	CFR (%)	New Districts Added	Cumulative District
2001-2005	104	78	75.00	-	11
2006-2010	51	33	64.71	6	17
2011-2015	143	101	70.63	15	32
2016-2020	22	16	72.73	1	33
2021-2025	27	21	77.78	2	35
Total	**347**	**249**	**71.76**	-	**35**

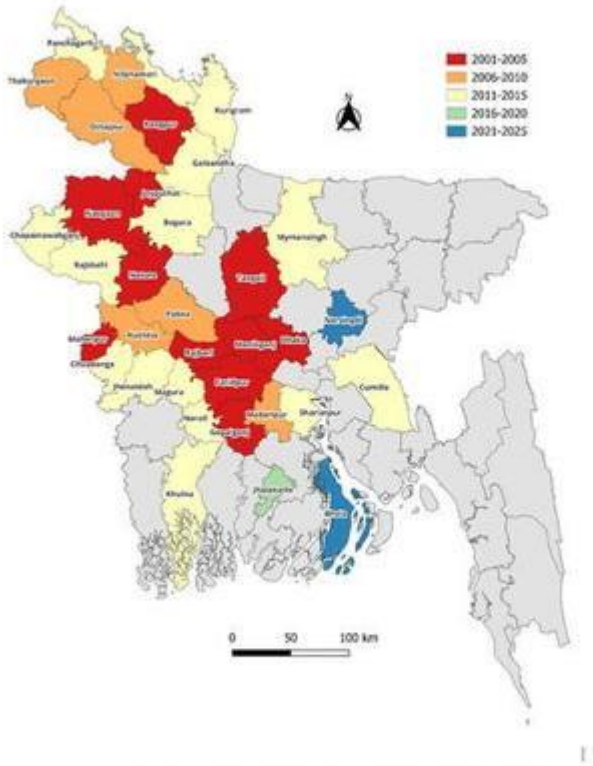


Figure 1. Spatiotemporal expansion of NiV infection between 2001 to 2025.

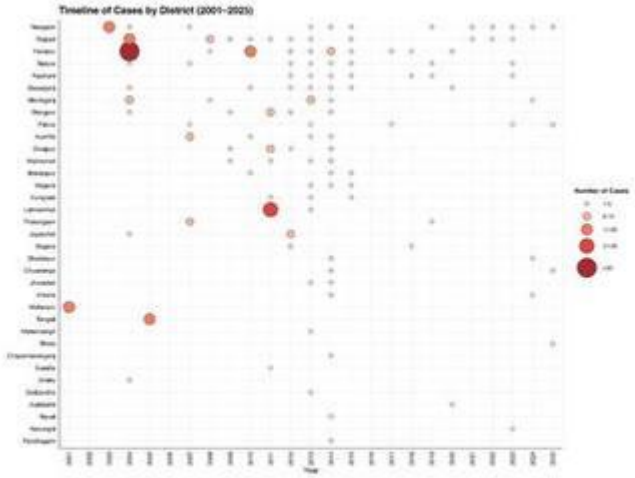


Figure 2. Timeline bubble plot of cases by district from 2001-2025.

1468 – Co-creating Community Engagement Strategies to Increase Rabies Post-Exposure Prophylaxis Uptake: A Multicountry Study in Tanzania, Côte d'Ivoire, and Chad

Monique LÉCHENNE (1,2), Kennedy Selestin LUSHASI (3), Kathrin HEITZ-TOKPA (4), Toguina MADJIADE (5), Bognan KONE (4), Nodjimbadem MBAIPAGO (5), Moussa Hassan YOUSSOUF (5), Rose Delima N'GUESSAN (4), Christian Tetteh DUAMOUR (3), Farida HASSAN (3), Salvador CAMACHO (1,2), Mahamat BECHIR (5), Bassirou BONFOH (4), Florence SECULA (1,2), Katie HAMPSON (6,7), Guillaume DESCHAMPS (1,2)

1: Swiss Tropical and Public Health Institute, Allschwil,Switzerland; 2: University of Basel, Basel, Switzerland; 3: Environmental Health and Ecological Sciences Thematic Group, Ifakara Health Institute, Tanzania; 4: Centre Suisse des Recherches Scientifiques en Côte d'Ivoire, Abidjan, Côte d'Ivoire; 5: Alliance Sahélienne des Recherches Appliquées pour le Développement Durable, N'Djaména, Chad; 6: School of Biodiversity, One Health and Veterinary and Life Sciences, University of Glasgow, Glasgow, UK; 7: University of Glasgow MRC/CSO Social and Public Health Sciences Unit, Glasgow, UK

Background:

Preventable rabies deaths prevail in many low-resource settings due to limited access to and low uptake of post-exposure prophylaxis (PEP). In preparation for the potential roll-out of PEP integration into the Expanded Program for Immunization (EPI), Gavi commissioned work to evaluate how co-created community engagement strategies (CES) may increase demand for PEP after potential rabies exposure.

Methods:

A multicentric qualitative study was conducted in Tanzania, Côte d'Ivoire, and Chad using transdisciplinary and participatory approaches to co-develop CES for PEP uptake. The Human-Centered Design framework followed three phases. In the inspiration phase, qualitative interviews and focus groups were conducted with identified stakeholders (community members, leaders, healthcare providers, civil society, teachers etc.). Discussions with adolescents and school groups captured perspectives from populations at higher risk of exposure. Results were analyzed following the WHO framework on behavioral and social drivers of vaccination. In the ideation phase, participatory co-design workshops were conducted to refine and adapt the CES proposed from the inspiration phase. The implementation phase piloted and evaluated the CES through follow-up interviews and discussions, complemented by monitoring indicators on bite reporting and care-seeking at health facilities.

Results

Persistent barriers to timely PEP included high costs, long travel distances, and limited awareness of services. Inconsistent PEP delivery contributes to loss to follow-up, reduced trust in health services, and reliance on traditional healers. General knowledge of rabies and its fatal outcome is high, but awareness of appropriate post-bite actions (exp. wound washing, timely PEP) is limited. Children were identified as

the most vulnerable group due to close contact with dogs, lower risk awareness, and unreported dog bites linked to fear of punishment. Participants emphasized the need for child- and mother-focused awareness strategies, including school-based education and engagement with women's and community groups to improve exposure detection. Co-creation workshops highlighted strong demand for context-adapted sensitization materials and engaging communication formats, such as theatrical performances and audio sketches. Trusted community actors such as religious leaders and community health workers were identified as preferred vehicles for message dissemination. Supporting materials co-developed with community members, including leaflets and picture boxes, enable local actors to better share key messages. The co-creation process represents a valuable learning opportunity, bringing together community members with representatives from the human and animal health sectors, fostering shared ownership and strengthening community-wide engagement.

Conclusion:

Co-creation approaches that engage trusted community actors and develop context-adapted communication tools can strengthen awareness efforts and foster shared and sustainable ownership. Results from the study's pilot phase will further inform context-specific recommendations for demand generation to ensure PEP uptake by those at risk. Strengthening PEP supply systems alongside community demand generation will also be essential during Gavi's rollout of PEP to build trust in health services.

1478 – One Health in Motion: Livestock Trade and Infectious Diseases Pathways in Rwanda

Soledad COLOMBE (1), Hugor SHEMA (2), Katharina KREPPEL (1), Wim VAN BORTEL (1), Fabrice NDAYISENGA (3), **Anselme SHYAKA** (4)

1: Institute of Tropical Medicine, Antwerp, Belgium, Belgium; 2: Africa Centre of Excellence for Sustainable Cooling and Cold Chain (ACES), Kigali, Rwanda; 3: Rwanda Agriculture and Animal Resources Development Board, Kigali, Rwanda; 4: Center for One Health, University of Global Health Equity, Butaro, Rwanda

Background

Livestock production supports global food security, but increased animal trade enhances the risk of animal and zoonotic diseases' spread across regions and borders – a critical One Health challenge. This study investigates how livestock movements from Rwanda's Eastern Province may drive diseases' spread and identifies priority intervention points within the trade network.

Methods

We collected official data on international live imports/exports as well as intra-national movements of live cows, sheep, and goats traveling by truck from Rwanda's Eastern Province, comprising seven districts (Nyagatare, Gatsibo, Kayonza, Rwamagana, Kirehe, Ngoma, Bugesera). Movement data included species, number of animals, origin and destination districts, dates, purpose, and season. Movements were mapped, and a directional network was built with nodes as district centroids and edges weighted by frequency, volume, and seasonality. Centrality measures were calculated, and seasonal variations analyzed. We assessed network resilience for species-specific networks using Giant Weakly Connected Component (GWCC) and Giant Strongly Connected Component (GSCC), performing sequential removal analyses: random, centrality-based, and greedy percolation (sequential removal of most-connected nodes). We quantified differences via Area Under the Curve (AUC), Relative Efficiency Index (REI), and bootstrap random resampling. Analyses were conducted in R v4.4.2.

Results

International movements were limited with 79 permits issued between 2020 and 2025 for 3375 animals. Most exported animals went to the Democratic Republic of the Congo, and most imports originated from Kenya. Intra-national movements were far more abundant, with 2132 permits issued in 2024**.** Most permits were for cows (68%) and most livestock originated from Nyagatare district. Rwamagana district issued the fewest permits. Shipments ranged from 1 to 300 animals of the same species and typically lasted 24h. The highest number of animals transported occured during the short rainy season (October - January). The majority of livestock was transported to other provinces in Rwanda (72%), primarily for butchering, with most going to Kigali, followed by the Western province. Key network parameters are summarized in Table

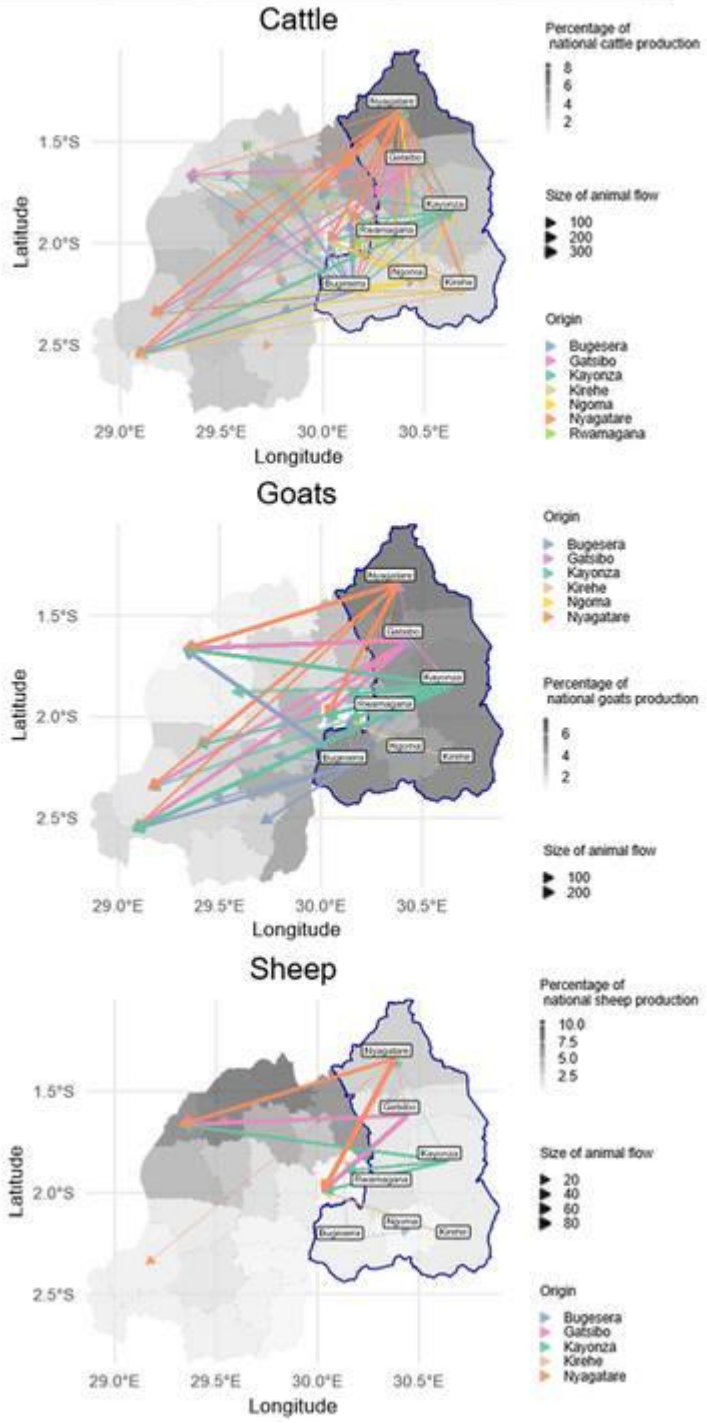
1. There were large differences in movement patterns between cattle, goats and sheep (Figure 1). Movement patterns did not differ per season but movement intensity did. Removing districts based on degree centrality for cattle and betweenness centrality for small ruminants reduced the GWCC almost as effectively as the greedy percolation strategy (REI = 0-0.190), indicating that degree and betweenness centralities are strong heuristics for identifying high-risk districts (Table 2). Analyses with GSCC provided similar results.

Conclusions

This study provides novel insights into livestock movement patterns in Rwanda and their potential role in infectious diseases' transmission. It revealed critical differences in the epidemiological roles of districts. Transport across the country within the span of 48h explains how outbreaks could spread nationally. Targeting centrally positioned districts could disrupt transmission pathways and limit disease spread.

Cows	Long Dry	19	79	4.52	34.85 (4.25-113.04)	5.26 (0-44)	0.01 (0.01-0.02)
	Long Rain	20	67	4.67	29.27 (0.69-109.72)	6.45 (0-58)	0.01 (0.01-0.02)
	Short Dry	21	69	5.65	28.54 (0.69-125.46)	6.43 (0-32)	0.01 (0.01-0.01)
	Short Rain	21	72	4.85	29.08 (2.64-121.91)	5.48 (0-35)	0.01 (0.01-0.01)
	Overall	**24**	**114**	**5.49**	**51.47 (1.1-196.61)**	**4.54 (0-40)**	**0.01 (0.01-0.01)**
Sheep	Long Dry	7	9	5.28	13.57 (3.43-24.12)	0 (0-0)	0.12 (0.06-0.29)
	Long Rain	10	11	4.23	10.09 (1.1-21.2)	0.2 (0-2)	0.17 (0.06-0.46)
	Short Dry	7	9	5.1	13.71 (1.95-22.07)	0.14 (0-1)	0.06 (0.05-0.08)
	Short Rain	6	7	6.63	15.47 (2.4-23.8)	0 (0-0)	0.07 (0.06-0.07)
	Overall	**12**	**15**	**4.68**	**13.35 (1.1-34.47)**	**0.33 (0-4)**	**0.17 (0.03-0.46)**

Figure 1: Movement of animals from the Eastern province in 2024 in Rwanda (cattle, goats and sheep from top to bottom).



1482 – Strengthening AMR Governance through Legislation: Lessons from the Quadripartite One Health Legislative Assessment Tool for AMR (OHLAT) Implementation

Carmen BULLON CARO (1), Aitziber ETCHEVERRIA (2), Camille LOI (3), Jorge MATHEU (4), Angelique MUHAVANI (2)
1: Food and Agriculture Organization of the United Nations (FAO); 2: United Nations Environment Programme (UNEP); 3: World Organisation for Animal Health (WOAH); 4: World Health Organization (WHO)

Background Antimicrobial resistance (AMR) arises from complex interactions across human, animal, plant and environmental domains, requiring coordinated responses across sectors and institutions. While the One Health approach has gained widespread recognition as a framework for addressing these interconnected risks, governance structures and surveillance systems remain largely fragmented across sector-specific authorities. The Quadripartite One Health Legislative Assessment Tool (OHLAT) was developed to support countries in strengthening legal preparedness for AMR under a One Health approach. Its first chapter focuses specifically on cross-sectoral governance mechanisms and other integrated responses constituting the key institutional foundations for coordinated AMR responses. This abstract presents a study that draws on two examples, the governance and surveillance components of OHLAT, to analyse how regulatory frameworks can support the establishment of sustainable One Health governance architectures for AMR.

Methods The study combines doctrinal legal analysis with comparative examination of national regulatory frameworks relevant to AMR governance and surveillance. The analysis draws on legislative assessments conducted using the Quadripartite OHLAT methodology in selected countries, complemented by review of legal datasets compiling national AMR-relevant legislation. The study also integrates findings from the literature on AMR integrated surveillance systems and AMR governance under a One Health approach. Particular attention is given to legal provisions establishing interministerial coordination mechanisms, institutional mandates for surveillance, data sharing arrangements, and accountability mechanisms across human, animal, plant and environmental health sectors.

Results Preliminary findings indicate that effective AMR governance requires a dual legal architecture combining cross-sectoral governance mechanisms with sector-specific regulatory frameworks. Legislation can play a critical role in institutionalising interministerial coordination platforms, clarifying mandates across ministries responsible for human health, agriculture (animal and plant health), food systems and environment, and establishing sustainable financing and operational structures for integrated surveillance systems. However, analysis also reveals persistent fragmentation across regulatory domains. Integrated surveillance systems remain unevenly developed and often lack clear legal mandates for cross-sectoral data sharing, joint analysis and coordinated decision-making. Where regulatory frameworks explicitly establish governance mechanisms and responsibilities for integrated surveillance, they provide a more stable institutional basis for One Health collaboration.

Conclusions Strengthening AMR governance requires moving beyond policy coordination towards legally grounded governance architectures capable of sustaining multisectoral collaboration over time. Legislation provides an important entry point for operationalising One Health governance by establishing institutional mandates, accountability mechanisms, and sustainable financing arrangements. The governance and surveillance components of OHLAT provide a practical framework for identifying legal gaps and supporting countries in building more coherent regulatory responses to AMR under a One Health approach.

1496 – Evaluation of Zika and Langat virus infections in Galapagos tortoise cells

Edwin OGOLA (1), Danielle K. OFFERDAHL (1), Ann MISURACA (2), Marshall E. BLOOM (1)
1: Laboratory of Virology, Division of Intramural Research, NIAID, NIH; 2: Conservation Science Wildlife Health, San Diego Zoo Wildlife Alliance

Tortoises are suspected reservoirs of arthropod-borne viruses that include viruses of major clinical and epidemiological significance, such as Western equine encephalitis virus and Crimean–Congo hemorrhagic fever virus. Further, we recently identified Jingmen tick virus (JMTV), a rapidly emerging segmented tick-borne orthoflavivirus-like virus, in tortoises. Phylogenetic analyses revealed greater genetic diversity in

tortoise-associated JMTV than in livestock-associated JMTV, suggesting the virus may have originated in tortoises. Tortoise-derived cell lines, as an *in vitro* analysis model, provide a valuable resource for studying viral biology, especially for emerging viral strains which are unable to replicate optimally in available cell lines. However, the biology of tick and mosquito-borne viruses in tortoises remains largely uninvestigated. Using complementary analyses combining immunofluorescence microscopy, plaque and immunofocus assays, and quantitative RT–PCR, we delineate replication dynamics of the mosquito-borne Zika virus (ZIKV) and the tick-borne Langat virus (LGTV) within Galapagos tortoise cells. Although both LGTV and ZIKV effectively established productive infections in Galapagos tortoise cells, LGTV exhibited higher mRNA replication activity and released a greater titer of infectious virions than ZIKV. Our results demonstrate that Galapagos tortoise cells support both LGTV and ZIKV infections, establishing a relevant *in vitro* system for investigating orthoflaviviruses infection dynamics. Evaluation of tortoise role in orthoflaviviruses transmission in disease endemic regions is warranted. This study is funded by the Intramural Research Program, NIAID, NIH.

1500 – Força_Saúde: Strengthening Public Health and Laboratory Capacities in Portuguese-Speaking African Countries through a One Health Cooperation Initiative

Isabel LOPES DE CARVALHO, **José MELO**, Força Saúde PROJECT TEAM, Sofia NÚNCIO
National Institute of Health, Portugal

Background:

Strengthening public health capacities is essential to address emerging health threats across interconnected human, animal and environmental systems. The Força_Saúde project was developed to reinforce institutional and laboratory capacities in Portuguese-speaking African countries through a collaborative One Health framework.

Methods:

The initiative is coordinated by the National Institute of Health Doutor Ricardo Jorge (INSA) in partnership with the National Institutes of Health of Angola, Cabo Verde, Guiné-Bissau, Moçambique and São Tomé e Príncipe. A hybrid capacity-building model was implemented combining synchronous online training, in-person courses, laboratory internships, technical workshops and specialised webinars. Training activities focused on priority public health areas including water and environmental quality, food safety, antimicrobial resistance, diagnosis of emerging infectious diseases, entomological surveillance, genomic sequencing and laboratory quality management. Participants came from diverse professional backgrounds across human and animal health sectors, reinforcing the interdisciplinary nature of the One Health approach.

Results:

Between 2024 and 2025, 62 training activities were conducted involving 472 professionals from partner institutions. Participant evaluations showed consistently high technical satisfaction levels, with average scores ranging from 4.3 to 4.8 on a five-point scale, reflecting the relevance of the training content and its applicability to professional practice. The hybrid training model enabled broad participation across participating countries while ensuring practical consolidation of technical skills through hands-on laboratory training and targeted technical support. Some logistical and institutional constraints partially affected implementation in specific contexts.

Conclusions:

Preliminary findings indicate that the project has contributed to strengthening technical expertise, improving laboratory practices and promoting the harmonisation of public health approaches across Portuguese-speaking African countries.

1502 – The impact of zinc oxide withdrawal in commercial UK pig herds on the presence of enterotoxigenic Escherichia coli and Rotavirus in weaner piglets

Andrew BEASE (1), Samuel CONNELLY (2), Nicky CRAIG (1), Jade DAVIES (2), Jas TIWANA (2), Muna ANJUM (2), Ilias KYRIAZAKIS (3), Sam BEECHENER (4), Abel EKIRI (5), Mark STEVENS (1), Nick WHEELHOUSE (6), Manal ABUOUN (2), Roberto LA RAGIONE (5), Ricardo CORONA-TORRES (1), Andy LAW (1), Linda OYAMA (3), Adrian MUWONGE (1), Amy TAYLOR (7), Deborah HOYLE (1)

1: The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, United Kingdom; 2: Animal and Plant Health Agency, United Kingdom; 3: Queen's University of Belfast, United Kingdom; 4: Scotland's Rural College (SRUC), United Kingdom; 5: University of Surrey, United Kingdom; 6: Edinburgh Napier University, United Kingdom; 7: AB Neo, United Kingdom

Background

Post-weaning diarrhoea (PWD) is an important disease of weaner piglets, resulting in morbidity and mortality. The primary causative agent is enterotoxigenic *Escherichia coli* (ETEC), with co-infecting pathogens, particularly Rotavirus (RV), contributing to disease susceptibility. Until recently, zinc oxide (ZnO) was added to feed at pharmacological levels (zinc, 2500 ppm) to reduce PWD. However, zinc is thought to contribute to antimicrobial resistance through common resistance mechanisms and contributes to environmental pollution. Zinc in feed above 150 ppm was therefore prohibited in the UK from June 2024. This study aims to investigate the impact of ceasing pharmacological ZnO supplementation on the presence of key ETEC and Rotavirus gene markers in weaner piglets, over the first 12 months following herd withdrawal.

Methods

Twenty-nine farrow-to-finish pig herds were recruited to a longitudinal study across the UK, running between 2022 to 2025. Herds were of median size 625 sows (range 100 – 1100). Sampling occurred at pre-ZnO withdrawal, and 3, 6 and 12-months post-withdrawal. Pooled pen faecal samples were generated by mixing 10 x 1 mL dropped pen-floor faeces within individual pens, for up to 10 weaner pens per herd, per time-point. Samples were snap frozen and stored at -80 °C. Metadata was collected at each visit, including information on vaccine use in sows/piglets, antimicrobial/coccidiostat use, and reporting of diarrhoea. Metagenomic DNA was extracted from faecal samples and tested by multiplex qPCR for ETEC-specific fimbrial and toxin genes[1]. RNA extracted from faecal supernatants was tested for Rotavirus species A, B, C and H by reverse transcription qPCR[2, 3]. Herd and sample level prevalence were determined for all targets, and for *E. coli* pathotype, according to combination of fimbrial and toxin signal. Relationships between the presence of ETEC genes and RV PCR signals, and key herd metadata variables will be determined using tabular methods, tetrachoric correlation and multivariate statistical analyses.

Results

Twenty-three herds completed the 12-month post-ZnO withdrawal sampling protocol, with six departing. Preliminary data showed F4 and F18 were the most common ETEC fimbrial genes, whilst F6 was rare; STa the most common toxin gene detected, at both sample and herd levels. Positive PCR signal for Rotavirus A, B and C was commonly observed across all study herds, with RVC the most frequent and RVH extremely rare. Following ZnO withdrawal, we observed an increase in reported diarrhoea in weaner pig cohorts, an increase in sow/gilt vaccination for ETEC and a slight uptick in coccidiostat use. Limited increase in antimicrobial use was reported following ZnO withdrawal, although product selection altered.

Conclusions

Further analyses are ongoing to determine herd and sample level prevalence of key PWD pathogen markers at all time-points, along with comparison of any changes to prevalence during the first 12-months following ZnO withdrawal.

1508 – Title: Blockchain-enabled Rabies control in Côte d'Ivoire and Mali: Ethical dimensions of technical and social adoption

Akissi Rose Delima N'GUESSAN (1,2), Kouamé Walter KRA (2), Kathrin HEITZ-TOKPA (1), Jakob ZINSSTAG (3), Bassirou BONFOH (1)

1: Centre Suisse de Recherches Scientifiques en Cote d'Ivoire, Côte d'Ivoire; 2: Université Alassane Ouattara de Bouaké, Côte d'Ivoire; 3: Swiss Tropical and Public Health Institute, Switzerland

Context: Rabies is a priority zoonosis targeted for elimination by 2030 in Côte d'Ivoire and Mali. However, fragmented inter-sectoral communication remains a significant barrier to coordinated control. Within a One Health framework, where data integration is paramount, blockchain technology offers novel avenues for strengthening stakeholder coordination through secure and transparent information sharing. To address these systemic gaps, the transdisciplinary BlockRabies App pilot test project based on blockchain was established for both countries. But technological hesitation, knowledge deficits about security, transparency, social, and ethical conditions of its adoption, in the pilot areas create uncertainty about the initial uptake of the application. This study analyzes the iteration of participatory testing and initial uses of the BlockRabies App with local actors, to identify ethical and socio-technical dynamics likely to determine its adoption, scale-up and long-term viability.

Methods: This inductive qualitative study was conducted in Côte d'Ivoire and Mali, the two countries where the BlockRabies App. is being implemented. A total of 35 involved participants of the project were recruited across both countries, including researchers, laboratory technicians, veterinary and public health professionals, software developers, decision-makers, and community representatives in the study sites. Data were collected through (i) participant observation during introduction workshops and field tests in rabies and veterinary centers; (ii) semi-structured interviews focusing on stakeholders' perceptions and representations; and (iii) a comprehensive desk review of project documents and ethical review process documents. The transcribed recording and paper-based data were both coded subjected to thematic content analysis assisted by Nvivo 14. The data analysis was guided by approaches from transdisciplinarity, new institutional economics, the ethics of health technology, and the sociology of innovation and use.

Results: The results highlight a dynamic of social interaction and inclusive participation among stakeholders around technology, thereby fostering its acceptance. The BlockRabies App was implemented through good collaboration between rabies centres, veterinary services researchers, IT-experts and laboratories. This cross-sector partnership was supported by mutual learning and institutional agreements, helped structure data governance and facilitate the circulation of Rabies cases information.

The results also show local adjustments and adaptations of the technology. Practical training was key to support users to gradually adjust and adapt the interface and functionalities of the application to professional needs and practices.

The initial use of technology reflected a gradual integration of it into existing professional practices. The application is not rejected, but its adoption remains limited. Information management continues to be hybrid, combining paper forms, telephone communication and digital tools, due to technical constraints, particularly unstable and irregular Internet access, highlight the need for an offline version.

Conclusion: The viability of blockchain depends on an appropriate legal framework, the availability of reliable IT infrastructure, the involvement and commitment of the relevant institutions, training, users' motivation.

1520 – Operationalizing One Health in Latin America: From Assessment to Investment-Ready Action

Mariela VARAS

The World Bank

Latin America sits at the frontline of emerging health threats at the human–animal–environment interface. Exceptional biodiversity, accelerating land-use change, expanding agricultural frontiers, and persistent social inequities increase the region's vulnerability to zoonotic diseases, climate-related hazards, and future pandemics. Although many countries have conducted One Health assessments and multisectoral diagnostics, a persistent challenge remains: translating gaps into prioritized, costed, investment-ready actions that inform policy decisions and attract sustainable financing.

This session presents an innovative approach designed to bridge that gap, developed through the PAHO-World Bank PROTECT project and strengthened through the FAO-IDB-IICA-PAHO-World Bank PIVOT initiative, both financed by the Pandemic Fund. In 2025-6, PROTECT conducted comprehensive One Health assessments in Colombia, Brazil, Chile, and Ecuador, integrating documentary review, aligned with international frameworks (SPAR, JEE, and PVS), multisectoral stakeholder interviews, technical capacity

analysis, and participatory, multidisciplinary workshops with national and subnational actors. Similar diagnostics conducted independently in Guyana, leading to the formulation of a costed National Action Plan for Health Security, provide additional insight into the challenges faced by small and vulnerable states, as well as an example of concrete implementation of One Health investments.

The key innovation is the transition from **diagnostic assessment to prioritization, costing, and operational and investment planning**through a structured continuum**.** In the abovementioned countries, this process supports the development of country-owned, multisectoral priority intervention packages designed to strengthen integrated surveillance, improve governance and coordination across sectors, and reduce zoonotic risk in priority territories. Crucially, the process also generates policy-relevant evidence to support decision-making, linking technical gaps to economic analysis and potential returns on investment in prevention, preparedness, and early detection.

To support this transition from evidence to action, an economic decision-support tool was developed and applied across the four countries to estimate implementation costs, identify multisectoral financing needs, and model the potential economic benefits of strengthened One Health systems. The tool enables governments and partners to translate technical recommendations into investment scenarios aligned with national planning cycles.

The assessments reveal both shared multisectoral challenges and context-specific implementation barriers. Common gaps include fragmented governance structures, limited interoperability between surveillance systems, and insufficient institutionalized mechanisms for cross-sector coordination. Additionally, territorial variation—particularly in Amazonian regions, border areas, and rapidly expanding peri-urban zones—requires differentiated strategies for implementation and investment.

By presenting comparative insights across multiple contexts, this session highlights how a consistent methodological framework can generate actionable evidence while remaining adaptable to diverse institutional, ecological, and epidemiological realities. Participants will gain practical insights into transforming One Health assessments into prioritized, costed, and financeable intervention pathways. The session demonstrates how strengthening the evidence base for multisectoral decision-making can accelerate the operationalization of One Health and support more strategic investments in health security and pandemic prevention.

Proposed Presentations

1. *From Gap Assessment to Prioritization: The PROTECT Multisectoral Methodology*

This will provide an overview of the diagnostic and prioritization framework used in Colombia, Brazil, Chile, and Ecuador, including capacity assessments, SPAR/JEE/PVS alignment, multisectoral consultations, and participatory territorial prioritization. The presentation will show how PROTECT generated actionable, country-owned priorities linked to implementation pathways.

2. *Comparative Regional Insights: Cross-Country Patterns and Territorial Differentiation in One Health Gaps*

This talk presents regional findings across Colombia, Brazil, Chile, Ecuador, and the independently developed diagnostic in Guyana. It highlights recurring cross-country patterns, including governance fragility, limited surveillance integration, and system interoperability barriers, while contrasting them with territorially differentiated needs in Amazon, border, and peri-urban settings. This comparative perspective underscores scalability and transferability.

3. *One Health and National Action Plan implementation: Insights from the Guyana Diagnostic*

A focused presentation on the independent One Health assessment, as well as the formulation, costing and implementation of the National Action Plan for Health Security (NAPHS) in Guyana will illustrate how small states with limited human resources, dispersed populations, and high ecological vulnerability face distinct One Health challenges and how Guyana has managed to secure resources and start implementing key One Health activities prioritized in the NAPHS.

4. *From Prioritization to Investment: The One Health Economic Decision-Support Tool*

A dedicated presentation on the economic tool developed under PROTECT and strengthened under PIVOT. It will describe how the tool estimates implementation costs, multisectoral investment needs, and expected economic returns from improved governance and surveillance. The talk will show how this tool supports budgeting, prioritization, and alignment with the Pandemic Fund and other financing mechanisms.

5. *From Assessment to Implementation: The PIVOT Model for Governance, Financing, and Economic Decision-Support*

An introduction to how PIVOT builds on the activities and results from PROTECT to create an operational package, including a systematic diagnostic, formalizable governance architecture, costed interventions and multisectoral capacity building at the nation level, as well as strengthened coordination mechanisms across LAC countries. The session will also describe the development and future refinement of the economic tool designed to estimate investment needs and expected returns for One Health interventions.

Session Structure and Agenda (90 minutes: 75 minutes and buffer time)

Time	Segment	Title / Focus	Speaker(s)*
10 min	Introduction & Framing	Overview of the assessment-to-investment pipeline and session objectives	Session Co-Chairs: Dr. Natalia Cediel & World Bank (TBC)
8 min	Presentation 1	From Assessment to Prioritization: The PROTECT Multisectoral Methodology	Dr. Natalia Cediel
8 min	Presentation 2	Regional Comparative Approach and Methodological Reflections	PROTECT team (Mariela Varas / Stefany Ildefonso / Phillis Kim)
8 min	Presentation 3	One Health and National Action Plan implementation: Insights from Guyana	Federica Secci / Ministry of Health of Guyana
10 min	Presentation 4	Costing and Investment Planning: The One Health Economic Decision-Support Tool	Carlos Castañeda-Orjuela
6 min	Presentation 5	From Priorities to Financeable Packages: Linking PROTECT and PIVOT	World Bank (Leah Germer / Melissa Brown)
15 min	Moderated Discussion	Translating assessments into investment-ready implementation pathways	All speakers
10 min	Synthesis & Closing	Key takeaways and reflections	Session Co-Chairs

*Gender balance is being considered

1524 – From Case Studies to Collective Problem-Solving: Insights from the Quadripartite One Health Governance Community of Practice

Marion SELOSSE (1), Katie WOOLASTON (2), Emilie Michelle RONIS (2), Cheng LIANG (3), Chadia WANNOUS (4), Mauro DE ROSA (4), Linda AWADA (1), Carmen BULLON (1), **Fairouz LARFOUI** (1)

1: FAO, Italy on behalf of the Quadripartite (FAO,UNEP, WHO,WOAH); 2: United Nations Environment Programme (UNEP), Nairobi, Kenya; 3: World Health Organization (WHO), Geneva, Switzerland; 4: World Organisation for Animal Health (WOAH), Paris, France

Effective implementation of One Health depends on governance systems that enable sustained coordination, collaboration and shared decision-making across human health, animal helath and the health of the environements sectors. While the importance of governance is widely recognised, practitioners consistently report a lack of practical, experience-based guidance on how One Health governance arrangements operate in real contexts, how they are maintained over time, and how common challenges can be addressed.

This session is grounded in the work of the Quadripartite's Community of Practice on One Health Governance (CoP), a global forum for shared learning and knowledge dissemination on governance design and implementation. Since 2025, the CoP has convened thematic webinars on regional experiences in Latin America and the Caribbean, environmental integration in the Asia–Pacific region, community governance in Africa, governance experiences in the EU, and global barriers and enablers for OH implementation. It has also developed a growing set of structured country case studies—including New Zealand, Brunei, Cuba and Peru—with additional cases in development.

During country support for JPA implementation, governments consistently sought guidance on One Health governance and frequently asked how cross-border countries had organized similar mechanisms, underscoring the value and relevance of the CoP on Governance.

The session will present a curated selection of governance case studies from the CoP, applying a common analytical framework that examines governance structure, multisectorality and inclusion, capacity building, sustainability, outcomes and challenges. Rather than highlighting "best practices", the cases illustrate diverse governance pathways across political, institutional and socio-ecological contexts, enabling meaningful comparison and learning.

An extended Ask-the-Expert forum will serve as the core interactive component. Case presenters and governance experts will address practical challenges such as institutional silos, legal anchoring, financing and sustainability, Indigenous and community engagement, and scaling governance mechanisms across levels of government. This format transforms the session into a collective problem-solving exercise, reflecting the ethos of the Governance CoP.

The session will be relevant to policymakers, OH platform coordinators, researchers and development partners seeking practical insights into governance design and sustainability.

Educational outcomes Participants will:• gain practical insight into how One Health governance mechanisms operate across different country contexts;• understand common governance challenges and enabling conditions identified through comparative case analysis;• learn how structured case studies can support implementation, learning and adaptation; and• engage directly with experienced practitioners to explore solutions relevant to their own contexts.

Proposed Session Structure (90 minutes)• Framing and Context (20 min): Overview of OH governance scope and CoP methodology.• **Lightning Case Studies (30 min):** 7–8 minutes each, using a structured presentation template.• **Ask-the-Expert Forum (40 min):** Moderated discussion on legal anchoring, financing, community engagement, institutional silos and sustainability, followed by audience Q&A.Further information on the agenda in the attached table. Particular attention will be paid to ensure gender balance.

Proposed WOHC Session

From Case Studies to Collective Problem-Solving: Insights from the Quadripartite One Health Governance Community of Practice

Segment	Talk title	Speaker(s)	
Opening & Context Setting (20 min)	The One Health Governance CoP and defining the scope of OH Governance	CoP on One Health Governance Representative	**Particular attention will be paid to gender balance representation in the Speakers**
Presentation 1 (10 min)	Lightning Case Study #1	TBC - Government representative from one of the case studies presented in the CoP already from	
Presentation 2 (10 min)	Lightning Case Study #2	TBC - Government representative from one of the case studies presented in the CoP already from Asia and the Pacific	
Presentation 3 (10 min)	Lightning Case Study #3	TBC - Government representative from one of the case studies presented in the CoP already from Africa	
Q&A (40 min)	Ask the Expert Forum: From case studies to collective problem solving, including audience Q&A	Panelists (including country, One Health practicioners, Quadripartite representatives)	

1537 – Knowledge co-production and One Health intervention co-design: A bottom-up model for community engagement around Taï National Park, Côte d'Ivoire

Gilbert FOKOU (1), Bognan Valentin KONE (1,2), Cyrille Aubin DOHO (1,3), Affoué Ruth Danielle KONAN (1,3), Seydou KONE (1), Bassirou BONFOH (1)

1: Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, Côte d'Ivoire; 2: Institut National de Santé Publique, Abidjan, Côte d'Ivoire; 3: Institut d'Ethnosociologie, Université Félix Houphouët-Boigny, Abidjan, Côte d'Ivoire

Background

The One Health (OH) approach that encompasses a holistic view of health linking the wellbeing of animals, people, and the environment aligns with the ways of knowing, doing, and being of indigenous communities. Stakeholders from different scientific disciplines, sectors and regions, increasingly collaborate in developing interventions that are related to contexts of the realities in which a particular complex problem or challenge is inserted. However, there has been little emphasis on understanding and incorporating local knowledges and communities within the One Health framework. The people-centred health care approach that organizes health systems around the comprehensive needs, preferences, and values of individuals, families, and communities, offers a solution that epistemologically considers the context. This study aims to assess the modalities for developing pathways of One Health Interventions in localised contexts with the views of communities.

Methodology

A mixed method approach was used to collect qualitative and quantitative data during two research studies in 2022 and 2025 in Taï (Southwest Côte d'Ivoire). The first study assessed anthropogenic risk factors for the emergence of zoonoses from wildlife around Taï forest using a household survey (n=331) and Focus Group discussions (FGD) with communities (n=5). The second study assessed behavioural change interventions over wildlife meat consumption using FGD (n=12) and key informant interviews (n=8). Quantitative data were collected with tablets equipped with Open Data Kit (ODK) application and imported into R software version 4.2.1 for statistical analysis. Qualitative discussions were transcribed on Microsoft Word, manually coded and analysed using a conventional content analysis.

Results

Populations living around protected areas are characterised by a localised pragmatism considering the dynamic needs of each specific community. They argue that the boundary between human, animal and ecosystem health is not clearly defined, with humans positioned at the centre of the system rather than

the periphery. They exhibit a “hybrid epistemology” as results of multiples and integrated health and conservation interventions and persistence of traditional knowledge, creating a space within the community for the integration of different types of knowledge, and for “co-design” of interventions. Local initiatives to structure OH operations from below are experimented through a local and decentralised platform for the control of epidemics and zoonosis emergencies involving policymakers, and sectoral government operational agencies. However, community voices remain overlooked at the health governance level, limiting community ownership and engagement on top-down interventions.

Conclusion

Understanding views, nuances and local meanings is likely to contribute to designing robust OH interventions in local communities. Privileging local voices, experiences and resilience patterns allows for the development of community-based understandings of how health risks play out and are conceived, perceived, and experienced in a specific context. Neglecting community voices could limit community engagement in zoonosis surveillance system.

1542 – COST Action BeSafeBeeHoney - BEekeeping products valorization and biomonitoring for the SAFEty of BEEs and HONEY

Laura GRÁCIO (1,2), **Marta LEITE** (2,3), **Andreia FREITAS** (2,3)

1: Faculdade de Ciências Universidade do Porto (FCUP), Rua do Campo Alegre, 4169-007 Porto, Portugal.; 2: Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Rua dos Lágidos, Lugar da Madalena, 4485-655, Vila do Conde, Portugal & REQUIMTE/LAQV, R. D. Manuel II, Apartado, 55142, Porto, Portugal; 3: REQUIMTE/LAQV, R. D. Manuel II, Apartado, 55142, Porto, Portugal

Honey has been a popular functional food since ancient times, due to its healthy properties. These are based on its bioactive compounds, which have antioxidant, antimicrobial, anti-inflammatory and anticancer properties. Furthermore, the European honeybee, *Apis Mellifera*, is one of the most important pollinators, playing a crucial role in food and plant production. However, bees are in decline, facing the threat of extinction in Europe due to anthropogenic activities, including agriculture intensification and pesticide application. This has resulted in a 40% decrease in domestic honey production, with the remaining 60% of EU consumption being imported. The present network is set to make a significant contribution to the field of beekeeping by facilitating cooperation between international stakeholders and driving progress in the sector. Key topics that will be explored include:

1. Honey and by-products: an exploration of their nutritional and medicinal properties.

2. The presence of abiotic stressors and anthropogenic contaminants in the environment can be determined using hive products as indicators.

3. The following report outlines the prevalent diseases and biotic stressors that threaten honeybee colonies.

4. The role of honeybees as pollinators in agriculture, and the consequences of lost colonies in agrarian ecosystems.

5. We specialise in policy research and market analysis related to beekeeping activities.

BeSafeBeehoney is a COST Action that adopts a multi-actor approach, bringing together distinct expertise in the fields of chemistry, biology, ecology, veterinary science, beekeeping, agrarian engineering, nutrition, economy and policy. This will ensure the delivery of breakthrough scientific developments. The importance of beekeeping is in line with Sustainable Development Goals 2, 12 and 15, which aim to promote sustainable agriculture, quality production and sustainable use of terrestrial ecosystems. Achieving gender equality is still a constant challenge, but it is an ongoing priority for the team. More than half of the team members are women, young researchers from inclusivity target countries, and they are committed to inclusivity.

Acknowledgements: This presentation is based upon work from COST Action CA22105 – BeSafeBeeHoney, supported by COST Association (European Cooperation in Science and Technology).

References:

1. Memorandum of understanding CA22105, available at https://www.cost.eu/actions/CA22105/

1549 – Community engagement as a driver of One Health implementation: perspectives from the World Bank Health Security Program in West and Central Africa

Carolyn SHELTON, Charlotte SCHRURS, Paul Jacob ROBYN, Collins CHANSA, Andre CARLETTO, Chijioke OKORO, Luis FLOREZ, Jorge BARRETO, Franck BERTHE
The World Bank Group

Background: West and Central Africa face persistent public health challenges, including recurrent outbreaks of zoonotic origin as well as a high burden of antimicrobial resistance (AMR). These threats emerge at the human–animal–environment interface and are often first detected at community level, where interactions between humans, livestock, wildlife, and ecosystems are frequent. Communities play a central role in supporting early detection and response to health threats.

Recent outbreaks, including Ebola and COVID-19, highlighted the importance of strengthening risk communication and community engagement (RCCE) and community-based surveillance as fundamental components of health security systems. Despite sustained investments and commitment to health security, several countries in the region still have gaps in community engagement, risk communication, and early detection mechanisms. To address this constraint, the World Bank Group established the Health Security Program (HeSP) in West and Central Africa to strengthen countries' capacities to prevent, detect, and respond to health emergencies while operationalizing the One Health (OH) approach.

Methods: HeSP integrates community engagement as a central pillar of OH implementation. Interventions align with National Action Plans for Health Security, International Health Regulations, and the World Organisation for Animal Health standards. HeSP activities focus on strengthening RCCE systems, community-based surveillance, and prevention messaging related to zoonotic diseases, infection prevention and control, AMR, and water, sanitation and hygiene.

In *Liberia, Guinea, and Cabo Verde*, community engagement activities support awareness campaigns and strengthen community-based surveillance. Community health and animal health workers detect and report unusual health events, linking community reporting mechanisms with national surveillance systems such as the Integrated Disease Surveillance and Response and Surveillance Outbreak Response Management and Analysis System (SORMAS).

In *Nigeria*, community engagement is reinforced through decentralized health security structures at federal, state, and local government levels, with training enabling community health and animal health workers to report unusual health events through digital platforms such as SORMAS.

In *Cameroon, Central African Republic, Chad, and Republic of Congo*, community engagement supports cross-border preparedness and response through participatory risk communication campaigns in border areas and outreach to mobile and pastoralist populations.

Results: Expected outcomes include strengthened community participation evidenced by enhanced community-based surveillance, stronger linkages between community reporting mechanisms and national surveillance platforms, and expanded training of community and animal health workers in prevention messaging and early detection of health threats. HeSP also supports RCCE strategies, stakeholder engagement plans, and grievance redress mechanisms to strengthen dialogue between communities and public health authorities.

Conclusions: HeSP demonstrates how community engagement can enable the operationalization of the OH approach in West and Central Africa. By strengthening RCCE, community-based surveillance and cross-sector collaboration, HeSP supports more resilient health systems while generating broader development benefits, including job creation and skills development in rural and underserved areas.

1551 – Migration strategy and stopover shape gut microbiomes of passerines across breeding sites in Eastern Europe and a Middle East stopover

Jeanne FAIR (1), Nisreen ALMOUND (2), Lela UNUSADZE (3), Denys MUZYKA (4), Jennifer OWEN (5), Jean TSAO (6), **Andrew BARTLOW** (7)
1: Global Conservation Institute, United States of America; 2: Royal Scientific Society, Jordan; 3: National Center for Disease Control, Georgia; 4: National Scientific Center Institute of Experimental and Clinical Veterinary Medicine, Ukraine; 5: Archbold

Biological Station, United States of America; 6: Michigan State University,United States of America; 7: Los Alamos National Laboratory, United States of America

Background:

Migratory birds connect distant ecosystems and may redistribute microbes and pathogens across flyways. However, it remains unclear whether migration strategy (resident vs partial migrant vs obligate migrant) consistently predicts gut microbiome structure on breeding grounds. It is also unknown whether spring stopover sites primarily create shared, location-specific microbiome signatures or increase microbiome instability. We evaluated two separate comparisons to evaluate migration and stopover effects on passerine microbiomes: (A) a three-species comparison across breeding locations in Georgia and Ukraine and (B) a stopover vs breeding-country comparison in two migratory warblers.

Methods:

Fecal samples were collected from three passerines representing resident (Blackbird), partial migrant (Eurasian Blackcap), and obligate migrant (Lesser Whitethroat) on breeding grounds in Georgia and Ukraine, including Ukraine samples spanning multiple sites. In a second dataset, Eurasian Blackcaps were sampled in Georgia and at a spring stopover site in Jordan, and Lesser Whitethroats were sampled in Ukraine and Jordan. Samples were preserved in RNAlater or DNA Shield and frozen within hours. DNA was extracted using the Zymo Quick DNA Fungal/Bacterial Miniprep kit and libraries were prepared with a Quick-16S V3–V4 workflow (Zymo). Libraries were sequenced on an Illumina NextSeq 1000. Reads were processed in QIIME2 in EDGE Bioinformatics with DADA2 and taxonomy assigned using a SILVA V3–V4 reference. ASVs, taxonomy, and metadata were analyzed in phyloseq in R with genus-level summaries; alpha diversity and community composition were evaluated using ordination and permutation-based tests, and dispersion was assessed to quantify inter-individual variability.

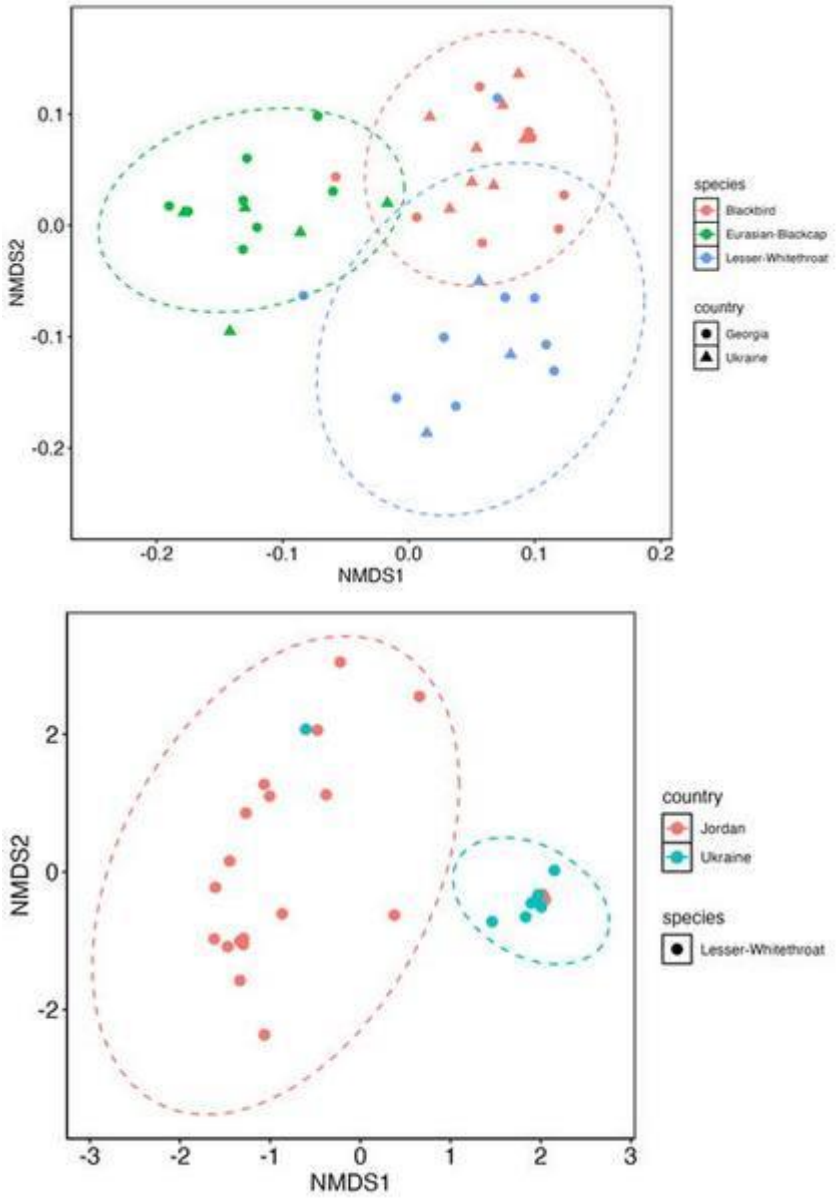
Results:

(A) Across the three-species breeding comparison in Georgia and Ukraine, host species explained more variation in microbiome composition than breeding location. Contrary to expectations that obligate migrants would show higher microbiome instability, dispersion (inter-individual variability) did not differ meaningfully among the three species, even with geographically distributed sampling within Ukraine.

(B) In the warbler stopover comparison, microbiome composition differed between the Jordan stopover and breeding-country sites for both species, consistent with location-associated shifts in community membership. Alpha diversity patterns were species-specific: richness differed by location while Shannon diversity was broadly similar. Evidence for stopover-associated instability was also species-dependent: Lesser Whitethroats showed greater dispersion at the stopover site, whereas Blackcaps showed comparable dispersion between locations.

Conclusions:

Together, these findings indicate that passerine gut microbiomes are strongly structured by host species, with location contributing additional compositional shifts. Migration strategy alone did not predict higher microbiome dispersion on breeding grounds, but stopover dynamics were associated with increased inter-individual heterogeneity in the obligate migrant. Because stopover and breeding-country sampling occurred in different months (April vs May), migration phenology and settlement on breeding grounds may contribute to observed location patterns.



1557 – One Health Approaches to Preventive Veterinary Medicine in Northern Canada Support Indigenous Community Health and Veterinary Training in Cultural Humility and Access to Care

Tessa BAKER (1), Jean WALLACE (2), Tacia TSIMARAS (2), Mikaela MACGILLIVRAY (2), Melanie ROCK (3), Cindy ADAMS (1), Frank VAN DER MEER (1), **Susan KUTZ** (1)

1: University of Calgary Faculty of Veterinary Medicine; 2: University of Calgary Faculty of Arts; 3: University of Calgary Faculty of Medicine

For 19 years, the Sahtu region of the Northwest Territories, Canada, has partnered with the University of Calgary to deliver a community-engaged veterinary outreach program aimed at improving dog health, supporting community wellbeing, and reducing risks at the human–animal interface. This long-running program is unusual in its continuity and offers a unique opportunity to evaluate change over time through a One Health lens. A mixed-methods program evaluation—drawing on medical record review, household surveys, dog census data, and thematic analysis of qualitative responses—was undertaken to assess longitudinal trends in dog health, community attitudes toward dogs, and the evolving experiences of veterinary service providers (VSPs).

Chart reviews of over a decade of clinic records (2008–2018) demonstrated substantial improvements in dog health and preventive care uptake across participating communities, including a marked increase in

vaccination (rabies: 26% to 78%; core vaccines: 15% to 73%) and deworming rates (15% to 86%). The median age of dogs increased significantly, suggesting enhanced survivability and overall health, while the proportion of dogs in ideal body condition rose from 38% to 70%. Sterilization uptake varied by community but remained consistently higher for female dogs than for males, reflecting local preferences and access considerations.

Household surveys and dog census efforts revealed that nearly half of all community dogs were captured in questionnaire data, enabling robust interpretation of changing human–animal relationships. Between 2008 and 2017, residents reported notable improvements in dog-related issues, including fewer concerns about overpopulation and increased access to dog-related resources. The proportion of respondents expressing an overall positive attitude toward dogs increased from 62% to 77%. Qualitative thematic analysis highlighted shifting norms around dog welfare, increased perceptions of safety, and strengthened community capacity to address dog-related challenges.

Complementing community-level findings, a parallel study of veterinary students, veterinarians, and technicians participating in the program (2015–2021) demonstrated that remote clinical outreach fosters cultural humility, client-centered care, and confidence practicing within resource-limited environments. Participants described meaningful relationships with community members, enhanced adaptability in clinical decision-making, and professional growth grounded in reciprocal learning.

This evaluation illustrates how sustained, community-driven veterinary outreach contributes to improved animal health, strengthens human–animal relationships, and supports culturally informed service delivery—key pillars of a One Health approach in remote and underserved regions. The findings underscore the importance of long-term partnerships and context-specific care models in achieving durable One Health outcomes.

1564 – Investigating the complex challenges within three Southern African livestock food systems to identify intervention points for systems resilience using One Health and Systems Thinking

Kevin QUEENAN (1), Michelle NORTH (2), Wilson NANDOLO (3), Nobuhle LUNGU (4), Andrew ARDINGTON (5), Vimbai HAMANDISHE (6), Vincent HENWOOD (7), Bettie KAWONGA (3), Mjabuliseni NGIDI (2), Stanford MUYILA (8), Julius MUSEVENZI (6), Liveness BANDA (3), Barbara HAESLER (1), Rob SLOTOW (2)

1: Royal Veterinary College, United Kingdom; 2: University of KwaZulu-Natal, South Africa; 3: Lilongwe University of Agriculture and Natural Resources (LUANAR), Malawi; 4: University of Cape Town, South Africa; 5: Regenerative Agriculture Association of South Africa; 6: University of Zimbabwe; 7: Department of Agriculture, Western Cape, South Africa; 8: Department of Animal Health and Livestock Development, Malawi

Livestock food systems in Southern Africa underpin human health and wellbeing by providing livelihoods, food and nutrition security, and significant socio-economic value. Yet these systems are increasingly exposed to, and contribute to, major global challenges, including climate change, pollution, biodiversity loss, natural resource degradation, and a wide range of health risks. Within the Wellcome Trust funded Sustainable and Healthy Food Systems - Southern Africa programme (SHEFS-SA), a One Health approach based on Systems Thinking was used to investigate the complex functioning of three livestock food systems in Malawi, South Africa, and Zimbabwe, and to identify interventions that would improve system resilience and sustainability while maintaining food and nutrition security.

A team of international and regional livestock academic researchers, and representatives from governmental departments and agriculture associations in the three countries met in a series of in-person workshops and virtual meetings, supported by the African Synthesis Centre for Climate Change, Environment, and Development (ASCEND), based in South Africa.

The Systems Thinking process that was followed included understanding the situation, defining the problem, determining boundaries, system conceptualisation, stakeholder mapping and engagement, and identification of interventions. An initial review of current trends in national livestock production and trade, nutrition and health challenges, and consumption patterns formed the foundation for the selection of a livestock system of interest in each country at the first in-person workshop, namely dairy in Malawi, beef in South Africa, broilers in Zimbabwe. For each system, a problem statement was developed and used to establish boundaries of scope for the system. Rough-draft systems maps were developed and formed the basis for the development of Causal Loop Diagrams (CLDs). The latter were generated in

Vensim PLE software through a series of virtual meetings to identify variables and causal links. Draft versions were shared and reviewed at a follow up in-person workshop and were revised and shared again in virtual meetings. This combination of in-person and virtual meetings allowed time for this iterative process beyond the confines of a workshop agenda.

These CLDs highlighted the system complexity, interconnectedness of variables, and feedback loops, and will be used during wider stakeholder engagement to identify potential areas of intervention based on the project's aim. Stakeholders from throughout the system were identified and mapped based on their degree of Interest and Influence. They will be recruited to review and validate the CLDs and to use them to engage in discussions to identify and prioritise feasible interventions. These results will provide the basis for subsequent scenario modelling and testing of interventions before policy recommendations are formulated. Comparisons between all three country's systems will provide a better understanding of the impact of climate change and other challenges across the region's livestock sector and guide regional policy recommendations.

1573 – Antibiotic Footprint Analysis as a One Health Tool to Estimate National Antimicrobial Consumption at human-animal interface: A Case Study from Pakistan

Muhammad Farooq TAHIR (1), Muhammad Usman ZAHEER (2)

1: Integral Global, Pakistan; 2: Food and Agriculture Organization, Regional Office for Asia and the Pacific, Bangkok, Thailand

Antimicrobial resistance (AMR) is a growing global public health threat driven largely by the irrational use of antimicrobials across human and animal health sectors. Monitoring antimicrobial consumption (AMC) is therefore essential for informing stewardship interventions and guiding policy responses aimed at mitigating AMR. The Antibiotic Footprint Analysis (AFA) framework has emerged as a One Health communication and analytical tool designed to quantify and visualize antibiotic consumption across sectors, analogous to the concept of a carbon footprint. By aggregating antimicrobial consumption data into a simplified metric, AFA facilitates comparison across sectors and helps highlight patterns of antibiotic use relevant for evidence-based policymaking.

This study applied the Antibiotic Footprint Analysis approach to estimate and compare national-level antimicrobial consumption across human and animal sectors in Pakistan for the year 2019, providing an initial baseline for future surveillance and stewardship efforts.

Human antibiotic consumption was estimated using a combination of pharmaceutical sales data, public sector procurement estimates, and import data for vertical health programs. Consumption was standardized using the World Health Organization Anatomical Therapeutic Chemical/Defined Daily Dose (ATC/DDD) methodology and expressed as Defined Daily Doses per 1,000 inhabitants per day (DID). Antimicrobial consumption in the animal sector was estimated using national import data extracted from the Pakistan Export-Import (EXIM) database. Veterinary antimicrobial quantities were derived from shipment records and expressed both as total metric tonnes (MT) and as milligrams per Population Correction Unit (mg/PCU) to account for livestock biomass.

Total human antibiotic consumption in Pakistan in 2019 was estimated at 18.6 DID, corresponding to approximately 1,652 metric tonnes of antibiotics. Fluoroquinolones accounted for the largest proportion of use (approximately 26%), followed by beta-lactam antibiotics including penicillins (22%) and cephalosporins, indicating substantial reliance on broad-spectrum agents. In the animal sector, antimicrobial consumption was estimated at approximately 876 metric tonnes, equivalent to 68.7 mg/PCU. Several critically important antimicrobials for human medicine, including colistin and fluoroquinolones such as enrofloxacin, were identified among commonly used agents in food-producing animals, raising concerns regarding potential drivers of antimicrobial resistance at the human–animal interface.

These findings highlight substantial antimicrobial consumption across both sectors and underscore the importance of integrated One Health surveillance systems for antimicrobial use. Strengthening routine antimicrobial consumption monitoring, promoting stewardship programs in both healthcare and veterinary practice, and regulating the use of critically important antimicrobials in food production are important steps for mitigating AMR risks. Establishing coordinated national surveillance across sectors would improve evidence generation and support policy implementation under Pakistan's National Action Plan on AMR.

1586 – Rapid host species identification from dried bloodspots of Culex mosquito blood meals using Mid-Infrared Spectroscopy and Machine-Learning

Erin S. JOHNSTON (1), Mauro PAZMIÑO-BETANCOURTH (1), Mary Elizabeth MIRANDA (2), Brandy ALABADO (2), Michael Ralph TANEDO (2), Mario GONZÁLEZ-JIMÉNEZ (8), Sarah CLEAVELAND (1), Troy Adam LAIDLOW (3), Michael WALSH (4,5), Cameron E. WEBB (4,5,6), Mafalda VIANA (1), Victoria BROOKES (3,5), Francesco BALDINI (1,7)

1: School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow, United Kingdom; 2: Field Epidemiology Training Program Incorporated, Quezon City, Manila, Philippines; 3: Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Camperdown, NSW, Australia; 4: School of Medical Sciences, Faculty of Medicine and Health, The University of Sydney, Camperdown, NSW, Australia; 5: Sydney Infectious Diseases Institute, Faculty of Medicine and Health, The University of Sydney, Camperdown, NSW, Australia; 6: Medical Entomology, NSW Health Pathology, Westmead, NSW, Australia; 7: Ifakara Health Institute, Environmental Health, and Ecological Sciences Department, Morogoro, United Republic of Tanzania; 8: School of Chemistry, University of Glasgow, Glasgow, United Kingdom

Background: Understanding mosquito blood feeding preferences helps clarify vector-borne pathogen transmission dynamics and informs control strategies for pathogens affecting both humans and animals. Gold-standard methods for identifying mosquito blood meals, such as PCR and ELISA, are costly, time-consuming, and can lose accuracy as blood meals are digested. Mid-infrared spectroscopy with machine-learning (MIRS-ML) can offer a rapid, cost-effective alternative approach to identifying host blood meals, as it does not require repeated purchase of reagents. Previous research shows MIRS-ML is successful in host identification from *Anopheles* and *Aedes* mosquito blood meals but has never been used to identify those from *Culex* species. *Culex* mosquitoes are important vectors of multi-host pathogens including Japanese encephalitis virus, West Nile virus, and filariasis. This study evaluated whether MIRS-ML can identify *Culex* mosquito blood meal hosts.

Methods: Laboratory-reared *Culex quinquefasciatus* were fed blood from six hosts (human, pig, chicken, cattle, dog and horse). Dried bloodspots (DBS) were created 6, 12, 24 and 30 hours after digestion in the mosquito by rolling abdominal contents onto filter paper and then scanned using a Bruker ALPHA Fourier-transform infrared spectrometer. The spectra generated were used to train a multilayer perceptron algorithm to predict blood meals from these six host species and then tested on mosquito blood meals from field-collected samples in the Philippines and Australia. Host identification for these DBS was validated by extracting DNA and amplifying the vertebrate cytochrome c oxidase 1 (CO1) gene via PCR followed by sequencing and GenBank comparison.

Results: For laboratory-reared mosquitoes, the model was 90.5% accurate in predicting host species in comparison to 16.7% random classification, with no decline in accuracy even 30 hours after digestion. Among field samples, PCR amplified blood meals in the Philippines were mainly from *Culex quinquefasciatus* (n=176), followed by *Aedes armigeres* (n=8) species. In Australia, the majority were from *Aedes kochi* (n=15), followed by *Culex sitiens* subgroup (n=9). MIRS-ML successfully identified hosts for 69.2% of the field-collected DBS which were from chicken, pig, human, dog, cattle or horse hosts.

Conclusion: MIRS-ML combined with DBS is a potential scalable tool for *Culex* blood meal analysis and would be of practical value for field sample collection, especially as DBS can be transported at room temperature. Whilst field-prediction accuracy was lower than laboratory DBS, these results suggest the presence of a strong blood-host specific spectroscopic signal with potential for further improvement by increasing the training dataset. We envision that MIRS-ML can be an alternative to the gold-standard PCR for blood meal identification with integration into vector-borne disease surveillance.

1591 – Antimicrobial-Resistant Gram-Negative ESKAPE Organisms in Commercially Available Raw and Alternative Pet Diets in the UK

Sophie HASLAM, Nicola WILLIAMS, Dorina TIMOFTE, Gina PINCHBECK, Genever MORGAN

University of Liverpool, United Kingdom

Background

The Gram-negative (GN) ESKAPE organisms *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp. are opportunistically pathogenic and frequently

multidrug-resistant. This group is of growing global concern due to their impact on patient mortality and treatment outcomes in human and veterinary medicine. Pilot work at the University of Liverpool identified these organisms in commercially available raw meat diets (RMD) for pets, suggesting RMD could be an unrecognised source. Alternative pet diets, including freeze-dried, cold-pressed, air-dried, and gently cooked products, are minimally processed yet have received little microbiological investigation despite increasing availability. This study investigated the prevalence of antimicrobial-resistant (AMR) GN ESKAPE organisms in commercially available RMD and alternative pet diets in the UK.

Methods

A cross-sectional microbiological study in the UK examined 100 RMD (10 brands, 9–11 samples per brand) and 55 alternative diets (13 brands; 22 freeze-dried, 15 cold-pressed, 10 gently cooked, 8 air-dried). Samples were cultured on selective media +/- cefotaxime (a third-generation cephalosporin (3GC)). Species-level identification was performed using MALDI-TOF mass spectrometry; antimicrobial susceptibility was determined by disc diffusion, following EUCAST guidelines and clinical breakpoints. Fisher's exact tests were used to assess associations between microbiological findings, protein group, and brand. Packaging was assessed for traceability information and any leaks or breaches.

Results

One cold-pressed alternative diet (1/55; 1.8%) yielded 3GC-resistant *Acinetobacter baumannii*. Fifty-four raw diets (54/100; 54%) contained ≥1 3GC-resistant GN ESKAPE organism: *Acinetobacter* spp. (28/100; 28%), *Pseudomonas aeruginosa* (24/100; 24%), and *Enterobacter hormaechei* (8/100; 8%). No significant association was identified in RMDs between protein composition (single vs. mixed protein) and ESKAPE presence (Fisher's exact test, p=0.22; Table 1), offal/tripe content and ESKAPE presence (p=0.053; Table X), or between brand and ESKAPE presence (p=0.06). Phenotypic resistance was demonstrated to highest priority critically important antibiotics (Table 2). Packaging concerns, including missing traceability information, poor integrity and external contamination, were observed across both diet types.

Conclusions

These findings highlight that RMDs represent an important and under-recognised source of AMR bacteria, demonstrating resistance to antibiotic classes critical for both human and animal health. The high recovery of GN-ESKAPE isolates on 3GC-supplemented media highlights a critical surveillance gap outside current pet food safety frameworks. The absence of a significant association between microbiological findings and protein group or brand suggests widespread issues across the raw pet food industry. From manufacture through transportation, retail, and consumer use, these products present multiple opportunities for AMR dissemination into human, animal, and environmental settings - risks deepened by observed packaging issues. Those at risk span One Health - animals, humans, and the shared environments they inhabit. With the continued popularity of raw feeding in the UK, these findings demonstrate the need for a One Health approach, including cross-sector surveillance, antimicrobial stewardship, and regulatory development.

Table 1. Distribution of Gram-negative ESKAPE organisms (%, n) across protein group and offal/tripe content in raw pet diets. All samples were raw pet food products (n=100 for tripe/offal analysis; n=99 for protein analysis*). *One sample containing horse (n=1) in which no ESKAPE organisms were detected was excluded from the protein composition table but retained in statistical analyses.

Protein Group	N	≥1 3GC-resistant GN ESKAPE organism	*Acinetobacter* spp. % (N)	*Pseudomonas aeruginosa* % (N)	*Enterobacter hormaechei* % (N)
Mixed	21	57.1 (12)	33.3 (7)	19.0 (4)	9.5 (2)
Beef	18	66.7 (12)	27.8 (5)	38.9 (7)	16.7 (3)
Chicken	15	26.7 (4)	6.7 (1)	13.3 (2)	6.7 (1)
Lamb	11	63.6 (7)	45.5 (5)	27.3 (3)	0.0 (0)
Turkey	11	45.5 (5)	9.1 (1)	27.3 (3)	18.2 (2)
Duck	8	75.0 (6)	12.5 (1)	62.5 (5)	0.0 (0)
Rabbit	5	40.0 (2)	40.0 (2)	0.0 (0)	0.0 (0)
Fish	3	33.3 (1)	33.3 (1)	0.0 (0)	0.0 (0)
Pork	3	33.3 (1)	33.3 (1)	0.0 (0)	0.0 (0)
Venison	3	100.0 (3)	100.0 (3)	0.0 (0)	0.0 (0)
Pheasant	1	100.0 (1)	100.0 (1)	0.0 (0)	0.0 (0)
Total	**99***	**54**	**28**	**24**	**8**
Tripe/Offal Group	**N**	**≥1 3GC-resistant GN ESKAPE organism**	***Acinetobacter* spp. % (N)**	***Pseudomonas aeruginosa* % (N)**	***Enterobacter hormaechei* % (N)**
Contains Offal	70	48.6 (34)	27.1 (19)	15.7 (11)	8.6 (6)
Contains Tripe & Offal	18	55.6 (10)	27.8 (5)	33.3 (6)	5.6 (1)
Contains Tripe	7	100.0 (7)	42.9 (3)	85.7 (6)	0.0 (0)
None	5	60.0 (3)	20.0 (1)	20.0 (1)	20.0 (1)
Total	**100**	**54**	**28**	**24**	**8**

Table 2. Gram-negative ESKAPE organisms isolated from raw pet food samples, sample protein and phenotypic resistance demonstrated.. A yellow box indicates susceptible and red indicates resistant.

Acinetobacter spp.										
Brand	**Sample**	**Protein Group**	**Tripe/Offal Group**	**GN-ESKAPE Organism**	**AK**	**CIP**	**MEM**	**MAR**	**ENF**	**GM**
B12	54	Lamb	Tripe	*Acinetobacter baumannii*						
Pseudomonas aeruginosa										
Brand	**Sample**	**Protein Group**	**Tripe/Offal Group**	**GN-ESKAPE Organism**	**AK**	**CIP**	**MEM**	**MAR**	**ENF**	**GM**
B12	50	Beef	Tripe	*Pseudomonas aeruginosa*						
	52	Beef	Tripe & Offal	*Pseudomonas aeruginosa*						
B13	59	Lamb	Tripe	*Pseudomonas aeruginosa*						
B3	84	Mixed	Tripe	*Pseudomonas aeruginosa*						
B15	100	Lamb	Tripe	*Pseudomonas aeruginosa*						
B17	115	Turkey	Offal	*Pseudomonas aeruginosa*						
B19	132	Turkey	Offal	*Pseudomonas aeruginosa*						
Enterobacter hormaechei										
Brand	**Sample**	**Protein Group**	**Tripe/Offal Group**	**GN-ESKAPE Organism**	**AK**	**CIP**	**MEM**	**AUG**	**AP**	**TGS**	**TS**
B14	72	Chicken	None	*Enterobacter hormaechei*							
	73	Mixed	Offal	*Enterobacter hormaechei*							
	75	Mixed	Offal	*Enterobacter hormaechei*							
B17	118	Beef	Offal	*Enterobacter hormaechei*							
	120	Beef	Tripe & Offal	*Enterobacter hormaechei*							
B19	135	Turkey	Offal	*Enterobacter hormaechei*							

Antibiotic abbreviations: AK, amikacin; CIP, ciprofloxacin; MEM, meropenem; MAR, marbofloxacin; ENF, enrofloxacin; GM, gentamicin; AUG, amoxicillin–clavulanate; AP, ampicillin; TGS, tigecycline; TS, trimethoprim–sulfamethoxazole.

1594 – Quantitative assessment of selective pressure driving antimicrobial resistance in dairy farm environments

Arianna PERUZZO (1,2), Stefano DALLE PALLE (1), Giorgia FABBRI (1,2), Silvano SALARIS (1), Luca VEDOVELLI (3), Cristiana BENETTI (4), Simone BELLUCO (5), Carmen LOSASSO (1)

1: Microbial Ecology and Genomics laboratory, Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Padova, Italy; 2: PhD National Programme in One Health approaches to infectious diseases and life science research, Department of Public Health, Experimental and Forensic Medicine, University of Pavia, Italy; 3: Unit of Biostatistics, Epidemiology and Public Health, Department of Cardiac, Thoracic and Vascular Sciences and Public Health, University of Padova, Padova, Italy; 4: Food Safety Department, Chemistry Laboratory, Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Padova, Italy; 5: Department of Food Safety, Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro, Padova, Italy

Background

Antimicrobial resistance (AMR) in livestock production is a critical environmental and public health concern, particularly due to the dissemination of mobile antimicrobial resistance genes (MARGs). In dairy farm systems, the combined use of antimicrobials, biocides and heavy metals such as copper and zinc may exert selective and co-selective pressure on microbial communities, enhancing antimicrobial resistance genes (ARGs) persistance and spread. This study aimed to quantitatively evaluate environmental selective pressures in dairy farms, compare ARGs abundance across production matrices, assess association between chemical residues and ARG selection, and define risk scenario and mitigation strategies within a One Health framework.

Method

Multiple matrices (faeces, feed, colostrum and milk) were collected from dairy farms. Antibiotic and metal residues were quantified using chromatographic and mass spectrometry techniques. Metagenomic shotgun sequencing was performed to determine ARG diversity and relative abundance across matrices. Co-occurance analysis evaluated associations between ARGs and mobile genetic elements (MGEs) to infer horizontal gene transfer potential. A modelling framework was applied to evaluate the association

between measured concentration of antibiotics, biocides, and heavy metal and ARG abundance in each matrix and to evaluate ARGs circulation among matrices to identify accumulation and dissemination hotspots.

Results

Faeces and feed showed the highest concentration of antimicrobial and metal residues, identifying these matrices as major sources of selective pressure. Metagenomic analysis performed on the whole sample detected 719 ARGs conferring resistance to multiple antibiotic classes, including β-lactams, aminoglycosides, tetracyclines, macrolides, fluoroquinolones, sulfonamides, glycopeptides, and disinfectants. Correlations between heavy metal residues and ARG abundance support a role of metals in the co-selection of multidrug-resistant bacteria. Milk and colostrum showed a high richness of resistome, following by calves feaces. This richness subsequently decreased in subsequent production categories, in parallel with the maturation of the fecal microbiota. Furthermore, a longitidinal flow of resistome transfer along the production chain was identifed. This inter-matrix gene transfer is supported by the concurrent detection of MARGs across all matrices, indicating shared resistance determinants and potential dissemination pathways throughout the production system.

Conclusions

This study identified critical stages of intensified resistome dissemination within the dairy production system, highlighting key points for intervention, including improved managment of feed residues, optimized colostrum practices and early-life microbiota-focused interventions. Overall, the proposed quantitative modeling framework provides a One Health-based tool supports the development of farm-level strategies aimed antimicrobial resistance mitigation.

1603 – Building economic assessment capacity for One Health AMR interventions in Africa (BEACOI-Africa): A regional curriculum development initiative

Mohamed Moctar MOUICHE MOULIOM (1), Mumba CHISONI (2), Juliana NDASI (1), Anafi MATAKA (1)
1: African Society for Laboratory Medicine (ASLM), Ethiopia; 2: University of Zambia

Background: Antimicrobial resistance (AMR) is a growing public health and economic threat in Africa. An estimated 4.1 million deaths are attributed to AMR each year, with projected economic losses of up to 5% of GDP by 2050. Despite the scale of this crisis, economic evaluations essential for planning, prioritizing and financing interventions are rare in African contexts because of four major gaps: limited technical capacity, weak one-health integration, poor contextual relevance of existing methods and lack of institutional sustainability. The African Society for Laboratory Medicine, through previous programs such as TADE (Technical Assistance for AMR Data and Evidence Use) and QWARS (Qualifying the Workforce for AMR Surveillance) programme, has demonstrated the ability to bridge data, policy, and economics to support AMR responses. The BEACOI-Africa initiative aimed to develop a sustainable, context-appropriate curriculum to strengthen regional capacity for economic evaluation of AMR interventions across one-health sectors in Africa.

Methods: A participatory curriculum development approach was employed to ensure alignment with regional needs and priorities. Stakeholder consultations and a literature review were undertaken to identify critical knowledge and system gaps limiting AMR economic evaluation in African low-and middle-income countries. Inputs were obtained from AMR and One Health stakeholders across sectors and informed the design of a regional curriculum aligned with African policy and practice needs. A regional consultation meeting convened key regional and continental stakeholders to comprehensively review and validate the curriculum architecture, content, and delivery mechanisms.

Results: Stakeholder consultations and a literature review identified six major barriers constraining AMR economic evaluation capacity, including limited training opportunities combining health economics with AMR and One Health concepts; concentration of expertise in human health with major gaps in animal and environmental sectors; weak institutional mechanisms for generating and using economic evidence in policy; limited peer-learning networks; absence of African case studies and context-adapted methodological guidance; and lack of practical tools. In response, a curriculum architecture of 10 modules was developed across four domains: foundational concepts, One Health integration, technical

economic evaluation methods, and policy and decision support. The programme includes online and in-person learning, mentored project work, and African case studies based on real-world.

Conclusions: This work provides a practical framework for strengthening African capacity to generate and apply policy-relevant economic evidence for AMR prevention and control. By integrating One Health principles, African case studies, and applied tools, the curriculum addresses critical regional capacity gaps and offers a sustainable foundation for improved AMR decision-making and resource allocation across sectors. Successful implementation of this capacity-building program is expected to enhance the generation of locally relevant economic evidence, strengthen institutional mechanisms for evidence utilization, foster regional networks of economic evaluation practitioners and ultimately contribute to more effective and efficient AMR response strategies across the African continent.

1609 – Randomised Controlled Trials on Zoonotic Diseases in Africa: A Scoping review and Bibliographic Analysis (ScoRBA).

Keitumetse LEBELO (1), **Mark E ENGEL** (2), Lorenzo DM BENNIE (2), Ameer HOHLFELD (2)

1: Desmond Tutu HIV Centre, Department of Medicine, University of Cape Town, Cape Town, South Africa; 2: South African Cochrane Centre South African Medical Research Council Francie van Zijl Drive Parowvallei 7500, Cape Town;

Background: Zoonotic diseases remain a major global public health concern, particularly in regions where close interactions between humans, animals, and the environment facilitate pathogen transmission. Prompt decision-making for effective control requires an understanding of the current literature landscape.

Objective: This ScoRBA review describes the geographic distribution of randomised controlled trials (RCTs) investigating zoonotic diseases in Africa. Additionally, we assessed the completeness of reporting across the included RCTs using the updated CONSORT 2025 checklist.

Methods: We conducted a rigorous literature examination of RCTs on zoonotic diseases in Africa, published between 1 January 2010 and 25 August 2025. We searched PUBMED, Cochrane Library, Scopus, Embase, Web of Science, and EBSCOhost. Two reviewers independently screened studies and extracted data. Any conflicts were resolved through consensus or by a third reviewer. Reporting completeness was assessed using the CONSORT 2025 checklist. Descriptive statistics summarised study characteristics, and a heatmap was used to report study quality. Quantitative analysis was conducted using R software.

Results: Of 4 764 records identified, 38 RCTs were deemed as eligible and included; (18 countries 287 study sites, 83 559 participants comprising children, adolescents and adults). Specific populations included healthcare workers, farmers and antenatal clinic attendees. Tanzania (4 studies; 76 sites), Uganda (7 studies; 71 sites) and Mozambique (2 studies; 40 sites) had the most study sites, while Malawi had the most participants (n=30 102) (figure 1). Reporting completeness varied across checklist items: core elements like study objectives, intervention descriptions, and outcome definitions were frequently reported, while method items such as randomisation implementation, sample size determination, blinding and protocol accessibility were reported less consistently (Figure 2).

Conclusions: RCTs on zoonotic diseases in Africa were geographically diverse, primarily concentrated in West, Central, and East Africa, with variability in reporting completeness. While key study characteristics are generally well described, important methods details are often insufficiently reported. Strengthening adherence to the CONSORT 2025 reporting items could improve transparency, facilitate evidence synthesis, and support the development of more effective strategies for the prevention and control of zoonotic diseases.

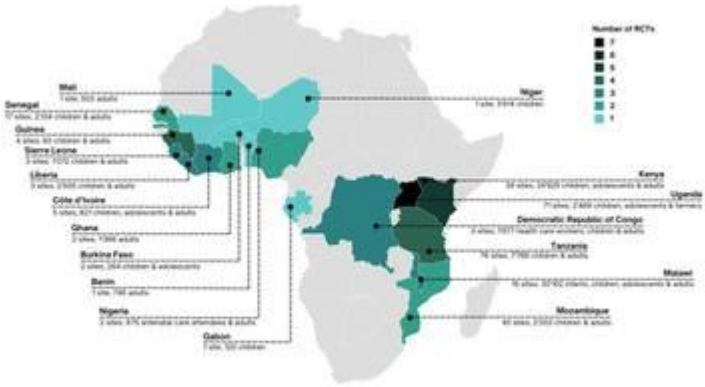


Figure 1. Geographic distribution of randomised controlled trials conducted in Africa. The map illustrates the number of trial sites and participant populations across countries in West, Central, and East Africa.

Figure 2. Heatmap of reporting completeness for randomised controlled trials on zoonotic diseases in Africa based on the CONSORT 2025 Essential Trial Reporting Items.

1616 – Tailoring innovations for antimicrobial resistance mitigation across sectors in low and middle income countries

Jonathan MAYITO
ICARS, India

Significance

Antimicrobial resistance (AMR) is a major global health challenge with low- and middle-income countries (LMICs) facing the highest burden. The development of innovation is crucial to tackle AMR but the adoption and sustainability remain a challenge in LMICs. Besides scientific rigour, an understanding of local conditions for acceptability & available infrastructure, Intellectual Property, etc., is essential to supporting innovations to cross the late-stage valley of death in field conditions.

In 2024, the International Centre for Antimicrobial Resistance Solutions (ICARS), Denmark, partnered with the Centre for Cellular and Molecular Platforms (C-CAMP) India, to support late-stage AMR-relevant innovations across the One Health sectors in India. C-CAMP has extensive experience in incubating and accelerating research and innovation in India, and ICARS brings expertise and experience on how to adapt interventions to real-life settings by using Intervention- implementation research (IIR) tools and frameworks with the aim to enable integration of innovations into existing systems within India and other LMICs.

This session focuses on how IIR can support the shaping of innovative AMR interventions into practical, scalable solutions across the One Health sectors by considering the cost-effectiveness, acceptability, and adaptability of innovations in the local context, and performance within the social, behavioural, and institutional factors of the country. Through presentations, case studies and expert panel discussions, participants will learn how IIR improves the design, delivery, and scale-up of interventions to mitigate

AMR and showcase how IIR knowledge and skills can support the successful translation of innovations and field validation for sustained impact.

Participants will gain knowledge on key concepts and practical approaches in IIR to understand the key enablers and barriers for the development, uptake and translation of innovation into policy, practice.

Aim: The session aims to:

Proposed talk titles and speakers for the panel discussion:

Proposed chairs: Discussion on supporting innovation uptake in LMIC realities

---

1620 – Microplastics as Selective Hotspots for Pathogens and Antibiotic Resistance in a Coastal Marine Ecosystem

Arianna PERUZZO (1,2), Davide ASNICAR (3,4), Vanessa MOSCHINO (5), Giulia BAGGIO (1), Eloisa TOSCAN MASSIGNAM (1,2), Giorgia FABBRI (1,2), Tihana MARCETA (5), Maria Gabriella MARIN (3), **Carmen LOSASSO** (1)

1: Microbial Ecology and Genomics laboratory, Istituto Zooprofilattico Sperimentale delle Venezie, viale dell'Università 10, 35020 Legnaro, Padova, Italy; 2: PhD National Programme in One Health approaches to infectious diseases and life science research, Department of Public Health, Experimental and Forensic Medicine, University of Pavia, Pavia, 27100, Italy; 3: Department of Biology, University of Padova, Via U. Bassi 58/B, 35131 Padua, Italy; 4: Aquatic Bioscience, Huntsman Marine Science Centre, 1 Lower Campus Road, E5B 2L7, Saint Andrews, NB, Canada; 5: Institute of Marine Sciences, ISMAR – CNR, Arsenale Tesa 104, 30122 Venice, Italy

Background Microplastics (MPs) are persistent pollutants that provide novel substrates for microbial colonization in aquatic environments. Whether MP-associated biofilms (the plastisphere) differ from surrounding water communities and contribute to the spread of potentially pathogenic bacteria and antibiotic resistance genes (ARGs) remains incompletely understood. This study aimed to determine whether environmental and experimentally aged MPs host distinct microbial communities, are selectively enriched in potentially pathogenic taxa, and harbor a more diverse and abundant resistome compared to surrounding marine and lagoon waters

Methods Environmental MPs (E-MPs) were collected from the Northern Adriatic Sea, while polyethylene MPs were cryo-milled and aged for eight months in a lagoon-supplied mesocosm system to obtain aged MPs (A-MPs). Microbial communities were characterized using 16S rRNA gene amplicon sequencing. Shotgun metagenomics was applied to assess resistome composition, and droplet digital PCR (ddPCR) was used to quantify selected clinically relevant ARGs normalized to 16S rRNA gene copies. Alpha- and beta-diversity analyses, taxonomic profiling, and pathobiome-focused filtering were performed to compare MP-associated and free-living communities

Results Both E-MPs and A-MPs hosted microbial communities significantly distinct from surrounding waters, with lower alpha-diversity and clear separation in beta-diversity analyses. Taxonomic profiling revealed matrix-specific assemblages and enrichment of Gammaproteobacteria on MPs. Potentially pathogenic genera were proportionally higher on MPs, with *Vibrio* dominating the MP-associated pathobiome. Shotgun metagenomics identified 605 ARGs, with higher richness and abundance on E-MPs compared to seawater. Several resistance classes were exclusively detected on MPs. ddPCR confirmed increased normalized abundances of key ARGs (e.g., *tetA*, *tetB*, *sul2*) on MPs and detected clinically relevant determinants such as *mcr-1* and *qnr* variants more frequently in MP-associated biofilms

Conclusions Marine microplastics act as selective and biologically active microhabitats hosting distinct microbial communities enriched in potentially pathogenic taxa and antibiotic resistance genes. These findings highlight MPs as potential reservoirs and dispersal vectors of antimicrobial resistance in coastal ecosystems. This study underscores the relevance of integrating microplastic monitoring into environmental antimicrobial resistance surveillance frameworks within a One Health perspective, linking marine pollution, food safety, and public health.

1642 – One Health in Theory, Not Practice: What's Holding US Back

Heidi BROWN (1), Amanda SORENSON (1,2), Tomothy OJODARE (1,2), Karly REASE (1), Julia JERNBERG (3), Jennifer WISHNIE (2)

1: University of Arizona, College of Public Health, United States of America; 2: University of Arizona, College of Veterinary Medicine, United States of America; 3: University of Arizona, College of Medicine, United States of America

Background: The growing complexity of One Health (OH) challenges requires a workforce capable of collaborating across disciplines. Academia plays a crucial role in cultivating researchers and educators skilled at working beyond professional silos to foster successful and sustainable solutions to complex OH issues. While the benefits and integration of OH in research has strong support, concerns remain that OH principles taught in academic settings may not align with how practitioners apply OH approaches in their daily work.

This qualitative study explored how veterinarians, public health practitioners, and medical professionals understand and apply OH in practice, identifying opportunities for strengthening OH training and enhancing the real-world integration of OH principles. We hypothesize that practitioners' perspectives will reveal whether (and where) misalignments exist between the way OH principles are taught in academic curricula and how practitioners implement OH approaches in their daily work, as well as highlight opportunities to address these gaps.

Methods: Participants practicing veterinary medicine, human health, and public health were recruited through professional networks and interviewed in two phases (June 2025 and Spring 2026). Prior knowledge of OH was not required for participation. Consented participants participated in a semi-structured interview recorded through Zoom, which was transcribed, cleaned, and de-identified prior to analysis. Transcripts were inductively coded by two independent reviewers to reduce bias. The team met to refine and determine the codebook, and interviews were then coded independently. Data collection aimed to (1) understand how practitioners view OH in their daily work; (2) explore OH success stories, including implementation processes, outcomes, and perceived facilitators; and (3) identify gaps in OH training.

Results: A total of 30 interviews were conducted (10 Vet Med, 10 Human Med, 10 Public Health) among practitioners in the US. Three themes emerged. First, OH is often conflated with climate impacts on health or vector/zoonotic disease transmission. Second, OH in practice was recognized to rely on communication and collaboration between the disciplines, though how to connect with other disciplines was a barrier. Third, OH was recognized as being a holistic approach, though we identified differences by discipline with respect to what that meant.

Conclusions: There remains a gap in the implementation of OH in practice across participants and professions, with understanding often limited to specific topics like zoonotic disease and climate change. Veterinary medicine seems to have more awareness of the concept and potential benefits of an OH approach; however, mechanisms to facilitate OH collaborations in practice are unclear or lacking across disciplines. Opportunities exist within academic settings to leverage interdisciplinary and transdisciplinary teaching and learning approaches that foster the collaborative skills practitioners need to successfully apply OH principles in practice.

1663 – From fragmentation to integration: addressing cooperation challenges through integrated surveillance and country level innovation

Jorge MATHEU (2), Yewande ALIMI (3), Kristina OSBJER (4), Theresa HØGENHAUG (4), Sunday OCHAI (4), Ute EILENBERGER (1), Beate HENRICHFREISE (1), Kirstin VITT (1)

1: GIZ, Germany; 2: WHO, Governance, Coordination and Monitoring Unit, Department of Antimicrobial Resistance, Quadripartite Core Group on OH Integrated Surveillance of AMR/AMU; 3: Africa CDC, One Health Unit Lead; 4: International Centre for Antimicrobial Resistance Solutions (ICARS)

Background: The emergence and spread of antimicrobial resistance (AMR) are inherently interconnected across all sectors of One Health (OH). Addressing this interdependence requires an integrated surveillance framework; however, data on AMR and antimicrobial use (AMU) across sectors has historically been fragmented. The absence of oversight prevents monitoring of cross-sector AMR dynamics by the international community. This collective contribution aims to provide examples on how AMR initiatives can support the translation of high-level commitments into operational systems at country level, enabling coordinated data generation, analysis, and specifically the use of integrated

surveillance for evidence-based policies and interventions. It also provides insights from country case studies and examines how national governments navigate the political and legal complexities of merging data from human health, animal health, agrifood systems, and the environment.

Methods: Toaddress the fragmented surveillance systems, the AMR Multi-Partner Trust Fund (AMR MPTF) finances national integrated surveillance of AMR and AMU in countries and the development of a Global Integrated System for Surveillance for AMR and AMU (GISSA) by the Quadripartite organisations (FAO, UNEP, WHO, WOAH). The system provides countries with guidance, tools, and technical instruments to develop integrated surveillance and to connect data streams from four sectors, thereby enabling comprehensive and coordinated understanding of AMR and AMU across the One Health sectors. Africa CDC and ICARS support countries to test solutions and generate practical experiences on the translation of data across multiple sectors at political, institutional, and technical level, thereby contributing to enabling platforms to integrate data across multiple sectors and strengthen national ownership of One Health integrated surveillance systems.

Results: Early experiences in some countries, Chile, Vietnam, Senegal, and Zimbabwe demonstrate both opportunities and challenges in establishing integrated AMR surveillance. Country case studies highlight the importance of strong national leadership, cross-sectoral collaboration, data sharing agreements and alignment of surveillance approaches across institutions. The examples demonstrate how international cooperation can support countries in overcoming technical and governance barriers, while ensuring that integrated surveillance systems respond to national priorities. Particular attention is given to strengthening environmental surveillance and its integration into broader AMR monitoring frameworks.

Conclusions: One Health integrated surveillance on AMR and AMU is essential to understand and address the interconnected nature of AMR. International initiatives can help bridge the gap between global AMR commitments and country-level implementation by supporting countries in building sustainable sector-specific and integrated surveillance systems that inform antimicrobial stewardship and strengthen global data linkages. The experiences shared provide valuable lessons on how collaboration, capacity strengthening, and coordinated approaches can enable countries to create ownership, generate actionable evidence to guide interventions and inform policies for sustainable AMR mitigation across sectors.

1667 – Under the Skin: development of a canine skin ex vivo model for tackling early Leishmania infection

Micheli FERLA (1), Juliana Inês WEBER (1), Marta MONTEIRO (1), Inês LOPES (1), Maria de Aires PEREIRA (1,2,3), Liege MARTINS (4), Vinicius SOUZA (4,5), Gabriela SANTOS-GOMES (1), Armanda RODRIGUES (1)

1: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisboa, Portugal; 2: Instituto Politécnico de Viseu, Escola Superior Agrária de Viseu, Campus Politécnico, 3504-510 Viseu, Portugal; 3: CERNAS-IPV Research Centre, Instituto Politécnico de Viseu, Campus Politécnico, Repeses, 3504-510 Viseu, Portugal; 4: Associate Lusophone Institute for Research and Development, ILIND, Faculty of Veterinary Medicine, FMV-ULusófona, Lisboa, Portugal; 5: Universidade Lusófona - Veterinary Sciences Research Center, ULHT-CICV, Lisboa, Portugal

Background: Canine leishmaniosis (CanL) is an important parasitic disease in dogs, with a wide clinical spectrum ranging from asymptomatic infection to severe systemic and potentially fatal disease. Beyond its veterinary relevance, CanL is also important in a One Health context, as dogs act as major domestic reservoirs for *Leishmania*, contributing to human exposure in endemic areas. Infection is initiated in the dermis during sand fly feeding, and the skin represents a key site for early host-parasite interactions that influence disease progression. Climate change, environmental disturbance, and urbanization are contributing to the expansion of sand fly vectors into previously unaffected areas, increasing exposure risk for dogs and humans. Early host-parasite interactions in canine skin are likely to play a key role in determining infection outcome, yet biologically relevant models to investigate these events remain limited. To address this issue, an ex vivo canine skin-PBMC model (ECS model) was developed to study the initial local response to *Leishmania infantum* infection.

Methods: Skin explants and autologous peripheral blood cells were obtained from healthy dogs and used to establish the ECS model. PBMCs were isolated and added to the explant culture medium. ECS were challenged with *L. infantum* and incubated for 72h. Explant structural integrity was assessed by histological analysis using hematoxylin and eosin coloration in formalin-fixed paraffin-embedded (FFPE) samples. Aiming to recover skin resident immune cells parallel samples were enzymatically digested with

dispase to separate dermal and epidermal fractions. Recovered cells were analyzed by multiparametric flow cytometry to identify resident dendritic cells, macrophages and lymphocytes. Major histocompatibility complex (MHC) class I and II were also analyzed for their ability to present antigens.

Results: Histological analysis demonstrates skin explant viability in culture, allowing the identification of an organized dermis and epidermis with no signs of necrosis. Parasite presence in skin explants was detected after 72h of incubation with *L. infantum*. Enzymatic processing yielded dermal and epidermal fractions, and recovered cells showed high viability. Moreover, resident macrophages, dendritic cells, and T lymphocytes were immunophenotyped.

Conclusions: The developed ECS model enables the study of early *L. infantum* infection events in a canine tissue context. By combining histological analysis and multiparametric flow cytometry, this *ex vivo* approach can help clarify early host-parasite interactions. It also contributes to reduce dependence of *in vivo* experimentation, and supports One Health strategies, advancing leishmaniasis control, as climate and environmental changes continue to reshape vector distribution, increasing exposure risk.

Funding/acknowledgements: This work was supported by FCT-Foundation for Science and Technology (FCT) through research grants 2023.11944.PEX (doi.org/10.54499/2023.11944.PEX) and by national funds GHTM-UID/04413/2025 and LA-REAL-LA/P/0117/2020. A. Rodrigues is supported by CEECIND/CP1725/CT0023 (10.54499/2022.00499.CEECIND/CP1725/CT0023). J. Weber (2022.13899.BD) and M. Monteiro (UI/BD/152819/2022) are beneficiaries of PhD studentships.

1673 – A New Frontier for Community-Driven Arbovirus Control: Translating Arbovirus Surveillance Strategies from The Amazon to the Atlantic Coastal Communities

Christina PETTAN-BREWER (1), David SOEIRO (2), Claudia PIMPAO (3), Livia CASSEB (4)

1: School of Medicine, University of Washington, Seattle USA and ABRASUNI Brazil; 2: Institute of Biological Sciences, Federal University of Minas Gerais (UFMG), Belo Horizonte, Brazil and ABRASUNI Brazil; 3: School of Medicine and Life Sciences, Pontifícia Universidade Católica do Paraná (PUCPR), Curitiba, Brazil and ABRASUNI Brazil; 4: Evandro Chagas Institute, Secretariat for Health and Environment Surveillance, Ministry of Health, Brazil and ABRASUNI Brazil

Aedes-borne arboviruses such as dengue and chikungunya are expanding in Brazil and Latin America due not only to climate change but also to human-driven pressures on ecosystems, including intense deforestation, biodiversity loss, pollution and densely populated areas. These factors alter climate ecology and the distribution of Aedes mosquitoes by disrupting natural habitats and the ecological balances that regulate vector populations, while increasing interactions among wildlife, domestic animals, plants, and human populations. These trends call for renewed emphasis on primary prevention at the source—combining environmental management, biodiversity conservation, Integrated environmental management, and integrated animal–human–ecosystem health surveillance. Indigenous and local traditional communities, often located in ecologically fragile and climatically sensitive territories, face heightened vulnerability due to limited access to health services and their close interactions with both domestic and wild animals affected by ecosystem degradation.

This project aimed to study the impact of climate change on Aedes-transmitted Arboviral diseases at multiple scales (meteorological, extreme events, land use change, vector, epidemiology, health policy, and population displacement) through the OH modelling approach.

The One Health (OH) modelling approach will lead to the understanding of interdependent relations and interactions to help as an early warning and monitoring system for arboviral disease outbreaks and management and contributing towards climate resilience at regional and national levels.

The integrated OH surveillance will be instituted as part of the Brazil national OH Plan, International Health Regulations, and pandemic preparedness by planning strategies while fostering an integrated understanding of health and epistemology that bridges research, policy and community with education, equity and inclusion from Para and Marajo Island (Amazon Region) to the Southern coastal traditional and indigenous communities in Brazil. Our study applied epidemiological and ecological modeling to predict climate-driven shifts in vector dynamics and identify priority areas for arboviral prevention. Modeling results guided community-based education programs, developed through collaboration among health, research and governance sectors, and supported by traditional and indigenous ecological knowledge (TIEK). Aligned with the COP30 resolutions, which emphasize the integration of health, biodiversity, and climate, this work underscores the central and leadership role in advancing prevention,

intersectoral strategies that strengthen resilience in both ecosystems and communities' engagement. Within an epistemological framework that values diverse forms of knowledge—scientific, traditional, and experiential—this approach reinforces the One Health perspective as both a scientific and politico-social paradigm. In alignment with Brazil's National Plan of One Health, these initiatives promote collaboration among the Ministry of Health, the Ministry of Agriculture and Livestock, Brazilian Association of One Health - ABRASUNI, ensuring coordinated action with universities and outreach research programs.

Acknowledgment: Gates Foundation Global Challenges and Ministry of Health – USA and BRAZIL

1679 – An Interdisciplinary One Health Approach to Antimicrobial Resistance in West Africa: Benefits and Challenges

Aurélia SOUARES (1,6), Carine BAXERRES (2), Anastasia SEFERIADIS (2), Maresa NEUERER (1), Mawuli L AGLANU (4), Charity W AKENTEN (4), Dramane KIEMDE (5), Neyaz KHAN (3), Stefan BERG (3), Ali SIE (5,6), John H AMUASI (3,4), Denise DEKKER (3)

1: Heidelberg Institute of Global Health, Heidelberg University Hospital, Heidelberg, Germany; 2: IRD, LPED, Marseille, France; 3: Bernhard Nocht Institute for Tropical Medicine, Hambourg, Germany; 4: Kumasi Centrer for Collaborative Research in Tropical Medicine, Kumasi, Ghana; 5: Centre de Recherche en Santé de Nouna, Nouna, Burkina Faso; 6: German Center for Infection Research (DZIF), Heidelberg, Germany

Addressing antimicrobial resistance (AMR) requires an integrated One Health approach that recognizes the complex interactions between human health, animal health, and environmental factors. Given the multifactorial nature of AMR, interventions must be tailored to local realities, taking into account social, cultural, economic, and ecological determinants of antibiotic use. This study adopted a mixed-methods design to measure resistance along the food chain and to capture both quantitative and qualitative dimensions of antimicrobial practices across human, animal, and community settings.

The research was conducted in Kossi Province, Burkina Faso, and the Ashanti Region, Ghana, involving livestock farmers, animal health practitioners, healthcare providers, pharmacists, and community members engaged in small-scale farming. Qualitative data included in-depth interviews and focus group discussions with farmers, healthcare workers, and community members to explore perceptions, decision-making processes, and cultural norms around antibiotic use. Policy and regulatory analyses examined how existing guidelines influenced local practices, and ethnographic observations documented human-animal interactions and local care practices. Using a design thinking approach, the project translated findings into locally relevant strategies for behaviour change. The interventions focused on strengthening awareness and understanding of AMR among farmers, healthcare providers, and communities, promoting responsible antibiotic use in humans and animals, and ensuring that strategies were culturally appropriate, feasible, and sustainable.

The project is distinctive in its integration of diverse disciplinary and epistemological perspectives. Microbiological and epidemiological findings were combined with anthropological and sociological insights to triangulate data and understand both the patterns and drivers of antibiotic use. Regular cross-disciplinary workshops ensured continuous dialogue among researchers and stakeholders, fostering a shared understanding of AMR dynamics and supporting the co-creation of context-sensitive intervention strategies. The study explicitly considered power relations and knowledge hierarchies that influence which perspectives are prioritized in decision-making. By actively involving local communities, healthcare providers, and farmers in research design and intervention planning, the project ensured that solutions were socially legitimate and locally grounded, reflecting the needs and priorities of all stakeholders.

The interdisciplinary results provided a comprehensive and nuanced understanding of AMR, revealing both convergent and discordant patterns across human, animal, and environmental health domains. To navigate these differences, methods of reconciliation and initiation were employed, facilitating the development of a new, integrated perspective that accounts for multiple epistemologies and disciplinary insights. By explicitly embracing interdisciplinarity and knowledge co-production, the study demonstrates how a One Health approach can generate interventions that are scientifically robust, contextually adapted, and widely accepted by stakeholders, including healthcare providers, farmers, and community members.

1688 – Acceptability of pig vaccination and deworming for cysticercosis (Taenia solium) in Rwanda: One Health implementation research

Eri TOGAMI (1), Ruth UWASE (2), Madeleine Ndegeya KAZINDU (2), Prince RWAGASORE (2), Community One Health Empowerment in Senegal and Rwanda CONSORTIUM (2), Shyaka ANSELME (2), Janna SCHURER (2), Meghan F DAVIS (1)

1: Department of Environmental Health & Engineering, Johns Hopkins Bloomberg School of Public Health; 2: Centre for One Health, University of Global Health Equity

Background

Cysticercosis, a parasitic infection caused by *Taenia solium* and spread through contaminated environments, causes neurologic disease in pigs and humans and impacts the quality and value of pork products. The acceptability of control measures for cysticercosis is context-dependent and influences the uptake and sustainability of interventions. The study objective is to characterize the acceptability of administering the TSOL18 vaccine and oxfendazole to pigs among rural smallholder pig farmers, pig vendors, butchers, veterinarians, community animal health workers, and public health officers, to prevent and control cysticercosis in Rwanda.

Methods

This qualitative, implementation research study involved key informant interviews in Nyamagabe District, southern Rwanda, in 2025. In Nyamagabe District, *T. solium* is endemic, and there is high pig ownership among smallholder farmers. It was embedded in a cluster randomized control trial named Community One Health Empowerment in Senegal and Rwanda (COHERS). Thematic content analysis using inductive coding was conducted to (1) map actor groups and their interactions in the pork value chain; (2) characterize intervention determinants using the Consolidated Framework for Implementation Research (CFIR); and (3) identify barriers to and facilitators of acceptability.

Results

Twenty key informants in the pork value chain were interviewed in 2025 during the delivery of the intervention. The key informants were rural smallholder pig farmers, live pig vendors, butchers, veterinarians, community animal health workers, and public health officers. Overall, the acceptability of deworming and vaccination of pigs was high, estimated to be over 90%. Farmers, animal health workers, veterinary professionals, public health officials, vendors, and butchers worked closely to raise, trade, process, and consume pigs. Acceptability was influenced by several factors categorized in CFIR domains, including local attitudes toward treating pigs and agricultural policies (Outer Setting), a tension for change and mission alignment with authorities (Inner Setting), partner engagement and reporting structure (Implementation Process). Barriers for acceptability included concern for adverse effects, sellability of the pigs, and religious beliefs. Facilitators included anticipated improvement in pigs' health that would result in economic benefits, and reported trust in authorities to recommend an appropriate treatment for community members. Participants recommended factors that would further improve their acceptability, related to delivery logistics and cost.

Conclusions

The acceptability of the pig intervention was shaped by health, economic, and social factors. The strengths of the study were triangulating perspectives across occupations and assessing the acceptability during the intervention, minimizing recall bias. One limitation was the possibility of social desirability bias, given that the researchers worked with local authorities. Understanding how pig vaccination and treatment are accepted among actor groups in the pork value chain helps the project improve the delivery and adaptation of the pig intervention and will ultimately lead to policymakers tailoring future One Health interventions to the community's needs.

Poster zone 3

Olive Tree

1696 – From Containment to Territory: Structuring Territorial Consequence Analysis in High-Containment Laboratory Risk Assessment

Erica GUERINO DOS REIS (1), Denise TORRES DA SILVA (2), Andressa GUIMARÃES DE SOUZA PINTO (2), Amanda PONTES LOPES (1), Halisson CAMPOS GONÇALVES (1), Flavia SARMENTO VIEIRA (1), Carla DE FREITAS CAMPOS (1)

1: Instituto de Ciência e Tecnologia em Biomodelos, Fundação Oswaldo Cruz, Brazil; 2: Instituto de Tecnologia em Imunobiológicos (Bio-Manguinhos), Fundação Oswaldo Cruz, Brazil

Background: Risk assessment in high-containment laboratories integrates evaluation of primary, secondary and tertiary containment systems with characterization of pathogen-specific attributes. Effluent inactivation, HEPA-filtered exhaust, structural integrity and emergency procedures are assessed alongside factors such as environmental persistence, wildlife reservoirs, and vector competence.

Although environmental considerations are formally included, consequence evaluation in practice remains focused on internal control and occupational exposure. The territorial dimension, meaning how consequences evolve beyond facility boundaries, is seldom examined in a structured manner.

A containment breach near a strategic watershed does not carry the same implications as one in an isolated setting. Sanitation fragility, dense urban settlement, or proximity to production systems may alter the scale and direction of consequence propagation, yet these conditions are rarely incorporated as explicit analytical variables during risk characterization.

Methods: We introduce an additional analytical step within WHO-aligned qualitative risk assessment processes, designated as the Contextual Impact Modifier (CIM), to examine territorial consequence dynamics (Figure 1). Probability estimation and engineering standards remain unchanged, and operational risk classification is preserved.

Conducted after conventional hazard evaluation, the CIM interrogates consequence propagation: if containment failure occurs, what territorial systems could mediate or amplify its effects?

The framework incorporates two analytical domains:

(1) Territorial Vulnerability Assessment, examining determinants such as water source proximity, sanitation infrastructure robustness, urban density, and flooding exposure; and (2) One Health Interdependence Analysis, evaluating amplification pathways through competent vectors, wildlife reservoirs, environmental persistence, and agricultural interfaces.

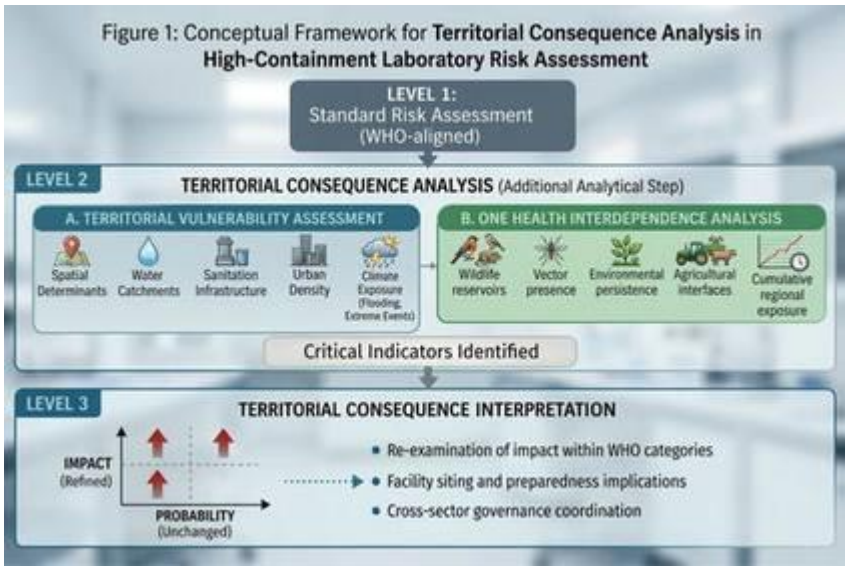
When identified, these critical indicators prompt systematic re-examination of impact interpretation within existing WHO categories, without altering probability assumptions.

Results: Application of the CIM to structured hypothetical scenarios showed that facilities under equivalent engineering controls and probability assumptions may differ significantly in territorial consequences after containment failure. Installations near sensitive water catchments, strained sanitation systems, or intensive production zones showed broader exposure trajectories than isolated facilities.

This territorial review clarified how consequences interact with surrounding systems without altering probability estimates or operational risk classification. The CIM is proposed as a decision-support tool for facility siting, preparedness, and governance, particularly where low-probability events carry disproportionate territorial implications.

Conclusions: High-containment biosafety assessment is technically robust at the level of engineered control. What remains insufficiently structured is how consequences unfold once those controls fail. The Contextual Impact Modifier (CIM) strengthens consequence interpretation while preserving severity and probability parameters.

This review is conceived as an institutional responsibility within biosafety governance, informing coordinated decision-making with environmental and public health authorities.



1701 – Implementation of the One Health Approach to Risk Assessment (OHARA) Framework in Canada: case studies and lessons learned

Sharon CALVIN, Antoinette LUDWIG, Irene LAMBRAKI, Dima AYACHE, Raquel FARIAS, Ben SMITH, Rukshanda AHMAD

Public Health Agency of Canada (PHAC), Canada

Background: In 2024, Canada completed its One Health Approach to Risk Assessment (OHARA) Framework, led by the Public Health Agency of Canada (PHAC) with a Multi-agency Technical Advisory Committee. The goal was to achieve high-quality risk assessments that will increase understanding of risks to enable prompt and effective action for the health of people, animals, plants and ecosystems in Canada. Since then, PHAC has implemented OHARA by working jointly with partners to conduct multi-sectoral risk assessments and other methods to understand a variety of risks and inform risk management.

Methods: Potential risk assessment topics requiring a multi-sectoral approach were brought to PHAC's One Health Risk Assessment team by a variety of mechanisms. The team then facilitated discussions with partners across sectors to scope the risk questions, clarify needs, and choose methods from a list of those appropriate for OHARA. The assessments were then conducted with teams of experts from different sectors and disciplines. Once drafted, multi-sectoral discussions informed approvals and communication of final products, as well as making the link between risk assessment and risk management across sectors.

Results: Several risk products were created to understand risks associated with animal/product importation, emerging pathogens, endemic pathogens, and regulatory review. Case studies that demonstrate the implementation of OHARA include: avian influenza A(H5N1), importation of bat guano, chronic wasting disease, and *Salmonella* in poultry. Based on multi-sectoral discussions, different methods were chosen for each file, to best fulfill the identified need. This included risk assessment, scenario analysis, an uncertainty algorithm, impact assessment, and a review of existing risk assessments. In one case, a multi-sectoral Risk Analysis Document was used to combine the results of risk assessment with other risk management and risk communication considerations, to better inform decisions.

Conclusions: The OHARA Framework has improved One Health collaboration in Canada by bringing sectors together to jointly assess risks. While the case studies demonstrate examples of multi-sectoral activities led by PHAC, OHARA is not limited to these examples. It provides a foundation and guidance for multi-sectoral work that can be used by anyone.

A number of lessons were learned in the first two years of implementation, including that every situation is different and requires tailored solutions to inform decisions and improve prevention, preparedness, and response. Early multi-sectoral discussions are needed to guide next steps and ensure resources are

used wisely and effort is not duplicated. Additionally, different perspectives have been encountered on suitable distribution of results, and communication specialists must be engaged early.

The evaluation of completed risk assessments and the associated process will help to improve One Health collaboration moving forward. To date, multi-sectoral collaboration using OHARA has been invaluable for Canada in addressing issues that overlap or fall between organizational mandates.

1705 – Looking ahead while looking back: climate risks and adaptation strategies at the human-wildlife interface in southern Africa

Oriane BASSO (1,2), Benjamin SULTAN (3), Larisa LEE-CRUZ (4), Annelise TRAN (2,4,5), Vladimir GROSBOIS (2), Tawanda TARAKINI (6), Rebecca MANZOU (7), Benjamin ROCHE (1,8), Eve MIGUEL (1)

1: MIVEGEC, University of Montpellier, IRD, CNRS, Montpellier, France; 2: ASTRE, University of Montpellier, CIRAD, INRAE, Montpellier, France; 3: Espace-Dev, University of Montpellier, IRD, Montpellier, France; 4: TETIS, University of Montpellier, AgroParisTech, CIRAD, INRAE, Montpellier, France; 5: CIRAD, UMR TETIS, Montpellier, France; 6: Department of Wildlife Ecology and Conservation, Chinhoyi University of Technology, Zimbabwe; 7: Meteorological Services Department of Zimbabwe (MSD), Harare, Zimbabwe; 8: International Joint Laboratory ELDORADO, IRD-UNAM, Mérida, Yucatán, México

Background:

Southern Africa is particularly affected by climate change and is already experiencing the adverse impacts of extreme weather events such as droughts and heat waves. Human-wildlife interfaces are critical areas where changes in climatic conditions may trigger cascading impacts with important public health implications, including infectious disease risk. Addressing these emerging threats requires locally grounded adaptation strategies that account for the interdependence of the processes at play and the inherent uncertainty of future climate scenarios.

Methods:

This study focused on the human-wildlife interface of conservation areas surrounding Hwange National Park and adjacent human settlements in Zimbabwe. A mixed-methods approach combining climate analysis and participatory workshop was used. Historical rainfall and temperature trends were analysed using remote sensing data and in situ observations from the Zimbabwe Meteorological Services Department (MSD). CMIP6 (Coupled Model Intercomparison Project Phase 6) climate projections were used to identify four plausible future climate scenarios. Local stakeholders involved in the workshop included farmers, representatives of government institutions, members of non-governmental organisations (NGOs), and stakeholders from the research and tourism sectors. The workshop was designed to elicit participants' assessments of historical impacts, future risks across diverse climate scenarios, and potential adaptation strategies.

Results:

Stakeholders reported numerous impacts from recurrent historical droughts and heatwaves, including reduced food security and water availability, and cascading impacts on human, livestock, and wildlife health. Climate analyses indicated historical and projected warming, but greater uncertainty in local precipitation trends across datasets and models. Stakeholders identified numerous cascading, interconnected future risks affecting multiple components of the system, including risks linked to public health, agriculture, food security, and environmental degradation. The participatory approach also revealed a broad set of adaptation proposals, with several options overlapping across scenarios and among multiple stakeholder groups.

Conclusions:

By combining climate analyses with a participatory approach, this study documents people's recollections of past impacts and their perceived future risks across diverse climate scenarios at the protected area interface. As climate change increases pressure on shared resources and threatens global health, inclusive dialogue among local actors is essential to identify collective adaptation pathways.

1708 – A Veterinary Sanitary Mandate for One Health: Rwanda's Public–Private Model for Veterinary Workforce and Disease Surveillance

Anselme SHYAKA (1), Pascal NYABINWA (2), Carine NYILIMANA (3), Jean Claude RUKUNDO (2), Isidore GAFARASI (2), Laurien NTAMUGABUMWE (4), Denyse MUGWANEZA (5), Fabrice NDAYISENGA (2)

1: Center for One Health, University of Global Health Equity, Rwanda; 2: Rwanda Agriculture and Animal Resources Development Board; 3: Ministry of Agriculture and Animal Resources, Rwanda; 4: Rwanda Council for Veterinary Doctors; 5: Rwanda Biomedical Centre

Background

Across many African countries and other low- and middle-income settings, veterinary service reforms have encouraged the privatization of clinical veterinary services while governments retain regulatory and public health functions. This transition has often faced challenges due to limited demand for paid services among smallholder farmers, weak incentives for rural private practice, and insufficient mechanisms to coordinate and supervise private veterinarians. As a result, gaps persist in animal health service delivery, disease surveillance, and early detection of zoonotic threats. Rwanda introduced a Veterinary Sanitary Mandate (VSM) to formally engage private veterinary practitioners within a structured public–private framework supporting animal health services, disease reporting, and national One Health priorities.

Methods

Through the COHESA Project, implemented in Rwanda by the Center for One Health at the University of Global Health Equity with national partners, targeted capacity building was provided to private veterinary practitioners participating in the VSM. Training focused on zoonotic disease recognition, surveillance reporting pathways, antimicrobial stewardship, and cross-sector collaboration. Knowledge assessments were conducted before and after training, and structured feedback was collected to identify operational barriers to mandate implementation.

Results

The Veterinary Sanitary Mandate is operational across Rwanda and engages private veterinary practitioners in key veterinary public health functions, including meat inspection, animal health care, veterinary pharmacy oversight, disease reporting, and animal welfare advocacy. Practitioners operate through private companies under the oversight of public veterinary services and the regulatory supervision of the Veterinary Council, working at the interface of animal, human, and environmental health while contributing to national disease surveillance systems.

Because the mandate involves veterinarians and veterinary paraprofessionals working in rural livestock systems, variations in baseline knowledge were observed. The COHESA project therefore supported targeted capacity building. A total of 80 practitioners participated in training across three cohorts. Median knowledge scores increased by 20–35 percentage points, with improvements in zoonotic disease recognition, antimicrobial stewardship, and surveillance responsibilities. Participants also reported greater awareness of their role in reporting priority diseases and collaborating with public health authorities. Challenges included limited diagnostic infrastructure, logistical constraints, and the need for clearer operational guidance as well as sustainable and continuous capacity building.

Conclusions

The Veterinary Sanitary Mandate represents a promising governance model for strengthening veterinary workforce capacity while improving zoonotic disease surveillance and animal health service delivery. Rwanda's experience shows how structured public–private collaboration can bridge gaps created by veterinary service privatization and support stronger One Health surveillance systems.

1712 – Uncovering hidden parasite-host communications in zoonotic infections caused by trypanosomatids

Armanda RODRIGUES (1), Mafalda MEUNIER (1), Ana VALÉRIO-BOLAS (1), Flávia FRÓIS MARTINS (1), Micheli FERLA (1), Juliana INÊS WEBER (1), Marta MONTEIRO (2,3), Rui FERREIRA (4), Inês CARDOSO (4), Joana PALMA-MARQUES (1), João OLIVEIRA-DURÃES (1), Telmo NUNES (5), Wilson ANTUNES (6), Graça ALEXANDRE-PIRES (2,3), Isabel PEREIRA DA FONSECA (2,3), Gabriela SANTOS-GOMES (1)

1: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade Nova de Lisboa, Lisbon, Portugal; 2: Center for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal; 3: Associate Laboratory for Animal and Veterinary Sciences, Portugal; 4: Banco de Sangue Animal, Porto, Portugal; 5: Faculty of Sciences, University of Lisbon, Lisbon, Portugal; 6: Unidade Militar Laboratorial de Defesa Biológica e Química (UMLDBQ), 1849-012 Lisbon, Portugal

Background: Leishmaniasis and trypanosomiasis constitute some of the most neglected zoonotic diseases (NZDs), and are caused *Leishmania* spp. and *Trypanosoma* spp. parasites, respectively. Together they constitute a serious threat to humans, wild and domestic animals, causing millions of deaths worldwide. Dogs constitute a major reservoir for these parasites and in a rapidly evolving world, trypanosomatids represent an emerging world health problem, posing important challenges to human health and veterinary sciences. As host-parasite immune interactions are key in determining infection outcome, several efforts have been made to unravel this communication. Macrophages are antigen presenting cells (APC) and constitute key elements in the immunological communication axis. However, these cells also constitute target cells for trypanosomatids infection. Thus, exploiting the immunological communication axis between macrophages and lymphocytes is essential to elucidate host immune regulation and pathogen persistence in infections. Moreover, in last years, extracellular vesicles (EVs) have emerged as important cell-to-cell and parasite-host communication systems. Thus, the present study focused on the role of macrophages-lymphocytes axis, aiming at unravelling parasite and parasite-derived-EVs communication.

Methods: Extracellular vesicles from *Trypanosoma cruzi* (*Tc*EVs) and *Leishmania infantum* (*Li*EVs) maintained in axenic culture were isolated using commercially available reagents. Scan electron microscopy (SEM) was used to characterize *Tc*EVs and *Li*EVs production in cultured parasites. Cellular co-culture systems based on APCs were established. Briefly, peripheral blood from healthy dogs was used to isolate monocytes and lymphocytes. Monocytes were *in vitro* differentiated into macrophages (MDM) and used to establish co-culture systems with autologous lymphocytes. Co-cultures were exposed to *Tc*EVs and *Li*EVs for 24 h and cellular interactions assessed by SEM and real-time (RT)-PCR for key immune mediators.

Results:*Tc*EVs and *Li*EVs were naturally produced and released by parasite membrane and have round morphology varying in size. Trypanosomatids and *Tc*EVs or *Li*EVs establish close interactions with MDM cell membrane with evidence for their internalization. Cells alter their membrane morphology after exposition to parasite-derived EVs. *Tc*EVs and *Li*EVs were able to induce a mix immune response of co-culture systems.

Conclusions: The established co-culture system with emphasis in macrophages-lymphocytes axis, allowed the detailing of the cross-talk between trypanosomatids and canine host. MDM were able to sense and react to *Tc*EVs or *Li*EVs presence. EVs are an integrant part of trypanosomatids biology and play an important immunomodulatory role in the host immune response, that may be explored for potential translational applications in the scope of diagnostic, prophylactic and therapeutic innovative strategies.

Funding/ acknowledgements: This work was supported by FCT-Foundation for Science and Technology (FCT) through research grants 2023.11944.PEX (doi.org/10.54499/2023.11944.PEX) and 2023.17706.ICDT and by national funding, GHTM-UID/04413/2025, LA-REAL-LA/P/0117/2020, CIISA-UIDB/00276/2025 and AL4AnimalS-LA/P/0059/2020. A. Rodrigues is supported by CEECIND/CP1725/CT0023 (10.54499/2022.00499.CEECIND/CP1725/CT0023). J. Weber (2022.13899.BD), M. Monteiro (UI/BD/152819/2022) and J. Palma-Marques (2021.05579BD) are beneficiaries of PhD studentships.

1718 – Zoonotic Endoparasites in Dog Feces from Urban Parks in Santiago, Chile: Environmental Risk Factors and Spatial Analysis

Galia RAMÍREZ-TOLOZA (1), Samuel LÓPEZ (1), Javier ACEVEDO (1), Fernando FREDES (1), Claudio ABARCA (1), Catalina ALFARO-GODOY (1), Camila MUÑOZ-ZANZI (1), Raúl ALEGRÍA-MORÁN (2)

1: Laboratorio de Parasitología y Enfermedades Parasitarias, Departamento de Medicina Preventiva Animal, Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile, Santiago, Chile.; 2: Escuela de Medicina Veterinaria, Facultad de Medicina, Facultad de Ciencias Biológicas y Facultad de Agronomía y Sistemas Naturales, Pontificia Universidad Católica de Chile, Santiago, Chile

Background: Dogs are deeply integrated into urban families, providing social and psychological benefits. However, shared public spaces like parks and squares represent a critical 'One Health' interface. High

concentrations of domestic animals lead to environmental contamination with resilient zoonotic parasites (e.g., *Toxocara* spp., *Ancylostoma* spp., *Giardia* sp., among others). This poses significant risks, particularly for children and vulnerable groups, through fecal-oral transmission. Monitoring environmental soil contamination is essential for understanding public health risks and developing prevention strategies in modern cities, where human-animal interactions are most frequent. This study aimed to characterize the presence of zoonotic endoparasites in dog feces collected from the main urban parks of Gran Santiago, determine risk factors, and identify high-risk spatial clusters.

Methods: A total of 492 samples were collected from public and private parks and squares from Gran Santiago, within the Metropolitana region. The fecal flotation technique was used to analyze samples. The association between environmental and anthropogenic variables and parasitism was evaluated using binary logistic regression, with the presence of any parasitic form in the sample as the response variable. Potential risk factors were initially screened using univariate analysis (p 0.20), and a multivariable model was subsequently constructed using backward stepwise elimination based on the Likelihood Ratio Test. The Kulldorff Scan Statistics were applied to identify spatial clusters, to distinguish "hotspots," and to assess whether the distribution of parasite cases deviates from randomness. The Bernoulli model of the spatial scan statistic, suitable for binary data like positivity to a parasite species, was used to analyze clustering.

Results:*Giardia* sp. was detected in 7.5% of samples (37/492), *Toxocara canis*, *Toxascaris leonina*, *Ancylostomidae*-like eggs, *Trichuris vulpis*, *Cystoisospore*-like eggs, *Sarcocystis* spp., and *Neospora* spp. were detected in 1% or less of the samples. Relative humidity was positively associated with the probability of parasitism (OR = 1.03; 95% CI: 1.001–1.063; p = 0.045), indicating increased odds of parasitism with higher humidity. UV index showed no significant independent effect (OR = 1.25; 95% CI: 0.949–1.660; p = 0.112). However, a significant interaction between UV index and humidity was detected (OR = 0.99; 95% CI: 0.987–0.999; p = 0.036). A total of 5 high-risk spatial clusters were detected, none of them statistically significant (p > 0.05). Only one of those clusters was at borderline significance (p = 0.07), located at San Borja Park in the center of the region.

Conclusions: Positivity was observed for several parasites with zoonotic potential in public spaces shared between animals and humans. Environmental factors indicate that humidity affects parasite positivity, which is also influenced by UV radiation. Potential spatial aggregation was observed at the center of the Metropolitana region.

1720 – From Sectoral Laws to Integrated Governance: One Health as a Guiding Legal Principle

Carmen BULLON CARO (1,2)

1: Universidade da Coruña; 2: FAO

BackgroundGrowing recognition that the health of humans, animals, plants and the environment are interconnected has led to widespread endorsement of the One Health approach. However, legal frameworks addressing interconnected health risks remain largely structured through sector-specific and often disconnected legislation governing public health, veterinary services, agriculture and environmental protection. This fragmentation can limit the capacity of governance systems to anticipate and manage complex challenges such as zoonotic diseases, antimicrobial resistance, biodiversity loss and pollution. Conceiving One Health as a legal principle, rather than as a fixed set of rules, may provide a flexible framework for strengthening coherence across sectoral legislation while allowing its application to be adapted to diverse institutional contexts and governance arrangements.

MethodsThis research proposes a legal analytical framework for operationalising One Health in regulatory systems. Building on existing scholarship, it identifies four legal pillars capable of guiding legislative design and interpretation: normative integration across regulatory domains; multisectoral and multidisciplinary collaboration; stewardship and the sustainable use of shared ecological goods; and access and participation rights. The study then examines how this framework could operate within selected administrative structures involved in the management of interconnected health risks.

ResultsThe proposed framework is applied to three governance domains where cross-sectoral integration is particularly relevant: disease surveillance systems, environmental impact assessment and pesticide management regimes. Examining these domains illustrates how the four pillars provide practical criteria for assessing whether existing legal arrangements enable or constrain the implementation of a One

Health approach. The analysis highlights the role of normative integration in strengthening coherence across sector-specific legislation; institutional mechanisms for collaboration in improving information sharing and coordinated responses; stewardship obligations in supporting the sustainable management of ecological goods underpinning health outcomes; and participation rights in enhancing legitimacy and inclusiveness in decision-making processes, facilitating whole-of-society engagement.

ConclusionsExamining One Health through the lens of concrete administrative structures illustrates how it could function as a guiding legal principle capable of supporting greater coherence in regulatory frameworks addressing interconnected health risks. By translating the principle into operational legal criteria, the proposed framework offers a practical methodology for assessing and strengthening legislation governing interconnected health risks. In doing so, it provides a flexible framework that can support more coherent regulatory responses across sectors, while allowing countries to adapt implementation to their institutional structures and policy priorities.

1727 – Costing One Health AMR surveillance in Africa to build a sustainable investment case

Mohamed Moctar MOUICHE MOULIOM (1), Ntombi Mudenda NKONDE (2), Ranyl Nguena GUEFACK NOUMEDEM (3), Dodoo Cornelius NII OTTO (4), Juliana NDASI (1), Anafi MATAKA (1)

1: African Society for Laboratory Medicine (ASLM), Ethiopia; 2: University of Zambia, School of Veterinary Medicine; 3: National Veterinary Laboratory (LANAVET), Cameroon; 4: University of Health and Allied Sciences, Ghana

Background: Antimicrobial resistance (AMR) surveillance is fundamental for guiding treatment, detecting emerging threats, informing stewardship, and supporting national decision-making. In many African countries, surveillance systems remain financially fragile. Investments often prioritize setup costs, such as equipment and infrastructure, while the recurrent costs required to maintain systems functioning, such as reagents, consumables, transport, and maintenance, are often poorly documented and insufficiently funded. This creates a sustainability gap in which laboratories may be established but cannot operate consistently. This study aimed to develop and apply a One Health costing framework to estimate the true cost of AMR surveillance across human, animal, and environmental health sectors and to generate an evidence-based investment case for sustainable financing.

Methods: A One Health costing model was applied across five African countries (Zambia, Ghana, Malawi, Tanzania and Cameroon), using data collected between 2020 and 2024. The model captured direct and indirect costs across sentinel sites, bacteriology laboratories, and national AMR coordination mechanisms. Cost categories included reagents and consumables, personnel, equipment, infrastructure, logistics and transport, training, quality assurance, data systems, and coordination. Data were gathered through standardized tools at sentinel sites and coordination levels and analyzed to estimate total costs, cost per laboratory, cost per sample or isolate, and contributions from governments and external partners. Cost effectiveness analysis, sensitivity analysis, and scenario planning were also used to explore efficiency, donor dependence, and financing options for long-term sustainability.

Results: Total surveillance costs ranged from USD 1.21 million to USD 14 million across countries and periods. The main cost drivers were reagents and consumables (52–65% of total costs), personnel (10–26%), infrastructure and renovations (14–44%), and equipment (8–14%). Donor funding accounted for most of the financing, contributing an estimated 55–90% across countries, and the Fleming Fund provided more than half of the total support in several settings. External partners financed more than 80% of the reagent costs, highlighting a significant sustainability risk. The cost per sample varied widely, with animal health surveillance costing three to ten times more than human health surveillance, largely because of lower sample volumes and the higher operational costs of active surveillance. Government funding accounted for approximately 28–36% of the total (staff salaries and utilities). These findings support a blended financing model in which governments fund stable core costs, while partners support catalytic and technical investments.

Conclusion: A granular One Health costing approach can help transform AMR surveillance from a poorly defined expense into a credible public investment. By making the cost drivers, recurrent needs, and domestic contributions visible, the model offers a practical basis for transition planning, budget advocacy, and sustainable financing. Institutionalizing costing tools, strengthening health economics capacity, and creating dedicated national budget lines will be essential to secure the future of AMR surveillance in Africa.

1731 – Assessment of the integration of One Health principles: the case of antimicrobial resistance governance in Senegal

Mouhamadou Moustapha SOW
Gaston Berger University, Senegal

Background

Antimicrobial resistance (AMR) is a major global health issue, particularly in sub-Saharan Africa, where structural, behavioural and institutional factors exacerbate its spread. In Senegal, AMR represents one of the leading causes of death, with an estimated 11,900 deaths in 2019, and its political management has led to the adoption of a political and institutional framework based on a One Health approach. This study assesses the extent to which One Health principles are integrated into AMR governance in Senegal, a pioneer in the adoption of an intersectoral framework in French-speaking country in Africa since 2017.

Methods

Based on 26 qualitative interviews conducted with 37 stakeholders from the human, animal, environmental and agricultural health sectors, the analysis draws on the conceptual framework developed by Ruckert et al. (2024), which identifies six principles of One Health governance: participation, coordination and collaboration, management, sustainability, accountability and transparency, and equity. This framework is particularly well suited for a critical evaluation of governance arrangements, with a view to informing the transformation of AMR management policies and the reform of existing power structures.

Results

The results reveal growing institutional integration of the One Health approach, but one that remains constrained by persistent sectoral silos, predominantly technocratic and weakly inclusive coordination mechanisms, and strong financial dependence on international donors. Governance arrangements are further characterised by inter-institutional tensions, limited enforcement of regulations and fragile sustainability due to insufficient domestic resources. In addition, limited sharing of surveillance data and insufficient financial transparency weaken accountability mechanisms. Sectoral and geographical inequalities compromise equitable access to quality antibiotics, as well as the effective integration of environmental and agricultural sectors.

Conclusions

The study highlights the limitations of technocratic assessment approaches, which often prioritise quantitative scoring over a contextualised understanding of governance capacities. It argues for the use of critical and systemic analytical tools that better integrate the political and social dimensions of One Health. Overall, the findings call for a rethinking of global health security assessment framework, in order to better reflect local dynamics and to foster sustainable national ownership of the One Health approach in the AMR management.

1739 – Free-Ranging Domestic Dogs as an Expanding and Under addressed One Health Challenge: Insights from Protected Area Managers

Lucy KEATTS (1), Christian WALZER (1), Diego MONTECINO (1), Lauren GAWEL (2), Catherine DOUGNAC (1)
1: Wildlife Conservation Society (WCS); 2: Cummings School of Veterinary Medicine, Tufts University

BackgroundDogs were domesticated approximately 15,000 years ago and remain closely associated with human settlements, yet many range freely beyond these areas. An estimated one billion dogs exist worldwide along a spectrum from dependent pets to feral animals. As human populations expand, dog populations increase correspondingly, escalating interactions at human–livestock–wildlife interfaces. Free-ranging dogs are increasingly recognized as a One Health concern affecting human health, livestock production, and biodiversity simultaneously. In conservation landscapes, dogs can prey on wildlife, disturb habitats, compete with native predators, hybridize with wild canids, and transmit pathogens such as rabies and canine distemper. Impacts can generate social–ecological consequences including wildlife

declines, livestock losses, disease transmission, and heightened human–wildlife conflict. Dogs also occupy important social and cultural roles in many communities, creating ethical, management and governance challenges.

MethodsA global survey was conducted across Wildlife Conservation Society country programs working in protected areas to assess the scale and nature of these impacts. Twenty-six programs from Africa, Asia, Central and South America, and North America participated. Respondents reported on presence of free-ranging dogs in protected areas, types of dogs involved (owned, feral, mixed), observed impacts on wildlife, human health and livestock, and management responses. A follow-up survey involving 18 programs collected additional information on interventions, governance and social considerations affecting management.

ResultsFree-ranging dogs were reported in protected areas in 25/26 participating programs, and identified as a direct threat to conservation in 22. Dogs were described as owned animals roaming from nearby communities as well as feral or semi-owned animals associated with ranger stations, livestock grazing, or hunting activities. Respondents reported impacts across wildlife groups including carnivores, ungulates, primates, small mammals, birds, reptiles, and amphibians. Predation was the most frequently reported impact, but disease transmission, disturbance, and competition were also documented. Threats extended beyond wildlife to livestock losses and human health risks, particularly through rabies transmission.

Despite the widespread nature of the problem, only half of participating countries reported active dog-management programs. Major barriers included limited research on dog ecology in conservation landscapes, lack of funding, weak legislation governing dog ownership, and insufficient technical expertise. Cultural attitudes toward dogs, strong human–dog bonds, and animal welfare concerns further complicated management approaches and policy implementation.

ConclusionsFree-ranging domestic dogs represent a widespread but under-addressed One Health challenge in and around conservation areas. Their impacts extend beyond wildlife predation to include pathogen transmission, livestock losses, and broader social–ecological consequences. Addressing these risks requires investment in integrated approaches combining wildlife conservation, public health, dog and livestock management, ethics, and community engagement. Strengthening surveillance of dog populations, expanding vaccination, sterilization, and other control programs, clarifying governance frameworks, and improving understanding of dog ecology in conservation landscapes are essential steps for operationalizing One Health responses to this growing threat.

1755 – One Health epidemiological research in West Africa: Preliminary results of a scoping review

Saidal Ali BAH (1,2), Sheriffo MK DARBOE (3), Eric M FÈVRE (4,5), **Tessa Rose CORNELL** (4)

1: Medical Research Council Unit The Gambia at the London School of Hygiene and Tropical Medicine, Fajara, The Gambia; 2: Department of Livestock Services, Ministry of Agriculture, Livestock and Food Security, The Gambia Government, Abuko, The Gambia; 3: Epidemiology and Disease Control Unit, Ministry of Health, The Gambia Government, Kotu, The Gambia; 4: Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, UK; 5: International Livestock Research Institute (ILRI), Nairobi, Kenya

Background

Across West Africa, formal adoption and operationalisation of the One Health (OH) concept have gained momentum. A wide spectrum of complex health and societal issues can now be examined through a OH lens. West Africa demonstrates a high burden of emerging, re-emerging, and zoonotic infectious diseases across human and animal populations, which represent a major focus of the OH agenda globally.

To date, a review of epidemiological OH studies in West Africa using a systematic approach has not been conducted. This scoping review aimed to examine the number, attributes, research themes, and geographic scope of existing studies across the region, to inform future research directions and to examine OH study reporting and quality.

Methods

The PRISMA-ScR protocol was applied to systematically search PubMED and Web of Science databases. The keyword search string comprised country names, OH and related terms, and eligible study types.

Epidemiological studies in West Africa, which reported data from at least two domains (out of human, animal, and environment health domains) and described the relationships or interactions between these domains, were eligible for inclusion. Articles in English, French, and Portuguese were included. No publication date restrictions were applied.

Using Covidence software, titles and abstracts of identified articles followed by full texts, were independently screened for eligibility by two reviewers, and conflicts were resolved by a third reviewer. Using a pre-developed form on Kobo Toolbox, data were extracted on article attributes (including author affiliations and disciplines, publication years, and study methodologies), OH research themes, and geographic scope. Extracted data were subject to descriptive data analysis.

Results

On electronic database search, 2850 titles and abstracts were identified following duplicate removal, of which 250 full texts were reviewed. Preliminary data extraction was conducted for 27 eligible full texts published between 1981 and 2024. Countries of focus included Nigeria (55.6%), Ghana (14.2%), The Gambia (7.4%), and Benin (7.4%). The following research topics were addressed: infectious disease or zoonosis (51.9%), antimicrobial resistance (22.2%), non-communicable disease (18.5), and human-animal interactions (7.4%). Variable infectious diseases were described, including malaria, Rift Valley fever, and rabies. Data on two and three domains were reported by 74.1% and 25.9% of articles, respectively. Articles reporting data from two domains most commonly reported human and animal domains (45.0%) or human and environment domains (45.0%).

Conclusions

Preliminary results of this review highlighted the range of epidemiological studies across West Africa which describe data from multiple health domains and address a variety of OH topics. Inter-country variations were demonstrated in the number of identified articles and the common OH research themes. The review highlighted heterogeneity in OH study reporting.

1765 – Health and Wildlife Knowledge (HAWK): a community-of-practice-built data platform to support the integration of wildlife health surveillance into One Health systems

Diego MONTECINO LATORRE, **Sarah OLSON**, Chris WALZER, Lucy KEATTS, Mathieu PRUVOT
Wildlife Conservation Society, United States of America

Wildlife health surveillance is a foundational component of One Health, providing early warning of emerging pathogens, detecting shifts in ecosystem health, and identifying risks at the wildlife–livestock–human interface before they escalate into broader public health or economic crises. Wildlife health surveillance (WHS) systems depend on highly diverse data—ranging from environmental variables to diagnostic test results—collected by multiple actors using varied methodologies and targeting diverse hazards, hosts, and vectors. However, these data are often fragmented, inconsistently stored and structured, and lack standardized vocabularies leading to data loss, inefficient sharing, and delayed responses to health hazards. These weaknesses undermine conservation efforts, impede the integration of wildlife health into One Health systems, limit early warning capacity, and constrain timely prevention of emerging threats to conservation, animal and human health.

Well-designed databases are foundational to the successful implementation and operation of WHS systems. Yet, access to comprehensive, purpose-built platforms remains a significant barrier, particularly in low- and middle-income settings. Existing databases are often private, costly, limited in scope, or available only to specific agencies. Chronic underinvestment in the environment sector and WHS has further constrained the development of interoperable, scalable digital infrastructure aligned with One Health goals.

To address this gap, WCS is developing the Health and Wildlife Knowledge (HAWK), a community-of-practice-driven digital data service platform to strengthen WHS. The platform is built around a comprehensive data structure co-developed by a globally distributed, diverse multidisciplinary expert network, aligned with established international standards and vocabularies. HAWK supports handling of diverse data, secure storage, and structured epidemiological and metadata capture across hazards,

hosts, vectors, and environmental contexts, while enabling modular expansion to meet country- and program-specific needs..

HAWK seeks to harmonize and consolidate wildlife health data that are often siloed and overlooked across institutions and sectors. By bringing these data together and enabling standardized data governance, interoperability, and controlled data sharing, HAWK supports strengthened risk assessments and integration of wildlife health into One Health frameworks. Data security, sovereignty, and ownership are protected through strict compartmentalization among organizations and user-specific permissions. HAWK supports data visualization (e.g., Ecoscope), analysis (e.g., AI and machine learning), and field data collection (SMART) allowing stakeholders to continue using preferred local systems. Conceived as a global public good, HAWK promotes equitable and multilingual access and operates on a collaborative model driven by continuous user feedback and shared costs and stewardship through an inclusive governance model.

HAWK is not a data repository and represents not merely a database, but a scalable interoperability and governance data service to strengthen WHS as a core pillar of operational One Health systems. The platform's data structure, functions, governance framework and implementation pathway will be presented.

1767 – From animal surveillance to human sampling: a practical and efficient approach for One Health zoonotic disease research

Katie CORRIDAN (1), Guy MCGRATH (1), Daniel COLLINS (1), Rory HORGAN (1), Eoghan DE BARRA (2), Eoin FEENEY (1), Conor MCALOON (1)

1: University College Dublin, Ireland; 2: Royal College of Surgeons Ireland

Background Practical examples of operationalising the One Health approach in field research remain limited. Public health research requires population-level perspective, but prospective human sampling is often constrained by limited resources, logistical barriers, and difficulties in participant recruitment. Furthermore, animal health surveillance systems generate large datasets under-utilised to inform human health research.

This pilot study aimed to develop and test a practical One Health research approach integrating animal health data, targeted human sampling, and community engagement. The objective was to design a resource-efficient, multidisciplinary process facilitating collaboration between sectors while improving recruitment and engagement with at-risk populations for zoonotic disease.

Methods This study formed part of a public health medical doctorate project with multidisciplinary supervision from veterinary public health and human infectious disease specialists. Secondary animal health datasets from public and private sources were analysed to identify areas with elevated prevalence of a selected zoonotic pathogen in food-producing animals. These findings informed a targeted human sampling strategy focusing on high-risk occupational groups.

Prospective human sampling was conducted at six community events involving veterinary and agricultural stakeholders, providing access to a “captive audience” and improving accessibility. Study information and zoonotic risk messaging were disseminated in advance through event organisers, a dedicated website, and educational resources.

A bespoke GIS-enabled application supported data collection and integration. The platform enabled real-time data capture with GDPR-compliant safeguards protecting herd-owner and participant data, while allowing spatial mapping and visualisation of integrated animal and human datasets. Feedback from participants and event organisers informed iterative refinement of the approach.

Results The approach facilitated collaboration between veterinary, agricultural, and human health sectors and demonstrated a feasible, resource-efficient model for zoonotic disease research. A total of 160 high-risk participants were sampled across six community events conducted over four months.

Community-based events proved effective for engagement, enabling peer discussion and informal knowledge exchange. The GIS platform supported efficient data collection and transparent data protection practices, increasing participant confidence in the research process. Spatial visualisation of integrated datasets also helped demonstrate the practical application of One Health analysis.

Participant feedback indicated strong interest in contributing to One Health research. Many participants demonstrated an intuitive understanding of links between animal and human health, even where the formal One Health framework was unfamiliar. Most participants opted to receive individual results, highlighting the importance of reciprocal engagement. The events also enabled opportunistic health promotion, including discussion of occupational zoonotic risk reduction and farm biosecurity.

Conclusions This pilot study demonstrates a practical and scalable approach to operationalising One Health principles in zoonotic disease research. Integrating animal surveillance data, targeted human sampling, digital spatial tools, and community engagement provides a replicable model for collaborative, resource-efficient research while strengthening relationships with populations at risk.

1770 – Operationalizing equity and inclusivity in One Health prevention: A systems thinking perspective from PREZODE

Kelly Marie SAMBUCCI (1,2), **Elsa LEGER** (3,4), Rico ANCOG (5), Nicolas ANTOINE-MOUSSIAUX (6), Salomé R. A. BUKACHI (7), Max CLARON (8), Amélie DEVARS-LARRIVE (9,10), Andres GARCHITORENA (11), Fatma GUERFALI (12), Manon LOUNNAS (4,11), Lina MEGO (13), Dien NGUYEN THI (14), Marisa PEYRE (4,15), Magda ROBALO (16), Margarida SIMOES (17), Sandul YASOBANT (18), Robyn ALDERS (19)

1: Institute of Vertebrate Biology, Czech Academy of Sciences, Brno, Czech Republic; 2: Masaryk University, Department of Anthropology, Brno, Czech Republic; 3: Institut national de recherche pour l'agriculture, l'alimentation et l'environnement (INRAE), France; 4: PREZODE (PREventing ZOonotic Diseases Emergence) International Initiative; 5: University of the Philippines Los Baños (UPLB), The Philippines; 6: University of Liege, Belgium; 7: University of Nairobi, Kenya; 8: Friendship NGO; 9: University of Veterinary Medicine Vienna, Austria; 10: Complexity Science Hub Vienna, Austria; 11: Institut de recherche pour le développement (IRD), Montpellier, France; 12: Institut Pasteur of Tunis, Tunisia; 13: University of Montreal, Canada; 14: Vietnam National University of Agriculture, Hanoi, Vietnam; 15: Centre de coopération internationale en recherche agronomique pour le développement (CIRAD), Montpellier, France; 16: The Institute for Global Health and Development (IGHD), Guinea-Bissau; 17: University of Évora, Portugal; 18: Indian Institute of Public Health Gandhinagar (IIPHG), India; 19: The Australian National University (ANU), Canberra, Australia

Background Preventing zoonotic disease emergence requires coordinated action across human, animal, and environmental systems, as promoted by the PREZODE (Preventing Zoonotic Disease Emergence) initiative. However, recent global health emergencies have demonstrated that inequitable access to surveillance systems, countermeasures, and decision-making power undermines both preparedness and public trust. Structural inequities rooted in colonial legacies, unequal research partnerships, funding asymmetries, and epistemic hierarchies continue to shape global health governance. If unaddressed, these dynamics risk weakening prevention strategies by excluding key knowledge systems, marginalizing vulnerable populations, and limiting the effectiveness of interventions. Within a One Health framework, equity and inclusivity must therefore be understood not only as ethical imperatives but as systemic determinants of prevention effectiveness.

Methods This work presents the conceptual and operational framework developed by the PREZODE Equity Group to embed equity and inclusivity across the five pillars of the PREZODE Strategic Agenda: understanding zoonotic risk, co-designing preventive solutions, strengthening early warning systems, developing global information infrastructures, and supporting inclusive governance. Drawing on systems thinking, participatory research principles, and a review of emerging literature and case studies, we analyse structural and epistemic barriers affecting prevention systems. Particular attention is given to feedback mechanisms through which inequities influence surveillance sensitivity, intervention uptake, and policy legitimacy.

Results Our analysis identifies reinforcing feedback loops through which structural inequities—such as unequal research capacity, limited community participation, and exclusion of Indigenous and local knowledge—perpetuate zoonotic vulnerability. Conversely, inclusive governance structures, equitable research partnerships, and community-based surveillance systems function as balancing mechanisms that improve early detection and intervention effectiveness. The framework highlights practical leverage points across the PREZODE pillars, including equity-sensitive risk assessment, participatory co-design of interventions, community-led early warning systems, inclusive data governance models that respect data sovereignty, and funding structures that support transdisciplinary collaboration. These mechanisms strengthen trust, improve policy uptake, and enhance the legitimacy of One Health prevention strategies.

Conclusion Positioning equity and inclusivity as operational drivers of prevention performance enables PREZODE to strengthen the interface between science, policy, and society. Embedding these principles in

governance, research partnerships, and surveillance infrastructures enhances system sensitivity, intervention effectiveness, and public trust. Integrating equity into One Health prevention strategies therefore represents not only a matter of justice but a practical requirement for building resilient and globally effective zoonotic disease prevention systems.

1779 – Connectedness Across Human, Animal, and Environmental Systems: A Scoping Review of One Health and One Welfare in Social Work

Janine NOORLOOS

Ontario Veterinary College, University of Guelph, Canada

Background

Social work is increasingly called to respond to complex challenges shaped by interconnected human, animal, and environmental systems. One Health and One Welfare are interdisciplinary frameworks that emphasize collaboration across sectors to address multisystem determinants of wellbeing. While these frameworks are widely discussed in veterinary medicine, public health, and environmental sciences, their uptake within social work scholarship remains unclear. Understanding how One Health and One Welfare are currently engaged in social work literature is important for identifying opportunities to strengthen ecological and interdisciplinary approaches within social work education and practice. This scoping review examines how One Health and One Welfare are referenced, defined, and applied across social work-relevant scholarship.

Methods

A scoping review was conducted following PRISMA-ScR guidance. Searches were performed across six academic databases (Web of Science, PsycINFO, Social Services Abstracts, CINAHL, PubMed/MEDLINE, and ProQuest Dissertations) from database inception to December 2025. The search strategy combined the terms “One Health” OR “One Welfare” AND “social work.” Two reviewers independently screened titles and abstracts, with disagreements resolved through consensus. Eligible sources included peer-reviewed journal articles, books or book chapters, and dissertations explicitly referencing One Health or One Welfare in relation to social work education, research, or practice. Data extraction captured publication characteristics, depth of engagement with the frameworks, positioning of social work, educational relevance, and attention to equity and Indigenous knowledge. Descriptive statistics and thematic synthesis were used to summarize patterns across sources.

Results

Nineteen sources met the inclusion criteria. Most publications were conceptual or synthesis-based, including commentaries, book chapters, and a smaller number of empirical studies. One Health was the most frequently used term, with fewer sources referencing One Welfare or both frameworks. Across the literature, One Health and One Welfare were often framed as interdisciplinary approaches aligned with social work’s ecological and justice-oriented foundations. However, engagement was uneven and frequently remained conceptual rather than operationalized within practice models or educational frameworks. Human–animal relationships were more consistently addressed than environmental dimensions. Approximately half of the sources discussed implications for social work education, though few articulated specific competencies, curricula, or pedagogical strategies. Equity considerations were commonly acknowledged, but Indigenous knowledge systems and land-based understandings of relationality were rarely integrated. Overall, the literature reflected growing interdisciplinary interest but limited empirical evidence and few clearly articulated examples.

Conclusions

Interest in One Health and One Welfare within social work scholarship is growing but remains uneven in its translation into applied guidance for education and practice. Strengthening integration of these frameworks requires clearer competencies, curriculum models, and evaluation approaches that address interconnected human, animal, and environmental determinants of wellbeing. Greater engagement with Indigenous knowledge systems and ecological justice perspectives may further strengthen the ethical and relational foundations of One Health-informed social work.

1788 – Needs and challenges for FAIR data implementation in a One Health research programme: a qualitative study using the Double Diamond methodology in the PEPR PREZODE

Paula CACERES (1), **Sari TANIKAWA** (1), **Manon LOUNNAS** (2), Eric CAHUZAC (1), Serge MORAND (3), Hadi QUESNEVILLE (1), Elena ARSEVSKA (4), Fanny BOUYER (5), Amandine COURNIL (2), Xavier BAILLY (1), Pierrine DIDIER (1), Natacha ROUSSEAU (4), Bruno ROSSET (4), Agnès LEBLOND (1), Thomas BALENGHIEN (4), **Christine CITTI** (1)

1: INRAE-PREZODE, France; 2: IRD, France; 3: CNRS, France; 4: CIRAD, France; 5: MOOD Programme

BACKGROUND

In the context of open science policies and the growing adoption of FAIR principles to improve research data management and reuse, the PEPR PREZODE, a French priority research programme dedicated to the prevention of emerging zoonotic diseases, established an action focused on data management and sharing for its funded projects.

To this end, the PEPR Data Working Group (PEPR DWG), a multidisciplinary team of experts, was created to anticipate the needs of future funded projects and propose solutions promoting FAIR data implementation from the outset.

METHODSBefore projects had been selected, the PEPR DWG adopted the Double Diamond design methodology, commonly used when a final solution is not yet defined. This approach allows the identification of user needs and the exploration of potential solutions before implementing tools or infrastructures.

Through a transdisciplinary reflection process, the group defined the scope of the study and designed a survey targeting key stakeholder categories.

Between November 2023 and May 2024, 29 in-depth qualitative interviews were conducted with four categories of stakeholders: researchers comparable to future PEPR project leaders, funding experts, institutional data governance actors and managers of data platforms supporting research communities.

Each interview was transcribed, anonymised and analysed to extract verbatim statements expressing needs or suggestions. A total of 144 verbatims were extracted and categorised, reaching thematic saturation.

RESULTS

The analysis identified 54 needs grouped into seven thematic categories. The most frequently mentioned concerned storage infrastructure, data security and sovereignty (25% of verbatim statements), human resources, training and awareness in data management (14%), interoperability, data quality and standardisation (14%), the valorisation and visibility of research data (13%), and collaboration and trust-building among stakeholders (11%).

Findings indicate that many barriers to FAIR implementation could be addressed through training, technical and human support and improved use of existing research data infrastructures. However, needs related to teams and project visibility as well as data valorisation require additional mechanisms to strengthen collaboration and make prevention efforts more visible.

In 2026, a questionnaire was sent to the teams of the funded PEPR PREZODE projects to assess whether the identified needs reflected project realities. Results confirmed the consistency of the needs identified.

CONCLUSIONS

This study provides a structured overview of recurring data management challenges faced by researchers. The findings show that implementing FAIR principles requires institutional support, governance mechanisms, training and dedicated resources to accompany researchers throughout the data life-cycle.

The results have informed actions within the PEPR PREZODE programme, including awareness activities, support for data management plans, the development of a data community of practice responding to researchers' needs and the design of a module for the future PREZODE International Platform aimed at improving project visibility and fostering collaboration for zoonotic disease prevention.

1799 – Understanding and Overcoming Sociocultural Barriers in the Prevention of Emerging and Re-emerging Diseases: Communication Strategies Based on the One Health Approach

Florence NGOLOLE NZEMBA (1), Chris LUTONDA (1), Bibiche KAPINGA (1), Justin MASUMU (1,2)

1: National Institute for Biomedical Research, Democratic Republic of Congo; 2: Pedagogic National University, Democratic Republic of Congo

Background:

The emergence and re-emergence of infectious diseases pose a major challenge to global public health systems. In the face of these threats, the One Health approach has emerged as an integrative framework linking human, animal, and environmental health. Studies conducted as part of the INRB's DOPERAUS project in six provinces of the Democratic Republic of the Congo (Kinshasa, Kwilu, Kwango, Equateur, Haut-Katanga, and Kasaï-Oriental) aimed to analyze the role of risk communication and sociocultural factors in the prevention and control of emerging diseases. The underlying hypothesis is that the effectiveness of prevention strategies depends on their adaptation to local cultural contexts and community engagement.

Methods:

The study adopted a mixed methods combining semi-quantitative as well as qualitative and participatory approach. Field surveys were conducted in the six provinces mentioned, combining observations, questionnaires (3404 participants), interviews (180 participants), and focus discussion groups (30 participants). The analysis was based on an assessment of risk perception, cultural practices, trust in health institutions, and the role of community leaders in disseminating health messages.

Results:

The results show that sociocultural contexts have a strong influence on health-related behaviors. Certain traditional practices strengthen social cohesion but can also increase the risk of transmission. Mistrust of health authorities hinders adherence to preventive measures, while the trust and involvement of local leaders significantly improve the effectiveness of interventions. Participatory communication approaches, which actively involve communities in crafting messages, have proven to be more effective and sustainable than prescriptive or coercive strategies.

Conclusions:

Research from our study demonstrates that the prevention and management of emerging diseases require a deep understanding of local sociocultural dynamics. Integrating the social sciences into One Health approaches enhances the relevance and effectiveness of risk communication strategies. Close collaboration between human, animal, and environmental health professionals and community stakeholders is essential for building response systems that are more inclusive, sustainable, and tailored to local realities.

1801 – Brazil's Greatest Flood: Digital PCR as a tool for priority pathogen and carbapenem resistance gene surveillance in extreme climatic events

João Vitor Barboza CARDOSO (1,2), Dariane Castro PEREIRA (2), Gabriela Simões DE OLIVEIRA (1), William Latosinski MATOS (1,2), Artur Mattia ONGARATTO (1), Lucas BOHNENBERGER (1), Christian Araujo BARCELOS (1), Louidi Lauer ALBORNOZ (1), Afonso Luís BARTH (1,2), Salatiel Wohlmuth DA SILVA (1), Andreza Francisco MARTINS (1,2)

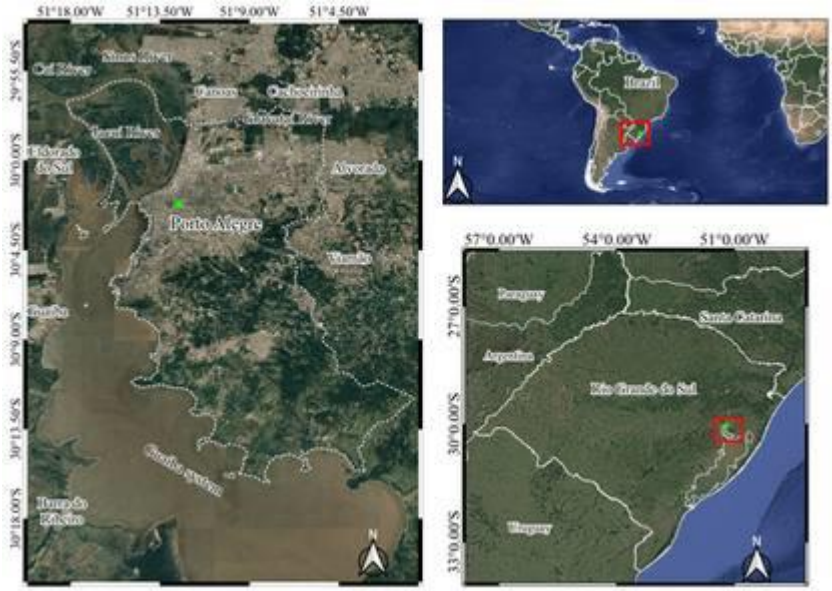
1: Universidade Federal do Rio Grande do Sul, Brazil; 2: Hospital de Clínicas de Porto Alegre, Brazil

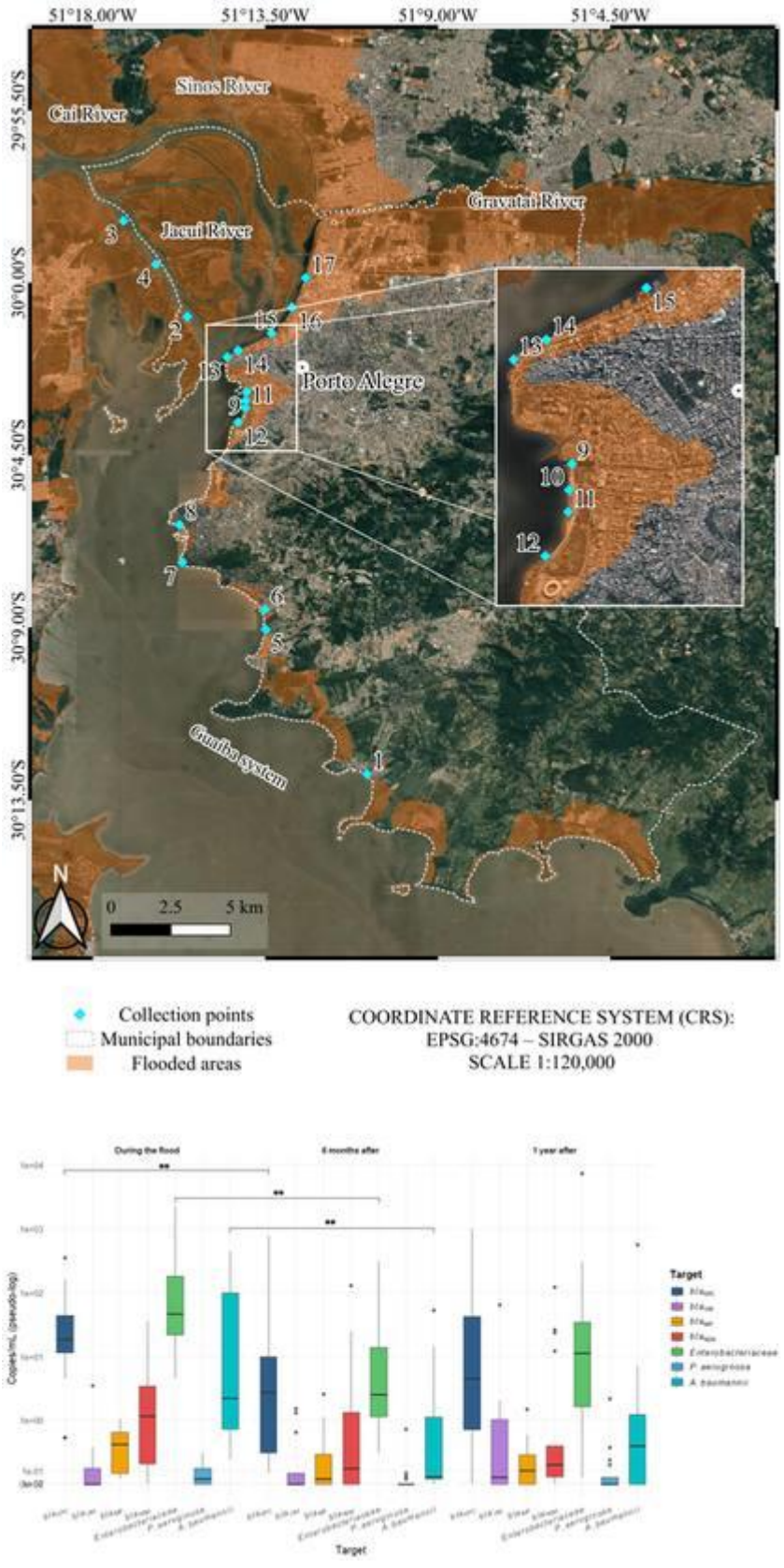
Background: Extreme climatic events, such as floods, pose a serious threat to public health by promoting the spread of antimicrobial-resistant (AMR) bacteria, particularly in urban areas with poor sanitation. In May 2024, the state of Rio Grande do Sul, Brazil (Figure 1), experienced the most severe flood in its history, affecting more than 2.3 million people and resulting in widespread sewage overflow and environmental contamination. Digital PCR (dPCR) is emerging as a promising approach for environmental and wastewater-based pathogen surveillance, owing to its high sensitivity, absolute quantification capability, and increased tolerance to PCR inhibitors. This study investigated the presence and absolute quantification of World Health Organization (WHO) priority pathogens and carbapenemase genes in floodwaters from Porto Alegre during and after the flood event.

Methods: A total of forty-six water samples were collected from seventeen sampling sites during three sampling campaigns: twelve samples in May 2024 (during the flood event), seventeen samples in November 2024 (six months post-flood), and seventeen samples in May 2025 (one year post-flood). The sites included previously flooded urban areas and strategic locations across Guaíba Lake (Figure 2). DNA was extracted using the DNeasy PowerWater Kit (Qiagen), and dPCR was performed on the QuantStudio™ Absolute Q™ Digital PCR System (ThermoFisher) with TaqMan multiplex assays targeting carbapenemase genes *bla*KPC, *bla*NDM, *bla*VIM, and *bla*IMP, and WHO priority pathogens: *Enterobacterales*, *P. aeruginosa*, and *A. baumannii*. A common threshold was applied across runs, and analyses were performed in R-studio.

Results: All targets were detected at least once across the three sampling campaigns. During the flood, higher concentrations were observed for *Enterobacterales*, *A. baumannii*, and *bla*KPC, with median values reaching approximately 122.15 cp/mL, 19.22 cp/mL, and 32.22 cp/mL, respectively (Figure 3). Six months after the flood, concentrations of these targets decreased to medians of approximately 2.54 cp/mL for *Enterobacterales*, 1 cp/mL for *A. baumannii*, and 2.74 cp/mL for *bla*KPC. Friedman test indicated significant temporal differences for *Enterobacterales* (p = 0.008), *A. baumannii* (p = 0.003), and *bla*KPC (p = 0.004). Pairwise Wilcoxon tests showed significant reduction between the flood and six months post-flood for *Enterobacterales* (adjusted p-value = 0.03) and *A. baumannii* (adjusted p-value = 0.01). Although *bla*KPC showed an overall significant trend, pairwise comparisons were not statistically significant (adjusted p = 0.07). Other targets showed lower concentrations, generally below 1 cp/mL, with no significant temporal variation.

Conclusions: Environmental findings mirrored the clinical epidemiology of the region, with *Enterobacterales* and *bla*KPC representing the most prevalent targets. The elevated concentrations detected during the flood indicate that extreme climatic events may enhance the environmental dissemination of antimicrobial resistance markers and clinically relevant pathogens, highlighting the importance of environmental surveillance to establish control politics.





1807 – Putting pandemic risk and resilience into a socio-ecological framework for risk mapping and policy

Marc YAMBAYAMBA, Simon RUEGG
Section of Epidemiologie, Vetsuisse Faculty, University of Zurich, Switzerland

Background Emerging infectious diseases (EIDs) arise from complex interactions between humans, animals, and ecosystems. Despite this growing recognition, pandemic preparedness efforts remain largely focused on downstream biomedical responses such as surveillance, diagnostics, and clinical countermeasures. Investments in upstream prevention and resilience remain limited. Furthermore, existing risk assessments often rely on anthropocentric indicators that inadequately capture the broader socio-ecological dynamics driving pathogen emergence and transmission. To address this gap, we propose a socio-ecological framework that integrates both risk and resilience dimensions to support more comprehensive pandemic preparedness, risk mapping, and policy planning within a One Health perspective.

Methods We are conducting a systematic literature review across major scientific databases to identify variables and indicators that characterize EID risk and resilience across human, animal, and environmental systems. Particular attention was given to governance, equity, and policy determinants that shape system capacity to prevent, detect, and respond to outbreaks. Drawing inspiration from risk assessment approaches used in the Sendai Framework for Disaster Risk Reduction, we aim to propose a weighted indicator methodology to capture the relative contribution of different socio-ecological factors. These indicators are organized within a multidimensional framework designed to support comparative risk mapping and resilience assessment. Future work will operationalize the framework using existing global and national datasets to generate composite indicators that can inform pandemic preparedness evaluation and policy prioritization.

Preliminary results We developed a four-layer socio-ecological framework describing the determinants of pandemic risk and resilience. At its centre, risk and resilience are conceptualized as two interdependent properties of the same system. The second layer captures key social, economic, and environmental determinants of health. These determinants are shaped by governance structures, institutional capacity, and equity considerations represented in the third layer. The outer layer encompasses broader structural drivers of pathogen spillover and amplification, including climate change, deforestation, biodiversity loss, rapid urbanization, extractive industries, food insecurity, conflict, human mobility, and behavioural practices.

Conclusion This framework provides a conceptual basis for integrating socio-ecological determinants into pandemic preparedness evaluation. By moving beyond purely biomedical indicators, it will offer a structured approach to identify upstream drivers of risk, strengthen system resilience, and support multisectoral decision-making aligned with the One Health approach.

1829 – Prevalence of Pesticide Residues in Akagera National Park Using Animal Wearable and Stationary Passive Samplers

Charline RUTAGENGWA (1,2), Jean ZHOU (3), Inumidun OYEBODE (3), Emmanuel IRIMASO (2), David MURENZI (1), Dawn ZIMMERMAN (4,5), Krystal J. Godri POLLITT (3)
1: Veterinary Initiative for Endangered Wildlife, Bozeman, Montana, USA; 2: University of Rwanda, School of Veterinary Medicine, Nyagatare, Rwanda; 3: School of Public Health, Environmental Health Sciences, Yale University, New Haven, CT, USA; 4: School of Public Health, Department of Epidemiology of Microbial Disease, Yale University, New Haven, CT, USA; 5: Smithsonian's National Museum of Natural History, Washington, DC, USA

Background

Agricultural activities surrounding protected areas can introduce pesticide residues into ecosystems managed for biodiversity conservation. However, contamination pathways within protected areas remain poorly characterized, particularly in landscapes where wildlife habitats interface directly with agricultural land. Passive sampling technologies provide a practical approach for assessing environmental contamination across complex ecosystems.

Methods

This study used silicone passive samplers (Fresh Air clips) to evaluate pesticide exposure in Akagera National Park, Rwanda, and integrated terrestrial and aquatic monitoring approaches. Samplers were deployed on anti-poaching dogs operating within the park and at key wildlife water bodies across

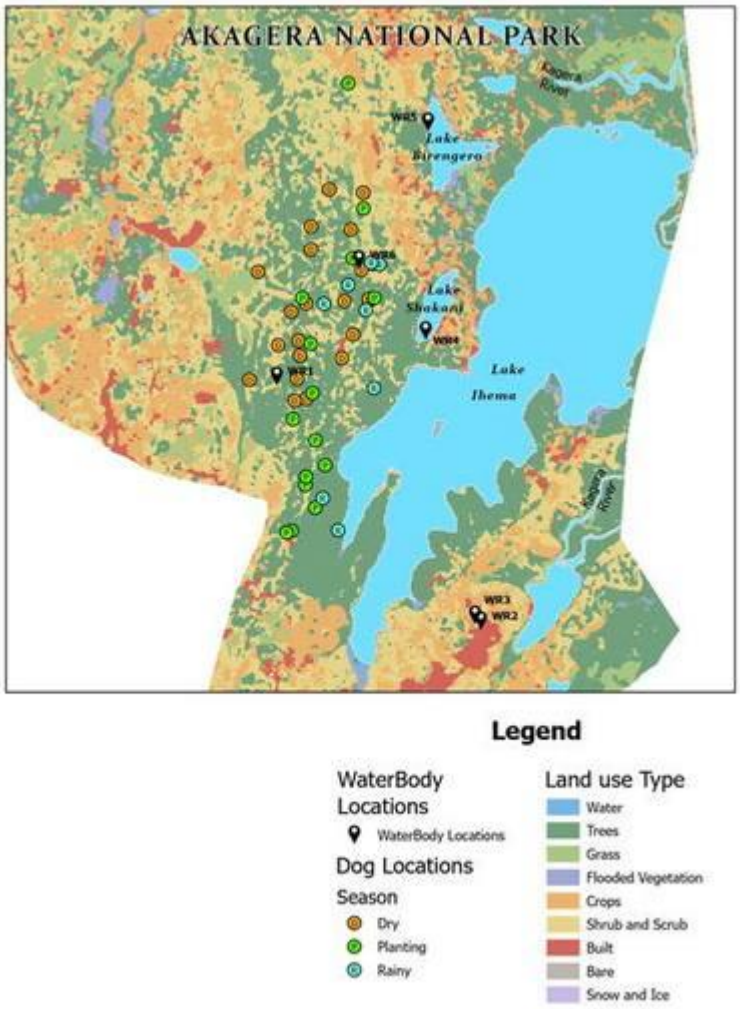
multiple seasons to assess potential contamination pathways. Waterbody samplers were deployed for approximately two weeks during each sampling period, conducted between September 2024 and April 2025, across the dry, rainy, and planting seasons. Chemical analysis targeted pesticides that have previously been used in agricultural activities.

Results

Diphenylamine, piperonyl butoxide, and myristicin were detected across sampling matrices. Diphenylamine was detected in 73% of dog-worn samplers but was absent in waterbody samplers, suggesting dominant terrestrial exposure pathways within the park. Piperonyl butoxide was detected in 100% of dog samplers and 19% of waterbody samplers, with concentrations reaching 3402 ng/m³, indicating consistent terrestrial exposure likely linked to pesticide use in surrounding agricultural areas. In contrast, myristicin was more frequently detected in waterbody samplers (38%) than in dog samplers (13%), suggesting hydrological transport processes during the rainfall season. Multivariate analyses further supported distinct exposure patterns between terrestrial and aquatic matrices.

Conclusion

These findings demonstrate that protected area boundaries remain permeable to agrochemical inputs originating from surrounding agricultural landscapes. Integrating sentinel animal monitoring with environmental passive sampling provides new insights into contaminant transport pathways within protected ecosystems and offers a scalable framework for monitoring chemical intrusion into conservation landscapes.



1834 – Widespread Exposure to Treponema pallidum in Wild African Nonhuman Primates: Implications for One Health

Clément LABARRERE (1,2), Charles KUMAKAMBA (1,2), Aboubacar DIAKITÉ (1,2), Inestin AMONA (1,2), Florence FENOLLAR (1,3), Oleg MEDIANNIKOV (1,2,4)

1: IHU Méditerranée Infection, France; 2: Microbes Evolution Phylogeny and Infections (MEPHI), Aix-Marseille Université, AP-HM, Marseille, France; 3: Infectious Risks in the Tropics and Emerging Microorganisms (RITMES), Aix-Marseille Université, SSA, AP-HM, Marseille, France; 4: IRD, Marseille, France

Human treponematoses are chronic infectious diseases caused by closely related subspecies of *Treponema pallidum*. While global eradication programs have historically focused on human populations, increasing evidence of treponemal infections in wild non-human primates (NHPs) raises concerns regarding their role as potential reservoirs. Understanding treponemal exposure in wildlife is therefore crucial from a One Health perspective.

We conducted a large-scale, non-invasive survey of *T. pallidum* circulation in wild NHPs across six countries (Senegal, Guinea, Republic of the Congo, Democratic Republic of the Congo, Algeria) and in captive chimpanzees in French zoos as negative controls. A total of 1,678 fecal samples were collected between 2018 and 2025. Host species were identified by sequencing of the mitochondrial 16S rRNA gene, and samples were screened for *T. pallidum* DNA using a real-time PCR targeting the *polA* gene. In parallel, the presence of anti-*T. pallidum* antibodies was investigated using an automated Jess Western blot platform with a recombinant antigen (TpN15, TpN17, and TpN47).

Of the 1,644 wild NHPs sample, 420 (25.0%) were seropositive, whereas all zoo control samples remained negative. Seroreactivity was detected across multiple primate taxa representing more than ten species, including great apes and monkeys: *Pan troglodytes verus* (177/676, 26.2%), *Gorilla gorilla* (17/50, 34.0%), *Papio papio* (59/124, 47.6%), *Erythrocebus patas* (57/109, 52.3%), *Cercopithecus ascanius* (67/354, 18.9%), and *Macaca sylvanus* in Algeria (33/96, 34.4%). Notably, this study provides the first evidence of *T. pallidum* exposure in NHPs from North Africa (*Macaca sylvanus* in Algeria, 33/96, 34.4%). All fecal samples were negative for *T. pallidum* DNA by qPCR.

These findings were corroborated by post-mortem analyses of bone samples from three wild chimpanzees from Senegal. All individuals were seropositive, and PCR analysis confirmed *T. pallidum* DNA in a vertebral sample. These molecular results, paired with observations of severe treponemal-like lesions in the field, provide definitive evidence of advanced treponematosis in West African NHPs.

Taken together, these findings suggest that exposure to *T. pallidum* is widespread among African NHPs across diverse ecosystems, including regions where human treponematoses persist. The high seroprevalence in some populations and the confirmation of advanced clinical disease highlight the importance of integrated surveillance. From a One Health perspective, the occurrence of treponemal infections across multiple primate species highlights the importance of integrated surveillance at the human–animal interface to better understand the ecology of treponemal diseases and evaluate the potential role of wildlife reservoirs in the persistence of human treponematoses.

1841 – Strengthening Pandemic and Transboundary Disease Preparedness Through Rapid Diagnostic Pipelines: The PREPARE-TID One Health Approach

Sara SAVIC (1), Rea Maja KOBIALKA (2), Kostas DELAKOUIDIS (3), Leonidas KAZATZOPOULOS (3), Dimitrios Victor EVGENIOU (3), Tobias SCHINDLER (4), Arianna CERUTI (2), Prakash GHOSH (2), Luisa BARZON (5), Tamas PETROVIC (1), Nazif ELALDI (6), Zati VATANSEVER (7), Manfred WEIDMANN (2), Julius Boniface OKUNI (8), Oumar FAYE (9), Dinesh MONDAL (10), Martin PFEFFER (2), Uwe TRUYEN (2), Marina ZEKIC (1), Ahmed Abd EL WAHED (2)

1: Scientific Veterinary Institute "Novi Sad", Serbia; 2: Institute for Animal Hygiene and Veterinary Public Health, Leipzig, Germany; 3: Repado Logismikotechniki-Ipiresiesereynas Kai Anaptixis Epe, Chalandri, Greece; 4: diaxxo, Zurich Switzerland; 5: Universita Degli Studi Di Padova, Department of Molecular Medicine (DMM), Padova, Italy; 6: Sivas Cumhuriyet Universitesi, Sivas, Turkiye; 7: Kafkas Universitesi, Kars, Turkiye; 8: Makerere University, Kampala, Uganda; 9: Institut Pasteur De Dakar, Dakar, Senegal; 10: International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh

Background: Timely detection of transboundary infectious disease threats is essential for effective global health security and outbreak control. Centralized laboratory diagnostics can delay pathogen identification and subsequent decision-making during emergencies. Grounded in a One Health framework, the PREPARE-TID project addresses this challenge by developing and validating a comprehensive, field-deployable diagnostic pipeline for rapid pathogen detection across human, animal, and environmental interfaces.

Methods: The project developed a modular diagnostic pipeline integrating advanced sample processing, rapid molecular assays, and mobile sequencing. We designed novel nucleic acid extraction chemistries adapted to a portable, automated extraction instrument. Diagnostic hardware platforms include the "One Health Pod," a point-of-need multiplex qPCR device utilizing ready-to-use cartridges, and a self-contained Mobile Suitcase Laboratory for on-site nanopore sequencing. To translate diagnostic data into actionable intelligence, we built an integrated digital surveillance platform combining a mobile data collection application with a real-time web dashboard. The pipeline was validated through analytical testing and real-world emergency deployments.

Results: Analytical evaluation demonstrated that the One Health Pod successfully detected targeted vector-borne and respiratory pathogens, performing reliably even under environmental stress conditions of 40°C and 80% humidity. The multiplex platform format allows simultaneous screening for up to 40 pathogens and antimicrobial resistance markers. During real-world deployments, the Mobile Suitcase Laboratory proved highly effective. In response to an mpox outbreak in Sierra Leone, the deployed system reduced diagnostic turnaround time from several days to just 1-2 hours. Over 150 samples were processed with an approximate 60% positivity rate, and isothermal amplification results showed 100% concordance with reference qPCR methods. Furthermore, following Cyclone Chido in Mayotte, a mobile water testing laboratory successfully analyzed surface and drinking water. It efficiently concentrated and detected bacterial pathogens like *Shigella* and *E. coli* directly in the field, confirming safe public water networks and identifying contaminated local sources.

Conclusions: Decentralized, mobile diagnostic technologies, such as the PREPARE-TID pipeline, significantly accelerate pathogen identification from sample collection to the point of action. By linking human, animal, and environmental health data through integrated digital tools, this One Health approach strengthens situational awareness and evidence-based decision-making during crises.

1847 – Advancing gender transformative One Health approaches: Insights from Female Genital Schistosomiasis

Jade WONG (1), **Sandra BODE** (2), **Sheila SANG** (3), Nina PUTNIS (3), Claudia ROBBIATI (4,5), Ariane MOSWETE (3), Lilian Wangechi WAIBOCI (6,5), Paula GRABIETZ (3), Gabrielle LAING (7), Hellen WAMBUI (6,5), Nina MILITZER (3)

1: Independent Researcher; 2: Independent Consultant; 3: Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH; 4: Italian National Institute of Health; 5: Women for One Health Network; 6: University of Nairobi; 7: Unlimit Health

Background:

In the current geopolitical climate, diversity, equity, and inclusion (DEI) considerations including gender are increasingly facing funding constraints and political deprioritization in global health and One Health (OH) agendas, affecting both policy-level engagement and community-based implementation. At the same time, diseases such as Female Genital Schistosomiasis (FGS), a neglected manifestation of schistosomiasis with profound gendered health and social consequences, highlight the urgent need to

address structural inequities in OH systems. FGS provides an entry point to rethink DEI integration from a bottom-up perspective while strengthening linkages between neglected tropical disease (NTD) communities and broader OH approaches. This study explores how DEI, including gender, can be systematically embedded within OH policies and programmes and derives actionable policy recommendations to improve health outcomes for humans, animals and the environment.

Methodology:

A scoping review was conducted mapping existing evidence on the integration of DEI, including gender, in OH and NTD-related policies and programmes. Peer-reviewed and grey literature were searched using predefined inclusion and exclusion criteria in NCBI and Google Scholar. In addition, semi-structured expert interviews are being conducted with multidisciplinary stakeholders from governments, civil society organizations, academia, and community-based actors in African countries where FGS and schistosomiasis are endemic. Preliminary findings were analyzed using qualitative thematic analysis. Findings are triangulated to give policy recommendations.

Results:

Context-specific gender roles and power structures strongly influence access to prevention, diagnosis, and care for FGS and broader OH issues. While FGS affects women, it is not solely a “women’s issue”. Operational guidance for integrating gender and equity into OH frameworks remains limited. Short-term, donor-driven, vertical, and disease-specific projects often fail to deliver impact. Equity analyses require dedicated financial and human resources and are highly context-specific. Effective programming needs structured multistakeholder engagement, civil society engagement, awareness-raising , and practices such as trust-building, community outreach and two-way communication between policymakers and local actors. Clearer normative guidance, stronger advocacy, and strategies are needed to navigate systemic barriers. Interdisciplinary, cross-sectoral collaboration and alignment, including water sanitation and hygiene, gender, and NTD priorities, can help collate multiple funding streams and increase effectiveness. Enablers include community-led approaches, systems thinking, capacity strengthening, inclusive research, disaggregated data (utilization), integration of services and an enabling environment including indicators.

Conclusions:

With shrinking support for DEI, multilevel action is essential to advance inclusive, equitable OH approaches. This policy brief uses FGS as a case study to show how integrating DEI perspectives informs disease prevention and control while addressing structural inequities, providing lessons to other diseases. Findings stress that integrating DEI needs institutionalized participation, context-driven approaches, dedicated resources, operational guidance and key standardized indicators. The study offers relevant policy recommendations with measurable steps for embedding DEI including gender into OH policies and programmes from local to global levels.

1852 – Associations Between Land Use and Land Cover Patterns and Yellow Fever Risk in Humans and Non-Human Primates in Brazil

Hilary MCLELAND-WIESER (1), Julianne MEISNER (2), Peter RABINOWITZ (1)

1: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, USA; 2: Department of Global Health, University of Washington, Seattle, USA

Background: The 2016-2018 yellow fever epidemic in Brazil was marked by a geographic shift in human cases towards major population centers, raising the risk of establishing an urban yellow fever cycle for the first time since the 1940s. To prevent this from occurring, a One Health approach is essential to minimize additional spillover events from non-human primates. Previous research has identified forest edge density, low levels of native vegetation, and other measures of landscape fragmentation as risk factors for yellow fever infection in non-human primates. Models focusing on human risk have included measures such as agricultural land use, fire, and vegetation greenness. However, much of this work occurred prior to the 2016-2018 epidemic or lacked spatial specificity. This project combines municipality level surveillance data on yellow fever in Brazil with high resolution land cover and land use data to identify associations between yellow fever cases and land use, land use change, and spatial heterogeneity in both humans and non-human primates.

Methods: This cross-sectional study uses pre-existing surveillance data on human and non-human primate yellow fever cases in Brazil from 2015-2024. Summary measures of land cover and land use, landscape heterogeneity, deforestation, and spatial heterogeneity are calculated annually at the municipality level using 30 meter resolution land cover and land use classification data from Map Biomass Brazil. Associations between yellow fever and land use metrics are assessed separately for humans and non-human primates using Bayesian hierarchical models to handle spatiotemporal autocorrelation.

Results: Data will be presented on trends in land use between 2015 and 2024 to characterize the scope and distribution of potential risk factors. Results of spatiotemporal models will also be presented showing statistical associations between yellow fever and land cover and land use metrics.

Conclusion: This analysis will help identify patterns of land use and land use change which are associated with risk of yellow fever in both humans and animals in Brazil. One Health comparison of environmental risk factors between non-human primates and humans can help with the development of strategies to prevent spillover and protect both human and non-human populations.

1860 – Phenotypic characterization of white-tailed deer-derived SARS-CoV-2 after reverse zoonoses

Sophie AICHER (1), Yaejin LEE (1), Bradley PICKERING (2), Jeff BOWMAN (3), Andrew DOXEY (4), Arinjay BANERJEE (5), **Samira MUBAREKA** (1)

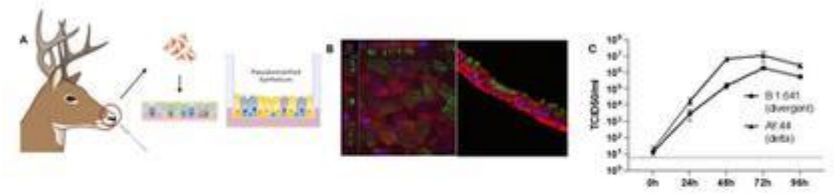
1: University of Toronto, Canada; 2: Canadian Food Inspection Agency; 3: Trent University; 4: University of Waterloo; 5: Vaccine and Infectious Diseases Organization

Background: During the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) pandemic, reverse zoonoses resulting from human to wildlife transmission were well-described. We detected a highly divergent variant (lineage B.1.641) of SARS-CoV-2 in white-tailed deer in Canada, reflecting protracted and sustained viral transmission among deer. In addition, this lineage clustered with a geotemporally-related human case, suggestive of deer-to-human transmission. We sought to determine the biological implications of this novel variant for 1) risk registration and 2) to address knowledge gaps in wildlife host-SARS-CoV-2 interactions.

Methods: First, we conducted a biological risk assessment inclusive of virus replication, host receptor binding, pathogenesis and transmission using human *in vitro* nasal epithelial cell and lung bud organoid models, and the Syrian golden hamster pathogenesis and transmission model. Next, to examine wildlife-host interactions, we established an *in vitro* model of white-tailed deer primary nasal epithelial cells and interrogated SARS-CoV-2 infected cells with RNAseq, followed by proteomics and molecular phenotyping.

Results: We did not find evidence of enhanced viral replication in human *in vitro* systems or pathogenesis on hamster histopathology for the B.1.641 virus, which also demonstrated a less efficient transmission phenotype relative to ancestral virus. In addition, weight loss was not statistically different for hamsters infected with B.1.641 and ancestral SARS-CoV-2 viruses. We then established primary deer nasal epithelial cells at an air-liquid interface from nasal brushings (A). Cells were fully differentiated and demonstrated formation of cilia and tight junctions (B). These cells also supported live virus infections in the order of 106 TCID50/mland 107 TCID50/mlfor the B.1.641 and a deer-derived Delta variant respectively (C). Deer-specific RSAD2 (viperin) and MX1 peaked at 72h for both viruses. We then examined the transcriptomes of primary deer nasal epithelial cells infected with B.1.641 and deer-derived Delta variants. At both 48h and 72h, there was greater induction of the innate antiviral response (particularly interferon-related) with B.1.641 infection relative to the Delta variant. Proteomic analysis of infected deer cells revealed production of innate immune components including MX1 and MX2. In order to gain insights into host determinants of response, we examined duplication events of innate immune genes in ungulate genomes. We noted significant duplication in type I interferon genes in white-tailed deer genomes. We are currently advancing deer-specific antiviral protein expression to further characterize host response from a functional perspective.

Conclusions: We demonstrate that the deer-derived B.1.641 variant is unlikely to pose higher biological risk, and ascertain induction of an antiviral innate immune response in an *in vitro* white tailed deer model. This approach also provides wildlife systems and tools to examine other zoonotic virus-host dyads.



1870 – Environmental Risk Factors of Coxiella burnetii in Small Ruminants: A One Health Perspective from Northeast of Portugal

Maria João CALDEIRA (1,2), João JACOB-FERREIRA (2), Tifany PEREIRA (1,4), Carina RODRIGUES (2,3), João R. MESQUITA (1), David GUALLAR (5,6,7), Pablo QUILEZ (5,6,7), Marta RUÍZ DE ARCAUTE (5,6,7), Delia LACASTA (5,6,7), Diana MARTELES (5,6,7), Sergio VILLANUEVA-SAZ (5,6,7), Hélder QUINTAS (2)

1: School of Medicine and Biomedical Sciences (ICBAS), University of Porto, 4050-313 Porto, Portugal; 2: Mountain Research Centre (CIMO), Polytechnic Institute of Bragança (IPB), 5300-253 Bragança, Portugal; 3: Research Center for Active Living and Wellbeing, Polytechnic Institute of Bragança (IPB), 5300-253 Bragança, Portugal; 4: University of Trás-os-Montes and Alto Douro (UTAD), 5000-801 Vila Real, Portugal.; 5: Animal Pathology Department, Veterinary Faculty and Instituto Agroalimentario de Aragón – IA2 (Universidad de Zaragoza-CITA), Miguel Servet 177, 50013 Zaragoza, Spain; 6: Clinical Immunology Laboratory, Veterinary Faculty, University of Zaragoza, Zaragoza 50013, Spain; 7: Ruminant Clinical Service, Veterinary Faculty, University of Zaragoza, Miguel Servet 177, 50013 Zaragoza, Spain

Introduction:

Q fever, caused by the zoonotic bacterium *Coxiella burnetii*, represents a significant challenge at the animal–human–environment interface. Due to its ability to form spore-like variants, the pathogen exhibits high environmental persistence, enabling long-distance windborne spread. This study aimed to evaluate seroprevalence trends over three years and to identify ecological risk factors associated with *C. burnetii* exposure in sheep and goats from Trás-os-Montes, in northeastern Portugal, a region characterised by high-density livestock farming and proximity between domestic and wild animal habitats.

Methods:

A cross-sectional study was conducted between 2020 and 2022. The study included 1,827 small ruminants (1,596 sheep and 231 goats) from 116 traditional farms. Blood samples were collected, and serological analysis was performed using a commercial indirect ELISA (ID Screen® Q Fever Indirect Multi-species, IDVet, France) to detect antibodies against *C. burnetii*. Data on farm management practices and the environmental interface were obtained through structured interviews conducted as part of a related study. Statistical analyses were performed using the R software. Chi-square tests were used to assess temporal and species differences, and logistic regression models were used to estimate odds ratios (ORs) and 95% confidence intervals (CIs) for several environmental variables.

Results:

The overall seroprevalence in the region was 40.4% (95% CI: 38.2–42.8). A significant temporal trend was observed, with prevalence increasing from 25.2% in 2020 to 40.2% in 2021, reaching a peak of 56.9% in 2022. Species-specific analysis revealed that goats had a significantly higher risk of exposure (52.8%) compared with sheep (38.7%) (OR = 1.78; 95% CI: 1.35–2.34; P 0.001). Regarding the animal–environment interface, multivariate analysis identified three main drivers of infection: contact with neighbouring flocks (OR = 1.58; 95% CI: 1.30–1.92; P 0.001), sharing water sources (OR = 1.53; 95% CI: 1.27–1.85; P 0.001), and potential contact with wildlife (OR = 1.32; 95% CI: 1.08–1.62; P = 0.008). The origin of replacement

animals (purchase from other farms vs on-farm replacement) was not statistically significant (P = 0.63), suggesting that the local environment, rather than animal movement, is the main source of infection.

Conclusion:

This study demonstrates an intensification of *Coxiella burnetii* circulation in northeastern Portugal, with exposure levels doubling within only three years. The results emphasise the pivotal role of shared environmental resources and farm proximity in transmission dynamics. From a One Health perspective, the high prevalence in livestock may increase the risk of pathogen spillover to the human population, particularly in rural communities. These findings underscore the need for integrated surveillance programmes and the implementation of environmental biosecurity measures to mitigate this public health threat.

1875 – Precision One Health: A Randomized Trial to Optimize Urban Rabies Elimination

Ricardo CASTILLO-NEYRA (1,2), Sherrie XIE (1), Elvis DIAZ (2), Jorge CAÑARI (2), Gian Franco CONDORI (2), Brinkley Raynor BELLOTTI (3), Valerie PAZ-SOLDAN (2,4), Maria RIEDERS (1), Bhaswar BHATTACHARYA (1), Michael LEVY (1,2)

1: University of Pennsylvania, United States of America; 2: Universidad Peruana Cayetano Heredia, Peru; 3: Wake Forest University School of Medicine, United States of America; 4: Tulane University, United States of America

BACKGROUND: Mass dog vaccination (MDV) is the cornerstone of human rabies prevention, yet conventional campaigns often result in "coverage gaps" where the virus persists. To reach the "Zero by 30" global target, we must move beyond uniform delivery toward data-driven precision. We hypothesized that combining mathematical spatial optimization with app-based 'precision vaccination' would significantly increase participation compared to traditional practices.

METHODS: We conducted a four-year stepped-wedge cluster randomized trial across 36 urban clusters, encompassing 322,000 households. We compared three strategies: (1) Current Practice; (2) Spatially Optimized Site Placement; and (3) Precision Vaccination with a mobile app that integrates spatial and historical participation data to guide door-to-door teams. To evaluate vaccination participation and its correlates, we conducted longitudinal door-to-door surveys of 8,000 households annually. Intervention effects were evaluated using a mixed-effects logistic regression model, adjusting for secular trends and cluster-level random effects.

RESULTS: Our results demonstrate that mathematical optimization of vaccination site placement alone did not significantly increase participation (OR = 1.05; 95% CI: 0.94–1.16; p = 0.39). However, the integrated precision vaccination approach—combining optimization with the data-driven app—increased the odds of participation by 26% (OR = 1.26; 95% CI: 1.08–1.58; p 0.01). This indicates that while site placement is important, the "last-mile" data provided to vaccinators is the critical driver of coverage. Notably, we observed a progressive decline in canine rabies cases citywide throughout the study period. Following three years of trial implementation and the delivery of our interventions across 96% of the urban area, canine rabies incidence reached zero. No new cases have been reported as of this submission, providing evidence for the successful interruption of viral transmission.

CONCLUSIONS: This trial provides some of the first experimental evidence that integrated "Precision One Health" strategies can significantly overcome urban vaccination barriers. By bridging operations research with zoonotic disease control, we demonstrate that effective elimination strategies must account for the spatial behavior of both the community and the vaccinators. This scalable, multimodal operational framework—integrating mathematical optimization, cross-sectoral stakeholder coordination, and precision field activities—offers a transformative model for global efforts to eliminate dog-mediated human rabies.

1883 – Co-creating One Health solutions: a community-led cleanup action to reduce dengue risk in urban informal settlements

Ana Maria BARRETO (1), Diogo DOS SANTOS FERREIRA (1), José Vitor ARAÚJO ROSA RIBEIRO (2), Elizete CARDOSO (3), Elenilda CARDOSO NEVES SANTOS (3), Suzana Cristina DOS SANTOS (4), Thiago DA MATA BARRETO (5), Yeimi ALEXANDRA ALZATE LOPEZ (1), Lucas DOS SANTOS PEREIRA (1), Hernán Dario ARGIBAY (1)

1: Instituto de Saúde Coletiva, Universidade Federal da Bahia, Salvador, Brazil; 2: Faculdade de Odontologia, Universidade Federal da Bahia, Salvador, Brazil; 3: Cia de Arte Cultural E ao Quadrado, Salvador, Brazil; 4: Associação Emília Machado Bahia, Salvador, Brazil; 5: Instituto de Biologia, Universidade Federal da Bahia, Salvador, Brazil

Background: In informal urban settlements, socio-environmental conditions often increase human exposure to zoonoses and other health threats. In these contexts, participatory governance processes are essential for developing sustainable and locally relevant solutions. For interventions to achieve meaningful impact, communities must be at the center of problem identification and the co-construction of responses. This study reports the experience of a transdisciplinary research group in co-constructing an intersectoral community action during World Cleanup Day to address dengue, the most prevalent arboviral disease in the community. **Methods:** On September 20, 2025, an intersectoral community action was implemented in the context of World Cleanup Day to mitigate dengue risk in the territory. The initiative was co-constructed through an ongoing participatory research process led by the Integrated Program in Environmental and Occupational Health (PISAT) at the Institute of Collective Health, Federal University of Bahia (ISC/UFBA), in partnership with the Teatro E ao Quadrado collective and the Associação Emília Machado da Bahia (AEMBA). The action took place in the informal urban settlement of Marechal Rondon, a territory characterized by low socioeconomic conditions and a high burden of dengue among residents. The intervention was collectively planned through four weekly meetings involving researchers, residents, and community leaders. During these meetings, participants identified dengue as a priority health issue, associated with accumulated waste that serves as potential breeding sites. Based on this shared diagnosis, participants proposed organizing a cleanup campaign during World Cleanup Day as a community-led strategy to reduce mosquito breeding sites, raise awareness about the health impacts of improper waste disposal, and promote reflection on the links between environmental degradation, health, and climate challenges. The meetings also defined community mobilization strategies and identified institutional partners, including the Municipal Urban Cleaning Company (LIMPURB), the Zoonosis Control Center (CCZ), and the philanthropic network Mãos Solidárias. **Results:** Approximately 120 garbage bags (100 L capacity) were removed during the activity. To encourage participation, a free anti-rabies vaccination campaign for domestic animals was conducted, resulting in the immunization of 162 dogs and cats. Additional activities included clothing donations, adoption of rescued puppies, and a collaborative snack. At the end of the event, a public talk on One Health highlighted the connections between human, animal, and environmental health and emphasized the importance of proper waste management for disease prevention and healthier environments. Native tree seedlings were planted in areas previously used for waste disposal. **Conclusions:** This experience demonstrates that co-construction processes involving universities, community members, local leaders, and public institutions can strengthen territorial governance and promote intersectoral responses aligned with One Health principles. Recognizing community knowledge and leadership can foster local capacity building, increase social engagement, and support sustainable strategies for disease prevention and environmental health improvement in informal urban settlements.

1893 – Impact of short-term reforestation on mosquito communities and disease risk

Petteri PUONTI, Frauke ECKE, Essi KORHONEN, Lorna CULVERWELL
University of Helsinki, Finland

Transmission cycles of zoonotic diseases are highly complex, shaped by interactions among pathogen, host, and environmental factors. This complexity is particularly pronounced in vector-borne zoonoses, where suitable conditions for both reservoir and vector hosts are required for transmission. Human activity has driven global losses of natural habitats and biodiversity, often creating favorable conditions for anthropophilic, disease-transmitting mosquitoes. Nature restoration aimed at biodiversity recovery has gained attention as a potential strategy for mitigating zoonotic disease risk. Ecosystem recovery certainly influences mosquito communities. However, its net effects on human and animal health remain uncertain. Madagascar is a global biodiversity hotspot, with over 90% of its wildlife being endemic. The island has lost more than 70% of its natural forest cover. Reforestation initiatives restoring native ecosystems in degraded areas provide an opportunity to investigate how biodiversity recovery influences the transmission dynamics of mosquito-borne zoonoses and the potential consequences for human and animal health. In this study, forest sites undergoing reforestation were surveyed to assess how short-term biodiversity recovery affects mosquito communities and associated disease risk.

The study was conducted at four forest sites in Madagascar: two on the Central Plateau and two in the eastern coastal lowlands. All sites had ongoing reforestation projects initiated no more than five years before the study began. Mosquitoes were collected over a two-year period from three habitat types: natural forest (positive control), deforested areas (negative control), and reforestation sites (impact), using BG-Pro traps.

Captured mosquitoes were identified to at least genus level using morphological keys and genetic analyses. Taxa were categorized according to their epidemiological role as primary vectors, bridge vectors, or non-vector species. Mosquito pools were screened for West Nile virus, Rift Valley fever virus, Chikungunya virus, and Babanki virus, all of which have previously caused epidemics in Madagascar.

Biodiversity data was collected using acoustic loggers, camera traps, and small mammal trapping. Environmental variables were quantified using drone imagery to derive indices such as canopy cover and surface water availability. The data, including mosquito community composition, vector status, pathogen detection, vertebrate biodiversity, and environmental variables, were integrated into statistical models to assess how reforestation and biodiversity influence the spatial risk of mosquito-borne disease transmission.

Reforestation sites resembled both deforested and natural sites in mosquito community composition, possibly representing a transition from communities in deforested areas toward those found in natural forests. Overall mosquito abundance was higher in forest sites than in reforestation or deforested sites. In addition, individuals belonging to the genus *Culex* were overrepresented in forest habitats.

Even short-term reforestation influences mosquito communities, increasing biodiversity and shifting community composition toward that observed in natural forests. However, it remains unclear whether these changes ultimately increase or decrease the risk of mosquito-borne disease transmission.

1900 – Mitigating Anti-Microbial Resistance in the Environment: A One Health Governance Analysis in Kenya

Srinivasa SRIGIRI (1), Morris BULIVA (2)

1: German Institute of Development and Sustainability, Germany; 2: Independent Consultant

Background

Antimicrobial resistance (AMR) poses a critical global health threat, with environmental transmission pathways – pharmaceutical waste, wastewater effluents, and agricultural runoff – increasingly recognised as significant yet inadequately governed. Despite international mandates for One Health approaches integrating human, animal, and environmental sectors, coordination across these domains remains weak. Kenya presents a paradox: a sophisticated formal governance architecture including national and county coordination platforms (NASIC, CASICs), technical working groups, and the One Health AMR Surveillance System (OHAMRS), yet persistently shallow environmental integration. This study examines why the environmental dimension lags in Kenya's AMR governance and identifies options for its effective integration.

Methods

The study employed a qualitative case study design grounded in polycentric governance theory, the Institutional Analysis and Development (IAD) framework, and the concept of Networks of Adjacent Action Situations (NAAS). The analytical lens focused on how authority, information, and resources (AIR) shape interactions among overlapping decision centres across constitutional, collective-choice, and operational levels. Primary data were collected through 12 semi-structured interviews with key informants – including government officials, environmental regulators, fisheries officers, wastewater treatment operators, and county-level AMR coordinators – conducted in Nairobi between 2023 and 2024. Supplementary data came from field notes from three stakeholder meetings and systematic analysis of policy documents and legal frameworks. Interview transcripts were analysed using qualitative content analysis via Atlas.ti, with six action situations delineated spanning planning, resource allocation, surveillance, stewardship, wastewater treatment, and regulation.

Results

The analysis reveals that constitutional-choice rules create formal institutional overlaps intended to foster coordination, yet systematic AIR asymmetries perpetuate the marginalisation of environmental issues. Boundary and position rules concentrate agenda-setting authority in health ministries, with National Environmentt Management Authority (NEMA) participating without voting rights and the Water Resources Authority (WRA) largely absent from coordination structures. Information rules exclude AMR parameters from environmental permits, inspection checklists, and Environmental Impact Assessments. Payoff rules reward clinical outputs while environmental investments compete against higher-priority expenditures. Scope rules omit explicit environmental accountability targets. These rule configurations attenuate feedback loops between environmental action situations and upstream planning, enabling human and animal health sectors to advance incrementally while environmental integration remains nascent – formally recognised in the second NAP-AMR (2023-2027) but operationally inert.

Conclusions

Effective One Health governance of AMR requires not merely including environmental actors in meetings, but fundamentally reconfiguring the rules that structure their participation and mandate. Targeted interventions – granting NEMA and WRA voting authority in NASIC/CASIC, embedding AMR parameters in regulatory instruments, institutionalising joint inspection protocols, ring-fencing environmental budgets, and establishing explicit environmental targets in monitoring frameworks – would realign authority, information, and resources to transform formal environmental inclusion into genuine operational integration.

1904 – Multidimensional exposures to domestic animals and household fecal contamination in rural Nepal

Caitlin HEMLOCK (1), Heather K AMATO (2), Aastha SHRESTHA (3,4), Shiva Ram NAGA (3,4), Nishan KATUWAL (3,4,5), Sabin B SHAHI (3,4), Sudichhya TAMRAKAR (3,4), Urusha RANJITKAR (3,4), Christopher LEBOA (6), Clara ZHONG (1), Rajeev SHRESTHA (3,4), Dhiraj POKHREL (7), Amod POKHREL (6), Dipesh TAMRAKAR (3,4), Amy J PICKERING (8), Laura H KWONG (6)

1: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA, USA; 2: Department of Global, Environmental, and Occupational Health, University of Maryland School of Public Health, College Park, MD, USA; 3: Center for Infectious Disease Research and Surveillance, Dhulikhel Hospital, Kathmandu University Hospital, Nepal; 4: Research and Development Division, Dhulikhel Hospital, Kathmandu University Hospital, Nepal; 5: Molecular and Genome Sequencing Research Lab, Dhulikhel Hospital, Kathmandu University Hospital, Nepal; 6: Division of Environmental Health Sciences, University of California, Berkeley, Berkeley, CA, USA; 7: LEADERS Nepal, Kathmandu, Nepal; 8: Department of Civil and Environmental Engineering, University of California, Berkeley, Berkeley, CA, USA

Domestic animals are common in rural settings and their feces may contribute to household contamination and potential exposure to enteric pathogens. We conducted a cross-sectional study of 277 households with a child under five years in 28 villages in Kavrepalanchok, Nepal (April - June 2023). Caregivers completed surveys on animal ownership, confinement, feces management, and child behaviors; enumerators conducted spot checks and collected soil from outdoor child play areas and child and caregiver hand rinses. E. coli counts were enumerated via IDEXX QuantTrays, and we included presence and log10-transformed concentration of MPN E. coli as outcomes. We used multivariable generalized estimating equations to assess animal and behavior-specific pathways and principal components regression to evaluate joint exposure patterns. We also used path analysis to examine

hypothesized pathways between animal free-roaming, feces presence, child behaviors, and hand contamination, and calculated standardized path coefficients to allow for comparison. E. coli was detected on 44% of child hands, 59% of caregiver hands, and 83% of soil samples. Chicken ownership and feces were consistently positively associated with E. coli contamination in soil and on child hands, while livestock exposures and feces management behaviors were more strongly associated with E. coli on caregiver hands. Keeping cows, buffalo, and goats outside the household compound was associated with lower soil contamination, however, owning a cow/buffalo shed and cleaning their feces with bare hands was associated with higher contamination on caregiver hands. Animal feces observed in child play areas were associated with higher E. coli concentrations on child hands, particularly poultry feces (mean difference in log10 MPN E. coli: 0.51; 95% CI: 0.04, 0.98). Joint analysis of exposures using principal components regression showed that the first component, which represented overall exposure intensity, was associated with contamination across all pathways. In the path analysis we found that free-roaming animals were significantly associated with increased child-animal contact ($\beta = 0.18$, $p = 0.004$) and higher presence of feces in child play areas ($\beta = 0.15$, $p = 0.015$), however reported direct child contact with animals was not associated with child hand contamination ($\beta = 0.23$, $p = 0.15$), but reported contact with animal feces was positively associated ($\beta = 0.63$, $p = 0.053$). These findings highlight the complexity of human-animal interactions, particularly in agricultural settings with multiple animal types owned and varied caretaking behaviors. Poultry feces in child play areas and child contact with feces highlight important exposures to target for interventions to reduce child hand contamination. Formative work on animal proximity and caregiver behaviors with livestock, including identifying barriers to safe feces management, may help identify feasible One Health interventions to reduce soil and caregiver hand contamination and potential dissemination of zoonotic pathogens in the household environment.

1912 – Integrating metagenomics, AI, and automation for precision microbial strain discovery

Angela HOOGENBOOM, Mara KRÖNER, Floyd WITTINK, Roland WESTVEER, **Astrid HEIKEMA**

Leiden University of Applied Sciences, Netherlands, The

Background: Targeted discovery of microbial strains with beneficial functionalities is needed to advance innovations in food processing and conservation, human health, sustainable agriculture and biomanufacturing. However, traditional isolation and characterisation methods are slow, labour-intensive, and challenged by the high complexity and diversity of natural microbial communities.

Materials and methods: To advance the discovery of natural microbial strains, we have implemented a workflow that comprises selective sourcing, enrichments under various conditions, shotgun metagenomic sequencing, AI-based image recognition applied to colony morphology for species prediction, automated colony picking, 96-well culturing, robotic DNA extraction, long-read Nanopore sequencing, and functional bioinformatic analysis.

Results: Initial results demonstrate that shotgun metagenomics successfully identified desired species in selected natural sources and enrichment cultures. Sequence date-guided culturing led to the isolation of multiple, diverse colonies of target strains. Early applications of AI-based image analysis showed accurate recognition of microbial species on agar plates, demonstrating great potential to improve colony selection prior to automated picking. Upscaling with 96-well culture formats, automated DNA isolation, and bioinformatics pipelines enabled fast, high-throughput genome analysis.

Conclusions: This workflow builds on existing approaches by integrating multiple technologies into one automated, scalable system. It enables faster, more precise discovery of microbial strains relevant to several applications and supports academic research as well as industrial innovation.

Result from an AI-based image recognition tool, which detects microbial colonies, classifies them based on morphological features, and identifies the species (input on the left, output on the right).

1915 – Funding landscape of One Health education research: a bibliometric analysis of funding sources

Lara FONTES (1), Mafalda LOPES (2,3,4), Daniel Martinho DIAS (1), Patrícia POETA (5,6,7), António José SOARES (1)

1: University of Trás-os-Montes and Alto Douro (UTAD), Portugal; 2: RISE- Health, Faculty of Medicine, University of Porto, Portugal; 3: Nursing School of the University of Porto, Portugal; 4: University of Salamanca, Spain; 5: Microbiology and Antibiotic Resistance Team (MicroART), Department of Veterinary Sciences, University of Trás-os-Montes and Alto Douro (UTAD), Portugal; 6: CECAV - Veterinary and Animal Research Centre, University of Trás-os-Montes and Alto Douro (UTAD), Portugal; 7: Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS), Portugal

Background

The growing recognition of the One Health approach has stimulated international investment in research and training initiatives aimed at addressing complex health challenges that span human, animal, and environmental systems. However, little is known about the funding landscape supporting research on One Health education for health professionals. Understanding which agencies and countries fund this research is essential to identify funding priorities, geographical imbalances, and opportunities for future investment. This study aims to analyze the funding patterns of scientific publications addressing One Health education.

Methods

A bibliometric analysis will be conducted using publications indexed in Scopus, Web of Science, and PubMed which provide detailed metadata on funding acknowledgements. The search strategy will identify publications related to One Health education using terms such as “One Health,” “education,” “training,” and “curriculum.” Funding information, including funding agencies, grant numbers, and funding countries, will be extracted from the records. Descriptive bibliometric indicators will be calculated to identify the most frequent funding sources and their geographical distribution. Network visualization will be used to explore relationships between funding agencies, research institutions, and countries.

Results

Initial (WoS, SCOPUS, Pubmed) database search identified 10,418 publications (2008-2026). After screening for health professionals focus, 889 records were selected. Preliminary observations suggest that research on One Health education is supported by a diverse set of funding bodies, including national research councils, international health organizations, and governmental agencies. Initial findings indicate that funding is concentrated in a limited number of high-income countries, particularly in Europe and North America. Some international organizations appear to play a key role in supporting collaborative research initiatives across multiple regions.

Conclusions

This study will provide the first systematic overview of funding sources supporting research on One Health education for health professionals. The findings may contribute to a better understanding of global investment patterns and help identify funding gaps that may influence the future development of transdisciplinary One Health training programs. These insights support the Quadripartite's One Health

Joint Plan of Action (2022-2026) by providing an evidence-based map of funding priorities for cross-sectoral workforce development.

1926 – Creation, validation and results from a survey on knowledge, attitudes and practices towards rabies in Kenya

Filipe MAXIMIANO SOUSA (1,2), Nicholas BOR (2), Nicholas NGWILI (2), Peterkin NZOMO (2), Ian MASAKU (2), Silvester MUTINDA (2), Siobhan MOR (2,3), Salome DÜRR (1), Lian THOMAS (2,4)

1: VPHI - University of Bern, Switzerland; 2: International Livestock Research Institute, Nairobi, Kenya; 3: Institute of Infection, Veterinary, and Ecological Sciences, University of Liverpool, UK; 4: The Royal (Dick) School of Veterinary Studies, Edinburgh, UK

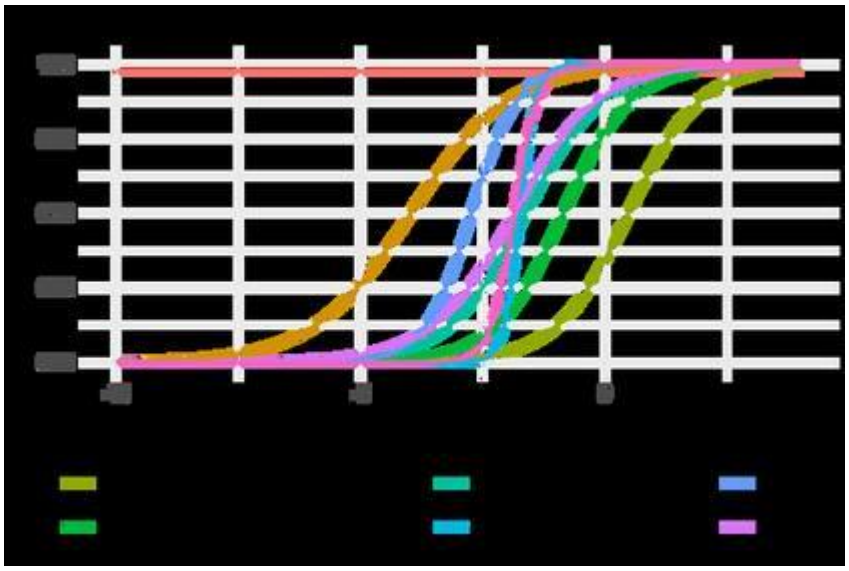
Introduction: Rabies is a zoonotic disease responsible for an estimated 59,000 human deaths annually worldwide. Dog-mediated rabies can be prevented and controlled by targeting the main source of human infection – dogs - and human communities. Long-term control requires mass dog vaccination. Until control is achieved, protecting human populations depends on adequate knowledge and access to resources that enable appropriate health-seeking behavior after exposure.

Knowledge, attitudes, and practices (KAP) surveys are widely used to assess community awareness of rabies, acceptance of dog vaccination and health-seeking behavior. These surveys can inform the design and evaluation of interventions aimed at disease control and improved health outcomes. However, published rabies KAP questionnaires are frequently developed and analyzed in highly heterogeneous ways and their validity is rarely assessed.

Cognitive interviews can be used to explore how respondents interpret and process survey questions, helping determine whether items are understood as intended, contributing to content validity and linguistic equivalence of the questionnaire. In addition, Item Response Theory (IRT) models can evaluate item characteristics and classify respondents according to their level of a certain trait.

Methods: We designed a questionnaire to measure respondents' KAP towards rabies based on literature and expert opinion. Questionnaire items were reviewed by experts and translated and back translated to Kikamba. It was then pre-tested using cognitive interviews in Makueni County of Kenya. Questionnaires were then pilot tested in Machakos county of Kenya. In each step it was updated accordingly. The final version was administered in two wards of Machakos County, Kenya. Finally, questionnaire items characteristics were further evaluated using IRT models.

Results and conclusion: In total, 1005 households were surveyed. Main gaps identified were related to some of the recommended post-exposure actions and the possibility of recovery after the onset of clinical signs. Just 54.82% of the dogs were vaccinated following free mass dog vaccination campaigns. The set of steps followed on the development of the questionnaire are crucial on the development of a proper tool. For example, following cognitive interviews the number of levels on Likert scales for attitudes were reduced, as respondents reported not finding them useful. Based on the results of the IRT models, the set of questions answered by all respondents are, in their great majority, relatively easy (Figure 1). IRT analysis revealed the instrument is more effective at discriminating among respondents with lower KAP levels, making it a valuable screening tool for identifying high-risk groups for educational interventions. Questions with low discriminatory capacity or information, (for example, increased roaming being a possible clinical sign of rabies), were dropped. Additionally, IRT allows for more robust comparisons of results across different studies or populations by placing individuals and items on a common scale of ability on a certain trait.



2328 – Quantifying household-level sharing of antimicrobial-resistant pathogens between pets and their owners: a systematic review and meta-analysis

Laurel REDDING (1), Charles MUTURI (2)

1: University of Pennsylvania, Philadelphia, PA, USA; 2: Temple University, Philadelphia, PA, USA

Background:

Companion animals are increasingly recognized as potential reservoirs of antimicrobial-resistant (AMR) bacteria; however, the frequency with which resistant pathogens are shared between pets and their owners within households remains unclear. The goal of this study was to conduct a systematic review and meta-analysis aimed at quantifying household-level sharing of AMR pathogens between pets and humans.

Methods:

We searched PubMed, Embase, and Web of Science for studies reporting concomitant sampling of pets and owners from the same household with assessment of genetic or phenotypic relatedness of AMR bacteria. Random-effects generalized linear mixed models were used to estimate pooled prevalences of sharing across studies. Subgroup analyses examined differences by host health status, pathogen group, molecular typing methods, study design, and study quality using a modified Joanna Briggs Institute checklist.

Results:

Across 152 extracted studies, the pooled prevalence of household-level sharing was 3.8% (95% CI=2.7-5.1%). It was similarly low among households in which both pets and owners were healthy or in which pets or owners were sick with conditions unrelated to the pathogen of interest (3.0%, 95% CI=2.0-4.0% and 3.0%, 95% CI=2.0-7.0%, respectively). In contrast, sharing was more frequent among households in which either a pet or an owner had a documented infection with the pathogen (9.0%, 95% CI=5.0-16.0%). Sharing prevalences were comparable for *Staphylococci* and *Enterobacterales*, despite differences in transmission routes and microbial ecology. Studies relying on phenotypic methods alone reported higher sharing prevalences than those using molecular typing, consistent with limited discriminatory capacity of phenotypic approaches. Substantial heterogeneity was observed across studies, but findings were generally robust across study design, geographic setting, and quality strata.

Conclusions:

Household-level sharing of antimicrobial-resistant bacteria between pets and their owners occurs but is relatively uncommon under typical household conditions, appearing to be more strongly associated with infection or active shedding than with routine cohabitation alone.

2342 – Continuous-Flow Removal of Rifampicin and Rifaximin Using 0.1% Alginate-Modified PET Fibers

Elena FASNIUC-PEREU, Alexandra Georgiana APOSTICA, Laura BULGARIU
Gheorghe Asachi Technical University of Iaşi, Romania

Background: Pharmaceutical pollution in aquatic environments is an increasing One Health concern, particularly due to the persistence of antibiotics and their potential contribution to ecosystem imbalance and antimicrobial resistance. This study evaluated 0.1% alginate-modified polyethylene terephthalate fibers as a biofunctionalized adsorbent for the continuous-flow removal of rifampicin and rifaximin from aqueous solutions. The work links plastic waste valorisation with a biopolymer-based surface modification strategy, supporting nature-based and circular approaches for water treatment and ecosystem protection.

Methods: PET fibers were functionalized with a 0.1% alginate solution, followed by ionic crosslinking with 2% calcium chloride in order to stabilize the alginate layer on the fiber surface. Dynamic adsorption experiments were performed in fixed-bed column systems at pH 2, separately for rifampicin and rifaximin. The influence of flow rate, initial antibiotic concentration and adsorbent amount was investigated. Residual antibiotic concentrations in the effluent were determined by UV-Vis spectroscopy, using 470 nm for rifampicin and 444 nm for rifaximin. Breakthrough curves were obtained by plotting C/C_0 as a function of time or treated volume. The experimental data were further interpreted using the Thomas and Yoon–Nelson models to estimate dynamic adsorption parameters, including adsorption capacity, kinetic constants and breakthrough time.

Results: The alginate-modified PET fibers showed measurable retention of both antibiotics under continuous-flow conditions, with different breakthrough profiles depending on antibiotic structure and operating conditions. Rifampicin removal was generally more efficient than rifaximin removal. For rifampicin, removal efficiencies reached approximately 70–77% under favourable flow-rate conditions, with dynamic adsorption capacities up to about 40 mg/g in flow-rate experiments and up to 63 mg/g at higher initial concentration. For rifaximin, removal efficiencies were lower and more variable, generally ranging from approximately 5% to 41%, with adsorption capacities up to about 22 mg/g. Increasing flow rate accelerated the passage of the antibiotic solution through the adsorbent bed and modified the breakthrough behaviour, while changes in initial concentration and adsorbent mass influenced both the shape of the breakthrough curve and the calculated adsorption capacity. The Thomas and Yoon–Nelson models were used to describe the dynamic retention process and to compare the performance of the tested systems.

Conclusions: 0.1% alginate-modified PET fibers demonstrated potential for the continuous-flow removal of rifampicin and rifaximin, with better performance for rifampicin and clear dependence on flow rate, initial concentration and adsorbent dose. By combining PET reuse with alginate-based biofunctionalization, this system supports a circular, nature-based strategy for reducing antibiotic pollution in water. These findings are relevant to ecosystem health and wastewater treatment, as limiting pharmaceutical contaminants may help reduce pressures on aquatic environments and the dissemination of antimicrobial resistance.

2369 – One Health Atlas: a visual guide to connect science, policy and action

Francois ROGER (1), Marie-Marie OLIVE (1), Marisa PEYRE (1), Dirk PFEIFFER (2), Jakob ZINSSTAG (3)
1: CIRAD, Montpellier, France; 2: City University of Hong Kong, Hong Kong SAR, China; 3: Swiss Tropical and Public Health Institute, Basel, Switzerland

BackgroundOne Health is increasingly mobilized in global health, biodiversity, food systems and pandemic prevention agendas. Yet its meaning can become diluted when used as a broad label rather than as an operational framework. There is a need for accessible resources that clarify the concept, document its scientific foundations, and support its implementation across sectors and scales.

MethodsThe One Health Atlas was developed as a collective, visual and interdisciplinary resource. Edited by Quae & CABI, it brings together contributions from more than 150 experts across disciplines and

continents. The Atlas combines concise texts, maps, timelines, diagrams and case studies. Its structure is organized into four parts: foundations and recent history; zoonoses, agriculture and food security; education, networks and governance; and future directions and emerging challenges.

ResultsThe Atlas documents the breadth of One Health applications, from zoonotic disease surveillance, antimicrobial resistance and food safety to soil health, plant health, education, stakeholder mapping, financing, social sciences, gender equity, climate change and artificial intelligence. Each double-page chapter can be used independently, making the Atlas suitable for teaching, professional training, policy dialogue and participatory workshops. By linking conceptual foundations with field-based examples, the Atlas provides a practical entry point for strengthening science-policy-society interfaces. The Atlas is freely downloadable as an open-access PDF through Quæ (https://www.quae.com/produit/1931/9782759240265/one-health-atlas) and CABI, increasing accessibility for students, practitioners and policymakers worldwide.

ConclusionsThe One Health Atlas is more than a book: it is a boundary object that helps diverse actors share a common visual language. It supports the transition from One Health as a concept to One Health as a set of teachable, governable and actionable practices. At a time when global health challenges require integrated responses, the Atlas offers a resource for education, dialogue and implementation.

2388 – Nanopore technology and AI for rapid integrated pathogen surveillance

Lara URBAN
University of Zurich, Switzerland

Background:

Genomics has become an integral part of One Health surveillance due to its unique ability to simultaneously identify and characterise outbreak clusters, transmission routes, virulence, and antimicrobial resistances, thus directly informing public health measures. Recent improvements in genomic sequencing through highly accurate nanopore technology now hold the promise of implementing on-site real-time genomics at the point of need with a previously impossible low upfront investment cost—rapidly and globally informing pathogen surveillance.

Methods:

We benchmarked whole-genome sequencing of foodborne and clinical pathogens by nanopore sequencing in comparison with established diagnostics and traditional centralised short-read sequencing technologies. We further developed metagenomic approaches by nanopore sequencing, which—unlike culture-based whole-genome sequencing—can be applied rapidly to any sample type and have the potential to holistically assess the presence of any pathogen, their genomic variation, and their virulence and antimicrobial resistance. By focusing on foodborne and clinical bacterial pathogens, we assessed how nanopore sequencing data and AI-informed can address the extant challenges of metagenomics that currently hinder its uptake in real-world pathogen surveillance—in terms of sensitivity, viability inference, and associations of virulence and resistance genes to their pathogenic hosts.

Results:

We were able to show that nanopore technology is mature enough to replace centralised genomic technology for clinical and foodborne pathogen surveillance and to provide essential additional

information regarding virulence and antimicrobial resistance genes, plasmids, genomic context, and epigenetic modifications. By comparing culture-based with metagenomic approaches in real-world datasets, we further confirmed the bias that culturing introduces in pathogen detections and characterisations. We finally obtained first evidence that the AI-based analysis of nanopore data can give us insights into a pathogen's virulence, and that epigenetic information intrinsincly encoded by nanopore data can deliver robust plasmid-host associations.

Conclusions:

We showcase the potential of nanopore technology-based genomics in application to global pathogen surveillance with a focus on clinical and foodborne pathogens. While already whole-genome sequencing by nanopore technology increase the accessibility of genomic diagnostics, the next crucial implementation of metagenomics will render pathogen surveillance truly accessible, rapid, and holistic. We will briefly talk about our real-world implementation efforts in collaboration with the global PulseNet network for foodborne pathogen surveillance.

2397 – Using an eco-climatic regionalisation approach for risk-based Vector-Borne Disease surveillance under a changing climate

Luca CANDELORO (1), Francesco VALENTINI (1), Carla IPPOLITI (1), Chadia WANNOUS (2), Laura AMATO (1), Susanna TORA (1), Alessio DI LORENZO (1), Paolo TIZZANI (2), Jonas PISCHKE (3), Paolo CALISTRI (1), Alessandro RIPANI (1), Rachid BOUGUEDOUR (4), Nicola D'ALTERIO (1), **Annamaria CONTE** (1)

1: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale'- Teramo, Italy; 2: World Organisation for Animal Health, Headquarters, Paris, France; 3: mundialis GmbH & Co. KG, Bonn, Germany; 4: World Organisation for Animal Health, Sub-Regional Representation for North Africa, Tunis, Tunisia

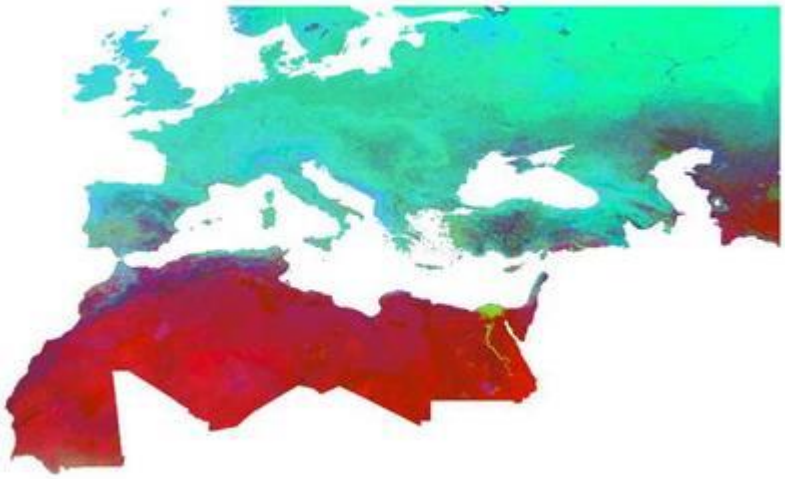
Climate change is reshaping environmental conditions worldwide, altering the spatial and temporal dynamics of vector-borne diseases (VBDs) and challenging existing surveillance systems. Although many VBDs share common environmental drivers, current risk-based surveillance approaches still rely largely on pathogen- or vector-specific models, limiting their scalability across multiple VBDs. The development of cost-effective integrated VBD surveillance would benefit from a transferable framework capable of capturing the shared eco-climatic drivers underlying multiple vector–pathogen systems. To address this challenge, the World Organisation for Animal Health (WOAH) and the Istituto Zooprofilattico Sperimentale dell'Abruzzo and Molise (IZS-Teramo) developed an Earth Observation (EO)-based eco-climatic regionalisation framework to support risk-based surveillance and epidemic intelligence for VBDs. Following a 2024 proof-of-concept application in North Africa (PROVNA project), the framework was further expanded methodologically and geographically across Europe through the PROVBAC project to support transferable multi-disease applications.

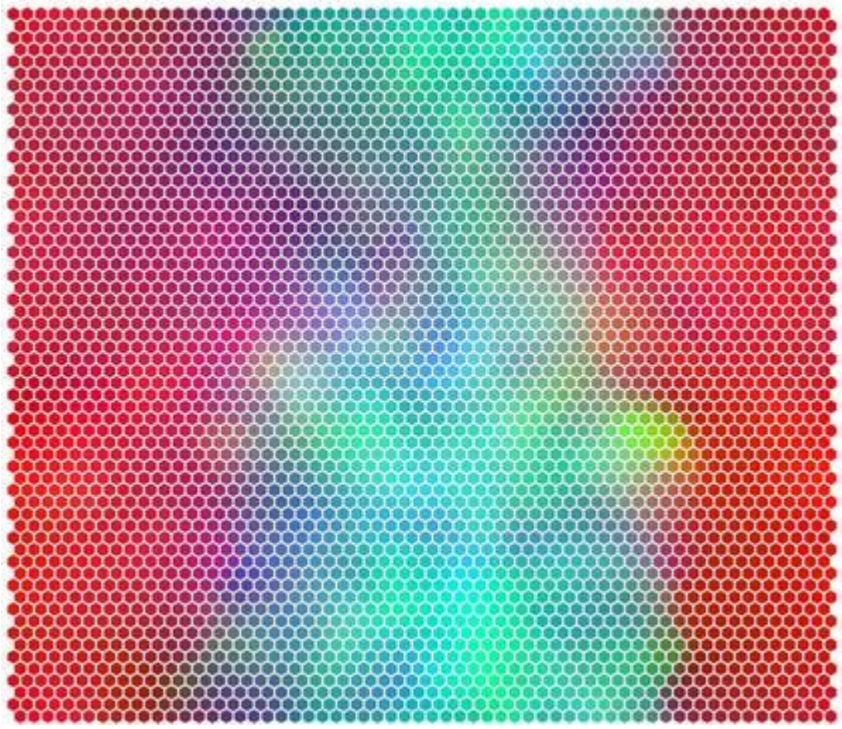
Multi-year EO time series from 2018 to 2025 (including MODIS Land Surface Temperature, MODIS Normalized Difference Vegetation Index, MODIS Normalized Difference Water Index, SMAP Soil Moisture, and TAMSAT/ERA5 rainfall) were harmonized to a common spatial resolution of 250 m and a temporal resolution of 16 days. These data were used to derive eco-climatic descriptors capturing thermal, vegetation, and hydrological dynamics relevant to VBD transmission. Recurrent environmental regimes were identified using an unsupervised Super Self-Organizing Map (SuperSOM) framework combined with affinity propagation clustering, enabling the delineation of ecologically coherent ecoregions.

The analysis generated a high-resolution eco-climatic regionalisation, delineating 3,600 environmental units that were subsequently aggregated into 94 ecoregions. These ecoregions captured major thermal, hydrological, and vegetation gradients across the study area, reflecting environmental conditions relevant to vector ecology and pathogen transmission. Their representation through RGB composites derived from dominant eco-climatic gradients facilitated the visual interpretation of environmental similarities and transition zones across Europe and North Africa. The annual EO-based characterisation enabled the monitoring of environmental variability and the identification of areas sharing similar suitability profiles for VBD transmission over time.

By deriving eco-climatic regions directly from EO through a data-driven and species-agnostic approach, the framework provides a scalable basis for adaptive multi-disease surveillance within a One Health context. The PROVNA outputs are already being integrated into WOAH epidemic intelligence and data integration activities to support preparedness and monitoring of animal health threats. More broadly, the

framework enables spatial risk stratification and supports Member Countries in implementing risk-based surveillance, targeted monitoring, and strategic allocation of surveillance resources for environmentally driven diseases.





2403 – Spatial patterns and environmental correlates of Aedes mosquito diversity at human–animal–environmental interfaces in Uganda's conservation areas

Dennison KIZITO (1,2), Rory James GIBB (3), Joseph MUTYABA (1), Brian KIVUMBI (1), Julius MUGGA (1), Fredrick SSENFUKA (1), John LWANGA (1), George ONGODIA (1), Patrick P'Odyek ABILA (4), Deo NTEEZA (1), Frank MWIINE (2), Julius Julian LUTWAMA (1)

1: Department of Arbovirology, Emerging and Remerging Infectious Diseases, Uganda Virus Research Institute, Entebbe-Uganda; 2: College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University; 3: Centre for Biodiversity &Environment Research, People &Nature Lab, Department of Genetics, Evolution, &Environment,University College London; 4: National Livestock Resources Institute, P.O. Box 5704 Kampala

Background:*Aedes* mosquitoes are primary vectors of arboviruses, including Rift Valley fever, dengue, chikungunya, yellow fever, and Zika, as well as parasites such as lymphatic filariasis. Acting as bridging vectors between sylvatic and human transmission cycles, their ecology is shaped by climatic variability and land use changes. The margins of protected conservation areas, where human settlements, livestock, wildlife, and ecosystems intersect, represent complex socio-ecological systems that may facilitate zoonotic and vector-borne disease transmission. Despite mosquito research in Uganda dating back to the 1930s and documentation of over 220 species, the diversity, distribution, and environmental drivers of *Aedes* mosquitoes in conservation interfaces remain poorly characterized.

Methods: Between August 2022 and June 2024, mosquito collections were conducted in six conservation interface areas along Uganda's cattle corridor: Queen Elizabeth (QECA), Bwindi–Mgahinga (BMCA), Lake Mburo–Nakivaale (LMNCA), Murchison Falls (MFCA), Pian Upe (PICA), and Kidepo Valley (KVCA). A cross-sequential design was employed to sample mosquitoes across domestic, peridomestic, and sylvatic settings, indoors and outdoors. Collections targeted multiple life stages using CDC miniature light and Biogents Sentinel traps. Morphological identification was performed to species level using standard keys, with additional characterization of sex, gravidity, and blood meal status. Climatic and environmental variables were derived from remote sensing and reanalysis datasets (2002–2024). Spatial analyses were conducted in QGIS (v3.40.7), with statistical visualization in RStudio (v4.4.1).

Results: A total of 67,921 mosquitoes were collected: *Culex* (42.7%), *Mansonia* (25%), *Aedes* (17.2%), *Coquillettidia* (16.2%), *Anopheles* (1.8%), and minor genera (*Uranotaenia*, *Lutzia*, *Ficalbia*, *Oranotania*, *Mimomyia*). Species richness varied across sites, with QECA (63 total; 17 *Aedes*) and MFCA (56 total; 14 *Aedes*) showing the highest diversity, while PICA (23; 11 *Aedes*) and KVCA (20; 7 *Aedes*) showed lower diversity. Dominant *Aedes* species differed by site, for example, *Ae. cumminsi* in BMCA, *Ae. circumluteolus* in LMNCA, *Ae. durbanensis* in QECA, and *Ae. ochraceus* in MFCA. MFCA displayed a more evenly distributed mosquito community, whereas QECA, LMNCA, and BMCA were dominated by one or two species.

Conclusion: This study demonstrated substantial heterogeneity in mosquito community composition across Uganda's conservation interfaces, underscoring the ecological complexity of these zones. Differences in dominant *Aedes* species across these various sites may have implications for the different arboviral zoonotic infections and vector-borne transmission risks. The findings highlight the need for spatially targeted surveillance and adaptive vector control strategies. Integrating ecological drivers with species distribution data advances One Health approaches to mitigate arboviral and parasitic disease risks in conservation landscapes.

2419 – Small Mammals (Rodents and Shrews) as Cryptic Reservoirs of Rift Valley Fever Virus at Wildlife-Human Interfaces in Uganda

Nackson BABI (1), Joseph MUTYABA (1), Phiona KATUSHABE (1), Caroline NADIRU (1), Tonny KAYIZI (1), Gladys K. NAKANJAKO (1,2), Charity A. NASSUNA (1), Swaib LULE (1), Wilber SSEMBAJJWE (1), Eric M. ENYEL (3), Elise RINGWALDT (4), Dennison KIZITO (1), Gladys K. ZIKUSOKA (5), Patrick ATIMNEDI (3), Luke NYAKARAHUKA (6), Deo B. NDUMU (2), Julius J. LUTWAMA (1)

1: Uganda Virus Research Institute, Uganda; 2: National Animal Diseases Diagnostics and Epidemiology Center (NADDEC), Ministry of Agriculture Animal Industry and Fisheries (MAAIF); 3: Uganda Wildlife Authority, Kampala-Uganda; 4: University College London, United Kingdom; 5: Conservation Through Public Health; 6: College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala

Background: Rift Valley Fever (RVF) remains a significant zoonotic threat in Uganda, with transmission primarily associated with livestock and mosquito vectors. The role of small mammals in Rift Valley Fever virus (RVFV) maintenance is poorly defined despite their ecological ubiquity and close association with human settlements. This study tested the hypothesis that rodents and shrews act as cryptic reservoirs sustaining RVFV circulation and facilitating spillover across wildlife-livestock-human interfaces.

Methods:A cross-sectional study was conducted across six wildlife conservation areas Queen Elizabeth (QECA), Bwindi-Mgahinga (BMCA), Lake Mburo (LMCA), Murchison Falls (MFCA), Kidepo Valley (KVCA), and Pian Upe (PICA) Conservation Areas. Small mammals were captured using Sherman and Tomahawk live traps deployed across domestic, peridomestic, and sylvatic habitats over two trapping nights per site. Species identification was conducted morphologically, and blood samples were collected on Dried Blood Spot (DBS) cards. RVFV exposure was assessed using an in-house validated ELISA. Geospatial and ecological metadata were collected using ArcGIS Survey123. Seroprevalence estimates were computed; overall, by species, site, and habitat type using STATA version 18. Comparative analyses assessed relative differences in exposure risk across ecological strata.

Results: Out of a total of 684 small mammals that were captured and sampled, overall RVFV seroprevalence was 28.4% (n=197), 95% CI (25.2%; 31.9%). Species-specific analysis showed highest exposure in *Rattus rattus* (37%; n=72), *Mastomys natalensis* (16%; n=31), and *Arvicanthis niloticus* (13.2%; n=26). Small mammals captured in peridomestic habitats had approximately 1.5-2 times higher likelihood of RVFV seropositivity compared to those sampled from sylvatic environments, suggesting amplification at the human-wildlife interface. Spatial variation in conservation areas was evident. Small mammals with the highest RVFV exposure were captured in QECA (42.1%; n=83) while those with the least exposure were captured in MFCA (8.1%; n=16).

Conclusions: The detection of antibodies among rodents and shrews across different habitats, coupled with the commensal behavior and ecological adaptability of the dominant rodent species (*Rattus rattus*), may support their role as cryptic reservoirs of RVFV. Elevated exposure in peridomestic and domestic habitats highlights their role in mediating spillover risk at human-wildlife interfaces. Current surveillance systems that exclude these reservoirs risk underestimating transmission dynamics. Integrating small mammal surveillance into One Health frameworks is essential for improving early warning systems and outbreak prevention.

2433 – Filovirus seroreactivity and exposure correlates in communities surrounding Mt Elgon National Park, Kenya

Moses MASIKA (2), Peter KIMELI (2), Zipporah BOSIBORI (2), Janet CHEBET (3), Leonid SEREBRYANNYY (4), Alicen SPAULDING (4), Daniel DOUEK (4), Jonathan TOWNER (5), George SIGAL (6), Benjamin PINSKY (1), Stephen LUBY (1), **Abraar KARAN** (1)

1: Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, Stanford, CA, USA; 2: KAVI Institute of Clinical Research, University of Nairobi, Nairobi, Kenya; 3: Bungoma County Department of Health, Bungoma, Kenya; 4: Vaccine Research Center, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, USA; 5: Viral Special Pathogens Branch, U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA; 6: Meso Scale Diagnostics LLC, Rockville, MD, USA

Background. Zoonotic spillovers of Marburg virus disease (MVD) have been documented at the Kenya–Uganda border region of Mt Elgon, including near Kitum Cave (1980, 1987) and the Kween District of Uganda (2017). *Rousettus aegyptiacus*, the Marburg virus reservoir, roosts in caves throughout the Mt Elgon region, and human communities may be at risk of infection. We aimed to characterize filovirus seroreactivity, identify associated exposures, and assess community knowledge of MVD.

Methods. We conducted a cross-sectional serosurvey at six health facilities surrounding Mt Elgon National Park in Bungoma County, Kenya in 2025. Participants aged ≥2 years were enrolled following age-stratified community mobilization. A structured questionnaire captured demographic information and key preidentified high-risk exposures. Serum was screened using a Meso Scale Diagnostics electrochemiluminescence (ECL) multiplex assay targeting Marburg, Ebola-Zaire, and Ebola-Sudan glycoproteins at 1:1,000 dilution. Presumptive reactivity was defined using a cutoff set at 5 standard deviations above the mean of our unexposed negative control cohort from Nairobi excluding 3 outliers. Serial-dilution testing (1:250, 1:1,000, 1:4,000) was performed on a subset of high-reactive samples to assess dilutional linearity. Multivariable logistic regression evaluated associations with self-reported exposures.

Results. 533 participants were enrolled. The mean age was 32 years; 51% were female; 51% were farmers; and 5% were healthcare workers. Self-reported exposures included recent bat exposure at home or work (38%), cave entry of any depth (33%), deep cave entry (12%), close bat contact in a cave (28%), bat-guano collection (4%), forest visit in the past year (59%), Uganda border crossing (20%), bushmeat consumption (8%), bat consumption (8%), hunting a wild animal (6%), severe undiagnosed febrile illness in the past 2 years (42%), and household/community member with sudden death from febrile illness with bleeding in the past 2 years (5%). Only 2% had heard of MVD before. Presumptive seroreactivity was 9.4% (50/533) for Marburg, 5% (25/533) for Ebola-Zaire, and 8% (41/533) for Ebola-Sudan. 19% (18/96) of reactive samples were cross-reactive against ≥2 targets. Selected high-reactive samples demonstrated dilutional linearity consistent with specific antibody binding. Age trended with Marburg reactivity (per-year aOR 1.01, 95% CI 1.00–1.03, p=0.06); no other exposure was independently associated.

Conclusions. Presumptive filovirus seroreactivity was detected in nearly one in five Mt Elgon residents using a multiplex binding assay. Awareness of MVD was low, while high-risk exposures including close human-bat contact were widely reported. Further testing will include orthogonal confirmation via soluble-antigen competition and pseudovirus neutralization. This study highlights the need for integrated One Health surveillance and improved community education as well as resources to reduce spillover risk in this transboundary region.

2462 – Building India's One Health Workforce : Experience from a National Online Certificate Programme

Sanghamitra PATI, Debdutta BHATTACHARYA

ICMR-REGIONAL MEDICAL RESEARCH CENTRE, Bhubaneswar, India

Background: The increasing frequency of zoonotic disease outbreaks, antimicrobial resistance (AMR), and environmental health challenges has underscored the need for a competent workforce capable of implementing the One Health approach. Despite growing policy recognition, structured capacity building opportunities in One Health remain limited, particularly in low -and middle-income countries. To address this gap, the Indian Council of Medical Research (ICMR), with support from the Department of Health Research, Government of India, developed and implemented a national online certificate programme on One Health through the National Programme on Technology Enhanced Learning (NPTEL) platform.

Methods: A multidisciplinary 12-week online course was designed through expert consultation and peer review. The curriculum comprised six modules covering One Health principles, emerging infectious diseases and AMR, zoonoses, applied epidemiology, health policy, and community engagement. The course targeted students, researchers, clinicians, programme managers, and policymakers. Participant enrolment, examination registration, certification outcomes, and programme implementation metrics from four consecutive course offerings (2023–2026) were analysed.

Results: Between 2023 and 2026, 18,561 participants enrolled in the programme, with 7,685 appearing for certification examinations and 6,678 successfully completing the course. Participants represented diverse professional backgrounds spanning public health, medicine, veterinary sciences, academia, research, and policy sectors. The programme facilitated interdisciplinary learning through structured assignments, discussion forums, and standardized assessments. The initiative received recognition from the Directorate General of Health Services, Government of India, and has been extended for continued implementation due to sustained demand and high uptake.

Conclusions: This national-scale online programme demonstrates the feasibility of rapidly expanding One Health competencies through digital learning platforms. The model offers a scalable and cost-effective strategy for strengthening multidisciplinary workforce preparedness, supporting national One Health priorities, and advancing pandemic preparedness, AMR containment, and zoonotic disease prevention. Our experience offers a doable framework for other countries seeking to institutionalize One Health capacity building. Moreover, large-scale digital learning platforms can serve as an effective and scalable mechanism for building multidisciplinary One Health competencies in LMIC settings.

2480 – Mapping Andes Virus and Its Rodent Reservoir Across South America

Jenicca POONGAVANAN

Stellenbosch University, Stellenbosch, South Africa

Background: Andes virus is a major cause of hantavirus cardiopulmonary syndrome in southern South America and is associated with a rodent reservoir, *Oligoryzomys longicaudatus*. Although Andes virus occurrence is concentrated in Chile and Argentina, the ecological conditions shaping virus and reservoir suitability remain incompletely characterized. We aimed to model the geographic suitability of the Andes virus reservoir-virus system across South America and identify the environmental drivers structuring suitability, with emphasis on differences between Chile and Argentina.

Methods: We compiled reservoir and virus occurrence records from South America and fitted ecological niche models separately for rodent occurrence, virus-associated occurrence, and a combined dataset pooling reservoir and virus records. Models were fitted using Generalized Linear Model, Boosted Rregression Trees, and Random Forest algorithms with pseudo-absence replicates. Environmental covariates included climate, vegetation classification, elevation, snow cover, precipitation, humidity, and human-interface variables including distance to the nearest waste site. Ensemble model performance was evaluated using AUC and TSS. SHAP analysis was used to quantify variable importance and interpret non-linear response curves. Country-specific SHAP outputs were compared for Chile and Argentina.

Results: Ensemble models showed strong calibration performance, with AUC values of 0.969 for the rodent model, 0.989 for the virus model, and 0.969 for the combined model. Predicted suitability was concentrated along the temperate Andean corridor of southern Chile and adjacent Argentina. The rodent model predicted a broader suitability envelope, while the virus model was more spatially restricted, suggesting that virus-associated suitability occurs within a narrower subset of the reservoir's ecological range. The combined model, fitted directly to pooled reservoir and virus records, produced a single suitability surface representing environmental conditions associated with the broader reservoir-virus system. SHAP analysis identified temperature as the strongest predictor of combined suitability, followed by distance to the nearest waste site and vegetation types. Forest-edge structure, elevation, snow cover, precipitation and humidity contributed additional but weaker effects. Response curves indicated non-linear relationships between environmental gradients and predicted suitability. Chile-specific patterns suggested stronger roles for forest-edge structure, snow cover, and vegetation types, whereas Argentina showed broader suitability gradients associated with vegetation, distance to the nearest waste site and elevation.

Conclusions: Andes virus suitability in South America is structured by interacting climatic, vegetation, topographic, and human-interface gradients. Reservoir suitability is broader than virus-associated suitability, emphasizing that host presence alone does not define the ecological conditions associated with Andes virus occurrence. These models provide a spatial framework for targeting ecological surveillance and field validation in Chile, Argentina, and other environmentally suitable regions of South America.

2538 – Mapping the Intersection of Artificial Intelligence, One Health, and Inclusive Education in Europe (2015-2026): A Thematic Network Analysis

Hatice BÜBER KAYA (1), Tuğba MUTLU (2)

1: Kırklareli University, Turkiye; 2: Yozgat Bozok University

Background. One Health depends on a workforce able to reason across human, animal, and environmental health, and artificial intelligence (AI) is now reshaping how such reasoning is taught. Three agendas are advancing across Europe at the same time yet along separate tracks. One Health education is being formalised through new competency frameworks, AI is entering schooling through AI-literacy frameworks released in 2024 and 2025, and inclusion principles set the terms of who can reach this education. Whether these agendas meet in inclusive secondary and higher education has not been mapped, and the window to align them is closing as each hardens on its own. This study asks what thematic structures and gaps characterise AI-supported inclusive education within One Health frameworks across European education from 2015 to 2026.

Methods. We apply Thematic Network Analysis (Attride-Stirling, 2001), supported by thematic synthesis (Thomas and Harden, 2008). The corpus draws on CORDIS, the Erasmus+ Project Results Platform, COST Actions, European Commission and international agency publications, and peer-reviewed case studies (2015-2026; secondary and higher education; six languages). Coding pairs a deductive skeleton (the Quadripartite One Health definition; UNESCO AI Competency Frameworks; the Salamanca Statement and the UN CRPD; Long and Magerko's AI-literacy competencies) with inductively derived categories. Two researchers code independently in a structured coding sheet, inter-coder reliability is assessed with weighted Cohen's kappa computed in R, and themes are synthesised into a basic, organising, and global network. Carried out during 2026 and pre-registered on OSF (https://doi.org/10.17605/OSF.IO/2YM39), the analysis to date covers a purposive screen of fourteen leading European and international initiatives and frameworks, with full-corpus coding ongoing.

Results. None of the fourteen initiatives screened integrated all three agendas. AI and One Health do meet: five of fourteen units position AI, in two cases as an object of critical and ethical inquiry and in three as a tool. Inclusion is the missing axis: eleven units never mention it, and the single unit that operationalises it positions no AI. One Health education concentrated at higher and doctoral levels and framed the human-animal-environment nexus largely through zoonoses and antimicrobial resistance; at secondary level, inclusion was absent throughout. Secondary education remained the thinnest cell in the map.

Conclusions. Across Europe, AI, One Health, and inclusive education are converging in time but not in content, leaving a shared yet largely empty intersection precisely as AI curricula and One Health education are being designed. Naming this gap now, together with the thematic network behind it, offers an evidence base for inclusive One Health curriculum and challenge-based learning, and timely guidance for the future One Health workforce. The thematic network for this orienting screen will be presented at the congress, with full-corpus analysis ongoing.

2547 – Seroprevalence, behavioural and sociocultural drivers of zoonotic disease exposure among Uganda's hunting communities: A One Health mixed-methods study

Mercy HAUMBA (1), Phiona KATUSHABE (1), Dennison KIZITO (1), Wilber SSEMBAJJWE (3), Ronald Ssali OGWAL (2), Joseph MUTYABA (1), Swaib A. LULE (1), Nackson BABI (1), Gladys Nakanjako KIGGUNDU (4), Ruth Stephens NALUKWAGO (1), Charity Angella NASSUNA (1), Carolyn NYAMOR (5), Elise RINGWALDT (6), Gloria AKURUT (7), Eric

Morris ENYEL (7), Rory J. GIBB (8), Gladys Zikusooka KALEMA (2), Musa SEKAMATTE (5), Laura FERGUSON (9), Nigel FIELD (6), Janet SELEEY (10), Julius Julian LUTWAMA (1)

1: Uganda Virus Research Institute, Uganda Plot51-59 Nakiwogo Road, Entebbe; 2: Conservation Through Public Health (CTPH), Entebbe-Uganda; 3: MRC/UVRI & LSHTM Uganda Research Unit, Plot51-59Nakiwogo Road, Entebbe; 4: National Animal Disease Diagnostics and Epidemiology Centre (NADDEC) Laboratories, Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Entebbe Uganda; 5: National One health Platform (NOHP), Coordination Office, Ministry of Health, Kampala, Uganda.; 6: Institute for Global Health (IGH), University College London, London, UK; 7: Uganda Wildlife Authority, Kampala; 8: Department of Genetics, Evolution and Environment, University College London, London, UK; 9: Institute on Inequalities in Global Health, University of Southern California, USA; 10: London School of Hygiene & Tropical Medicine, London, UK

Background

Wildlife hunting is illegal in Uganda, yet communities within conservation areas continue to depend on bush-meat for food and income, increasing opportunities for zoonotic disease exposure. Despite growing concern about zoonotic spillover risk at human-wildlife interfaces, few studies have integrated serological evidence with behavioural and sociocultural data to understand the drivers of disease exposure. This study investigated the seroprevalence of brucellosis, Rift Valley fever (RVF), and Crimean-Congo Hemorrhagic fever (CCHF), and examined how behavioural and sociocultural factors may influence zoonotic disease risk among hunting communities in Uganda.

Methods

A cross-sectional mixed-methods study was conducted in Bwindi-Mgahinga (BMCA), Lake Mburo (LMCA), Murchison Falls (MFCA), and Queen Elizabeth (QECA) conservation areas in Uganda, targeting active and reformed participants in the bush-meat value chain. Participants completed structured questionnaires, provided blood samples for serological testing for brucellosis, RVF, and CCHF, and participated in focus group discussions and in-depth interviews. Serum samples were analysed using in-house indirect ELISA assays, while Modified Poisson regression was used to identify factors associated with seropositivity. Qualitative data were analysed thematically, and findings from both components were triangulated to provide an integrated One Health interpretation of zoonotic disease exposure.

Results

Among 946 participants who consented to blood sampling, 53.9% were female, with a median age of 33 years. Seroprevalence was 77.7% for brucellosis, 41.5% for CCHF, and 26.5% for RVF. Modified Poisson regression showed that increasing age was associated with higher RVF (adjusted prevalence ratio [aPR] = 1.01; 95% CI: 1.00-1.02) and CCHF (aPR = 1.01; 95% CI: 1.00-1.01) seroprevalence, while males had higher RVF (aPR = 1.38; 95% CI: 1.12-1.70) and CCHF (aPR = 1.21; 95% CI: 1.05-1.38) seroprevalence than females. Brucellosis seroprevalence was higher among participants engaged in agriculture (aPR = 1.12; 95% CI: 1.01-1.24) and those reporting contact with rodents (aPR = 1.11; 95% CI: 1.04-1.19). Use of personal protective equipment while handling animals was consistently associated with lower seroprevalence of brucellosis (aPR = 0.7; 95% CI: 0.62-0.81), RVF (aPR = 0.06; 95% CI: 0.04-0.10), and CCHF (aPR = 0.58; 95% CI: 0.48-0.70). Qualitative findings showed that disease exposure was shaped by economic dependence on bush-meat, culturally rooted hunting practices, gendered roles across the bush-meat value chain, and limited understanding of zoonotic disease transmission, all of which reduced the adoption of protective behaviours and reinforced unsafe human-animal interactions

Conclusion

Our study findings demonstrate that hunting communities living at the human-wildlife interface experience substantial exposure to CCHF, RVF, and brucellosis and highlight the contribution of occupational, behavioural, and sociocultural factors to disease risk. Strengthening community-centred One Health interventions through improved risk communication, safer animal-handling practices, enhanced community disease surveillance, and providing alternative livelihood opportunities may reduce zoonotic disease exposure and spillover risk in conservation areas.

2558 – Updating Veterinary Antimicrobial Stewardship Resources to Address Emerging One Health Antimicrobial Resistance Priorities

Alexandra MEDLEY

US Centers for Disease Control and Prevention, United States of America

Background: Antimicrobial resistance (AMR) is a growing threat to human, animal, and environmental health and remains a priority within global One Health strategies. Veterinary professionals play a critical role in antimicrobial stewardship (AMS), infection prevention and control (IPC), and early recognition of emerging resistant pathogens. Since publication of the American Veterinary Medical Association (AVMA) report *Antimicrobial-Resistant Pathogens Affecting Animal Health* in 2019, substantial changes have occurred in the AMR landscape, including the emergence of new bacterial and fungal threats, evolving stewardship recommendations, and increased emphasis on One Health approaches to AMR mitigation. This project aimed to update the AVMA resource to better support veterinary AMS and align with contemporary One Health AMR priorities.

Methods: A multidisciplinary working group convened by the AVMA Committee on Antimicrobials conducted a structured review and revision of the 2019 report. Information from published scientific literature, surveillance reports, regulatory and public health guidance, and subject matter expert review was evaluated to identify pathogens of current clinical, epidemiologic, and stewardship significance. Pathogens affecting companion animals, equids, food-producing animals, aquaculture species, and veterinary healthcare settings were assessed. The review process examined changes in pathogen relevance, antimicrobial resistance patterns, stewardship implications, infection prevention, and diagnostic and treatment considerations. Updated content was synthesized into species-specific summaries and practical reference tools intended to support veterinary prescribing and stewardship decision-making.

Results: The 2026 report substantially expands the scope of the original publication. Newly identified antimicrobial-resistant bacterial pathogens and priority fungal pathogens were incorporated based on emerging evidence and evolving stewardship concerns. In addition to pathogens causing direct animal disease, the update includes organisms with importance for veterinary healthcare-associated infections and IPC programs. New summary tables were developed to facilitate interpretation of antimicrobial susceptibility information and support evidence-based prescribing practices. The updated resource provides pathogen-specific information across companion animal, livestock, poultry, and aquaculture sectors while explicitly incorporating One Health stewardship principles. The revision process also highlighted areas where surveillance data remain limited, emphasizing ongoing challenges in generating comparable AMR information across animal populations and sectors.

Conclusions: The 2026 AVMA report update reflects the evolving AMR landscape and demonstrates how veterinary stewardship resources can support broader One Health AMR mitigation efforts. By incorporating emerging pathogens, stewardship considerations, and IPC priorities across multiple animal sectors, the resource strengthens veterinary contributions to responsible antimicrobial use and cross-sector AMR prevention and control. Continued collaboration among animal, human, and environmental health stakeholders is needed to improve surveillance, stewardship, and coordinated responses to emerging AMR threats.

2568 – Towards Integrated One Health Surveillance in Ireland: A Roadmap for an All-Island Surveillance Platform

Erik P DE JONG (1,2), Jessica S HAYES (1), Máire A CONNOLLY (1)

1: School of Health Sciences, University of Galway, Galway, Ireland; 2: Insight Research Ireland Centre for Data Analytics, University of Galway, Galway, Ireland

Background

Emerging zoonotic pathogens, including highly pathogenic avian influenza (H5N1), highlight the need for integrated surveillance systems that connect human, animal, and environmental health sectors. The island of Ireland presents a unique epidemiological setting due to its location on a major avian migratory route in Europe the East Atlantic Flyway, significant livestock sectors, growing climate-related risks and a shared land border. Current surveillance systems are well established within sectors but are only partially integrated, limiting timely data sharing, cross-domain analysis, and capacity for early warning and response to emerging health threats. Through the EU4Health OH-ALLIES (One Health: All Ireland for European Surveillance) project, a roadmap was developed to guide future integration of One Health surveillance systems.

Methods

A mixed-methods approach was used to develop the roadmap. Evidence was synthesised from three complementary workstreams: (1) stakeholder mapping involving consultation and network analysis of organisations engaged in surveillance; (2) benchmarking of One Health surveillance systems and practices in three European countries: the Netherlands, Denmark, and Norway; and (3) landscape analysis of existing surveillance systems, data flows, and information technology infrastructure in Ireland, including qualitative interviews with key stakeholders. Findings were triangulated to identify system strengths, gaps, implementation priorities, and foundational requirements for future integration (Figure 1).

Results

The analysis identified strong existing surveillance capacity in animal and human health, supported by established laboratory and information systems; however, these systems remain largely domain-specific with data silos leading to fragmented, disconnected information. Key barriers to integration included limited interoperability between surveillance platforms, incomplete inconsistent (meta)data and data standards, disjointed cross-domain data sharing, underdeveloped integration of environmental surveillance monitoring (wastewater, climate, biodiversity and land-use data), and cross-border data sharing challenges. The roadmap proposes five strategic priorities: (1) strengthening governance and cross-border coordination; (2) modernising surveillance IT infrastructure; (3) improving data quality, interoperability, and automation; (4) expanding environmental and citizen-based surveillance; and (5) building long-term analytical and workforce capacity. A phased implementation pathway was developed (Table 1), covering short-term actions (year 1–2) focused on governance, digitisation, harmonised metadata standards, federated data-sharing mechanisms, unique case and sample identifiers, pilot integrated dashboards, and data-sharing protocols. Long-term actions (year 3–5) include automated interoperability, integration of genomic and environmental data streams, advanced analytics and artificial intelligence capabilities developed within appropriate governance and regulatory frameworks, and establishment of a fully operational all-island One Health Surveillance System.

Conclusions

This newly developed roadmap provides an evidence-based pathway towards integrated One Health surveillance on the island of Ireland. It underlines the urgent need to link human, animal, and environmental surveillance systems, to strengthen early warning, risk assessment and preparedness for emerging zoonotic threats. The roadmap also aligns with evolving European One Health surveillance priorities and contributes to broader regional and global health security objectives.

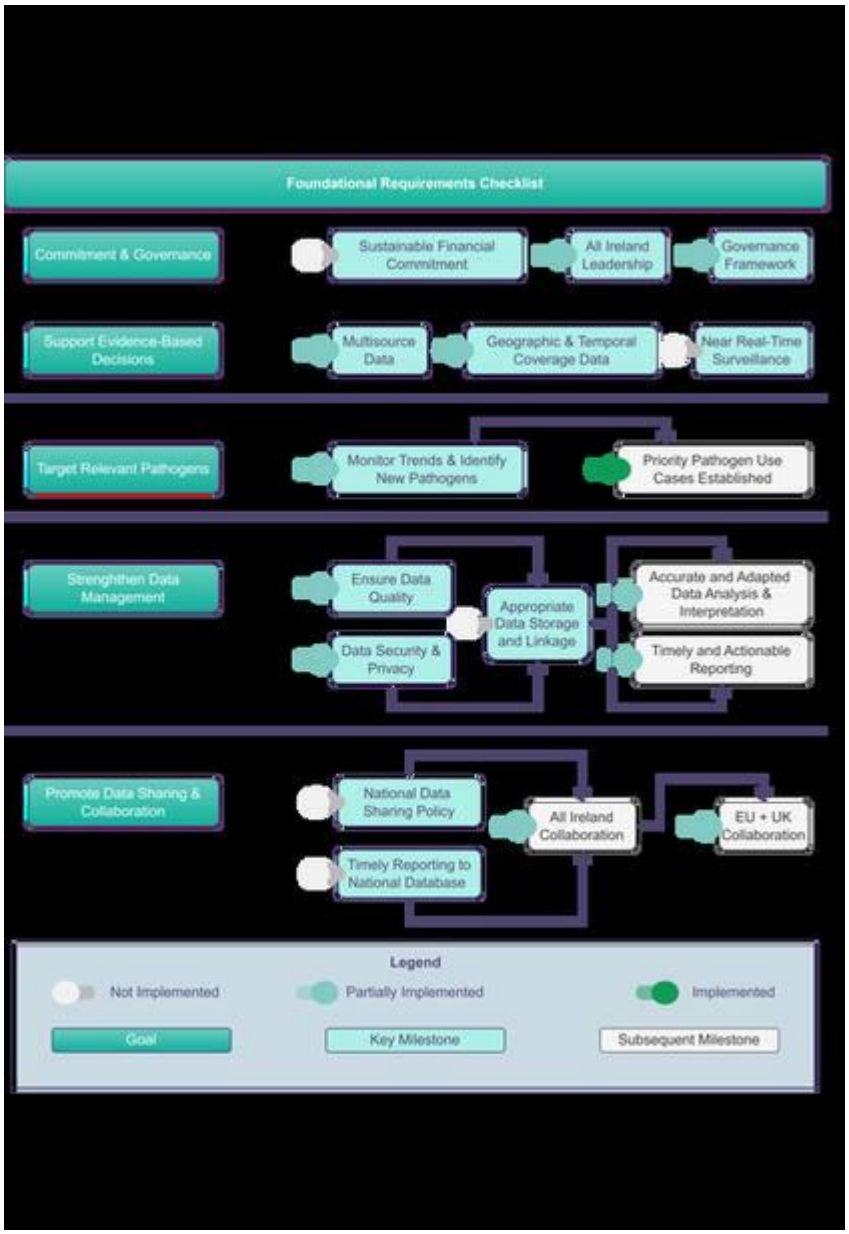

Foundational Requirements Checklist
Commitment & Governance
Sustainable Financial Commitment
All Ireland Leadership
Governance Framework
Support Evidence-Based Decisions
Multisource Data
Geographic & Temporal Coverage Data
Near Real-Time Surveillance
Target Relevant Pathogens
Monitor Trends & Identify New Pathogens
Priority Pathogen Use Cases Established
Strenghthen Data Management
Ensure Data Quality
Data Security & Privacy
Appropriate Data Storage and Linkage
Accurate and Adapted Data Analysis & Interpretation
Timely and Actionable Reporting
Promote Data Sharing & Collaboration
National Data Sharing Policy
Timely Reporting to National Database
All Ireland Collaboration
EU + UK Collaboration
Legend
Not Implemented
Partially Implemented
Implemented
Goal
Key Milestone
Subsequent Milestone

TABLE 1. ALL IRELAND ONE HEALTH SURVEILLANCE SYSTEM ROADMAP

Workstream	Phase 1 (Years 1-2) Foundation & Pilot	Phase 2 (Years 3-5) Integration & Scale-up
Governance & Policy	Secure long-term funding	Establish sustainable budget lines
	Establish OHSS implementation group	Establish cross-border steering committee
	Develop cross-border SOPs	Align with EU standards
	Define data-sharing frameworks	
Data & Infrastructure	Digitise surveillance submissions	Automate cross-sector data exchange
	Complete metadata inventories	Expand geospatial dashboard functions
	Map data flows and gaps	Enable automated reporting
	Design OHSS architecture	Achieve EU interoperability
	Develop pilot cross-sector dashboard	
Analytics & Innovation	Assess end-user needs	Expand predictive analytics
	Integrate environmental data	Integrate genomic surveillance
	Explore AI/ML application	Enable automated risk assessment
Stakeholder Engagement & Capacity	Engage surveillance partners	Expand wildlife surveillance networks
	Strengthen citizen science	Strengthen surveillance workforce capacity
	Promote cross-sector collaboration	Stakeholder feedback loop
	Identify training needs	
Expected Outcomes	Funding secured	Sustainable funding maintained
	Metadata catalogue completed	>90% automated data exchange
	Increased citizen participation	Routine cross-sector data sharing
	Cross-border SOPs implemented	Full EU interoperability achieved
	Pilot dashboard operational	
Challenges → Mitigation	Governance fragmentation →Harmonised SOPs	Interoperability issues →Data standards
	GDPR constraints →Sharing agreements	Workforce shortages →Targeted training
	Resistance to change →Pilot demonstrations	Funding risks →Dedicated budgets
	Limited engagement →End-user needs	EU alignment →Technical working groups

2572 – The Transatlantic Taskforce on Antimicrobial Resistance (TATFAR): Bridging a One Health Approach in Multisectoral AMR Collaboration and Best Practices

Ilya PLOTKIN

Office of Global Affairs, United States Department of Health and Human Services

Background

The Transatlantic Taskforce on Antimicrobial Resistance (TATFAR) was created after the 2009 United States (U.S.)-European Union (E.U.) Summit Declaration to address the urgent, growing threat of antimicrobial resistance (AMR). The Taskforce is co-chaired by the European Commission Public Health Directorate and the U.S. Department of Health and Human Services Office of Global Affairs. AMR leaders and subject matter experts across One Health sectors from Canada, the EU, Norway, the United Kingdom (U.K.) and the U.S. collaborate and share best practices to combat AMR. The Taskforce guides collaboration toward objectives defined in each TATFAR five-year workplan across several key areas, including antimicrobial use, AMR surveillance, communication, and innovation, integrating a One Health approach that convenes human, animal, and environmental health partners under a shared umbrella. This One Health approach recognizes the interconnection between human, animal, plant, and environmental health and is implemented according to national contexts and laws, as relevant.

Methods

A preliminary case study of the TATFAR 2021-2027 work plan implementation is used to analyze the extent of multisectoral engagement through a One Health approach, compared to past TATFAR work plan implementation and activities. Using available historical data, including agency participation records, governance documents, work plan structure and activities, and published information, a characterization of the level of engagement across One Health partners participating across the TATFAR member countries is evaluated.

Results

TATFAR, from its beginnings, built its functions around promoting information exchange, coordination, and cooperation between members, which grew to include Canada, the EU, Norway, the U.K. and the U.S., centered around the challenge of AMR. By providing technical and scientific statements or suggestions

rather than formal or binding positions, the partnership evolved to encompass partners across human, animal, plant, and environmental health sectors, and building upon a One Health lens for engagement to both understand and mitigate AMR. The current work plan reflects this evolution: 15 of 18 actions (83%) now engage agencies from more than one sector, though only three engage all four One Health sectors and just one explicitly uses "One Health" terminology, suggesting multisectoral collaboration has outpaced formal One Health framing. Not only was the discussion of One Health more prominent, but members also engaged a greater number of multisectoral partners within their country.

Conclusions

At a moment when AMR is increasingly recognized as a critical global health security threat, TATFAR offers a transferable model for sustained regional collaboration that bridges science, policy, and implementation across sectors and borders. By leveraging its foundations as a collaborative exchange of regional AMR information and expertise, and TATFAR's growth to incorporate greater One Health coordination across the intersection of human, animal, and environmental health, countries are better prepared to comprehensively address AMR domestically and globally.

2578 – High ambient temperature, humidity, heat index, and stroke risk in a Mediterranean region

Maya NEGEV, **Shlomit PAZ**, Shiraz VERED, Galit WEINSTEIN
University of Haifa, Israel

Background

Studies assessing the relationship between high ambient temperatures and stroke risk yielded conflicting results, while potential associations of humidity and heat stress with stroke risk remain underexplored. The objective was to explore the association of ambient temperature, humidity, and heat index (HI) with the risk of total stroke (combined ischemic/intracerebral hemorrhage [ICH]), ischemic stroke (IS), ICH, and transient ischemic attack (TIA) among older adults during the warm season in the Mediterranean region, a climate change hot spot.The hypothesis was that ambient heat stress acutely elevates stroke risk across temperature, humidity, and combined heat index exposures.

Methods

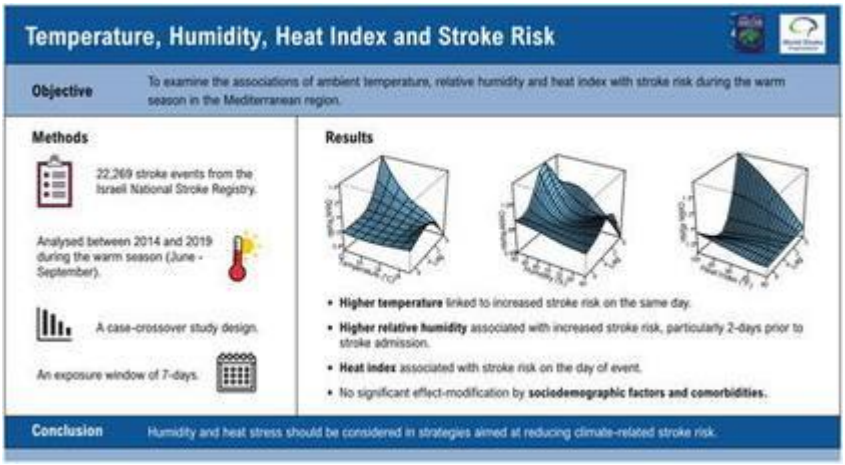
In this time-stratified case-crossover study, data were obtained from the Israeli National Stroke Registry. All first stroke and TIA events among individuals aged ⩾18 years that occurred during the warm season (2014– 2019) were included. Temperature and relative humidity were assessed using high-resolution satellite-based models and monitoring stations, based on patients' residential addresses. A heat index (HI) was calculated based on a combination of temperature and relative humidity data. Conditional logistic regression models with Distributed Lag Non-Linear Models were used with adjustment for potential confounders, including air pollution. The HI models were stratified by participants' demographic and health characteristics.

Results

The sample included 22,269 individuals with a first stroke (mean age 72 ± 14 years; 55% males) and 8728 individuals with a first TIA (mean age 69 ± 14 years; 52% males) during the warm season. Higher temperature (32°C vs. 27°C), particularly on the stroke event date, was associated with increased risk of total stroke (odds ratio (OR) = 1.32; 95% confidence interval (CI) = 1.23–1.41). The strongest association for relative humidity (90% vs. 70%) was observed 2 days before the event (OR = 1.09; 95% CI = 1.06–1.12). An HI of 100°F was associated with an approximately 40% higher risk compared to HI of 80°F on the event day (OR = 1.39; 95% CI = 1.32–1.47). Associations were slightly weaker for ICH, whereas associations with TIA were similar in magnitude to those observed for IS. No evidence of effect modification was observed across subgroups.

Conclusions

High temperatures combined with high humidity are associated with an immediate increase in the risk of stroke and TIA, even in a region where the population is acclimatized and most buildings are air-conditioned. Preparedness and prevention strategies may be crucial for reducing stroke risk during periods of heat stress.



2621 – WIViREIDS: Enhancing Field-to-Lab Surveillance for Emerging Infectious Diseases (EIDs) at the Wildlife, Livestock, and Human Interface in the Philippines

Edna FELIPE (1), Jonas Claude LAURENTE (1), Jenny-Rose MIRANDA (1), Rizza Araceli SALINAS (2), Imelda SANTOS (1), Jemma BERGFELD (3), Toan HONG (3), Patrick MILETO (3), Frank WONG (3)

1: Department of Agriculture - Bureau of Animal Industry, Philippines; 2: Department of Environment and Natural Resources - Biodiversity Management Bureau, PHilippines; 3: Australian Centre for Disease Preparedness, Australia

Emerging infectious diseases and potential zoonotic diseases pose significant threats to regional and global health security, particularly in regions with significant interacting human–livestock–wildlife interfaces. The Wildlife Interface Viromic Regional Emerging Infectious Disease Surveillance (WIViREIDS) project aims to strengthen surveillance and diagnostic capabilities across countries in Southeast Asia. Activities in the Philippines, initiated in June 2024 by the Department of Agriculture – Bureau of Animal Industry (DA-BAI), focused on enhancing national and regional veterinary field and laboratory capabilities and establishing sustainable surveillance methods for risk-targeted wildlife interfaces.

Under a One Health approach, the project prioritizes improving preparedness for Highly Pathogenic Avian Influenza by integrating field epidemiology, wildlife surveillance, and molecular diagnostics. The project also strengthens multi-sectoral national coordination through the operational collaboration of various sectors including DA Regional Offices, Regional Animal Disease Diagnostic Laboratories, the Department of Environment and Natural Resources, local veterinary services, and the BAI Animal Disease Diagnosis and Reference Laboratory, Project personnel actively participated in pathogen genomic surveillance training and discussed learnings and outputs with the other participating countries at regional project meetings held in 2024 and 2025, which fostered knowledge exchange and assessed surveillance strategies at a regional level.

The priority wildlife interfaces identified in the Philippines for active surveillance activities include those in which wild migratory or water birds overlap with poultry species or are in close proximity to people. From December 2024 to May 2026, a series of sample collection activities were conducted in Regions III (Pampanga, Nueva Ecija) and XI (Davao City, Davao del Norte). A total of 2,260 fecal, environmental, and oropharyngeal and cloacal swab samples were collected from wild bird species, including *Hirundo rustia, Nycticorax nycticorax, Egretta. garzetta, Alcedo atthis* and *Anas sp.* All samples from our active surveillance to date have tested negative for Influenza Type A using real-time PCR, noting that the majority were not from key avian influenza reservoir waterfowl species. Results from PCR screening of other viruses including avian coronavirus and paramyxovirus will also be presented. Furthermore, the project team is planning on widening the scope of sample collection sites in risk-targeted areas.

The project delivered local training on the application of Oxford Nanopore Technologies MinION sequencing technology and targeted amplicon sequencing workflows.

Importantly, such hands-on capability transfer activities delivered *in loco*, contribute significantly to improving the Philippines' preparedness and responsiveness to zoonotic disease threats. Although HPAI sampling from the active surveillance of targeted wild bird interface locations have yielded negative results to date, the project emphasizes the importance of establishing an ongoing surveillance and

methodological capability sustained through sample throughput and technical practice. The initiative contributes to the country's regional health security and implementation of the One Health approach in mitigating EID risks.

2637 – Exploring systemic drivers of Avian Influenza outbreaks in large-scale poultry productions in Denmark

Stine KJAER LEFÈVRE

Statens Serum Institut, Denmark

Background:

Recurrent outbreaks of Highly Pathogenic Avian Influenza (HPAI) continue to challenge animal health, public health, and the poultry sector despite substantial advances in surveillance, biosecurity, and One Health collaboration. While existing approaches have significantly improved our understanding of pathogen circulation and transmission, repeated high-impact outbreaks suggest that focus on hazard and exposure alone may not fully explain the recurrent magnitude of these events.

Methods:

This study explored systemic drivers of Avian Influenza in large-scale poultry productions in Denmark through a qualitative analysis of existing peer-reviewed literature. Based in conceptualisation from Disaster Risk Reduction, the analysis focused on qualitative deductive descriptions of the concepts of ´hazard´, `exposure´ and `vulnerability/amplifying factors´. These concepts was then analysed for internal coherence, being the initial claim/ study objective, the findings of each study and the subsequent conclusion in each of the included litterature, and also across the included litterature.

Results:

The findings shed light on the magnitude of the cascading adverse effects of current mandated outbreak response actions. The study found repeated shortcomings in internal coherence. The primary cause of outbreaks, being contact to wild birds, remained the conclusion of the studies, despite that they did not find statistically significant correlation to support the claim. This suggest a degree of paradigm maintenance within the literature and the academic field.

This potential paradigm maintenance becomes problematic as the risk assessments regarding control measures for the disease, are based on th litterature and further informs legislation and mandated response actions. Based on the included qualitative studies, it was possible to clearly differentiate between the disruptions of the production chains caused by the disease itself, and disruptions caused by the mandated response actions. Through a system dynamic mapping, it became evident that there are indications that current response actions might actually play a role in maintaining the recurrence and magnitude of these outbreaks. From these insights, leverage points and research gaps were identified.

Conclusions:

These insights open up for discussions on how data generated from mandated surveillance programs are informing research agendas, and how this shapes the conceptualisation of risk in literature and legal frameworks. This study demonstrates that complex socio-ecological problems benefit from multiple independent perspectives rather than multiple studies within the same conceptual framework. Integrating complementary disciplines creates opportunities to challenge existing assumptions, explore alternative explanations, and strengthen the overall understanding of complex system behaviour. This approach to behavioural reconfiguration of the entire system is closely linked to the One Health Key Principles.

2650 – Investigating the genetic pattern of essential Two-component Systems and associated MDR efflux pumps in proximity and inside E. coli prophages: a study from swine farm isolates from Piedmont Region, Italy

Miryam BONVEGNA (1), Maria Cristina STELLA (2), Laura TOMASSONE (2)

1: School of Veterinary Medicine, University College Dublin, Ireland; 2: Department of Veterinary Sciences, University of Turin, Italy

Two-component Systems (TCSs) are considered bacterial “core” genes, necessary to guarantee the microorganism survival across diverse stressful environmental conditions, such as the presence of toxic compounds. Specific TCSs, like the *evgS*/*evgA* system, are strictly affected by antibiotics, leading to the activation of bacterial MDR efflux pumps. Considering the raising concern about AMR linked to human-animal pathogens, such as *E. coli*, understanding if these genes are present on potentially mobile elements, such as bacteriophages, is of paramount importance.

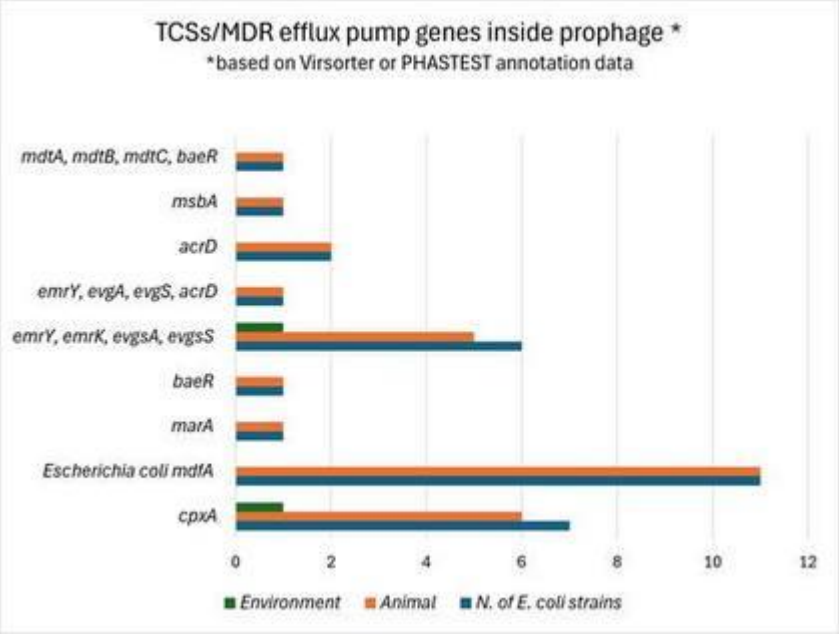
In this study, TCSs and associated efflux pumps’ genes were searched inside prophage regions or nearby (next to the last bp of viral origin) in MDR *E. coli* (N= 29) genomes, sampled between 2019 and 2020, from healthy animals and environment in 4 swine farms of Piedmont, Italy. WGS analysis was performed with assembled genomes (CLC Genomic Workbench v. 20.0.4), from two × 250bp paired end short-reads sequences’ output by Illumina MiSeq™. Through Proksee web platform, a combination of Mobile-OG db, PHASTEST and Virsorter 2.0 data were used for prophage annotation, while CARD was run to detect AMR genes associated to TCS type (cut-off perfect or strict). For prophages’ annotation, a cut-off of 1000 bp of minimum length and a minimum concordance of two tools was used.

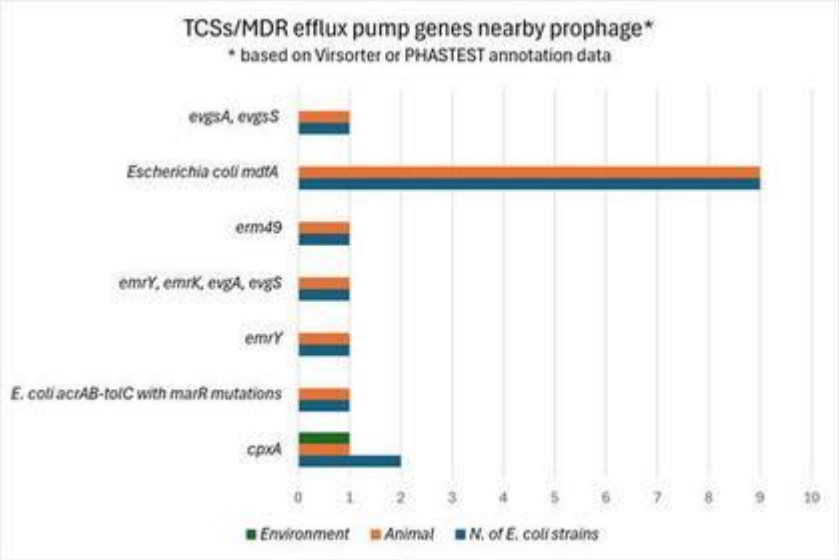
Results reveal that prophage regions were identified almost consistently by the three tools with minor differences, regarding region identification and the sequence length. The AMR TCSs genes *evgA* and *evgS,* were detected inside prophages by Virsorter in 7 different genomes (6 animal and 1 environmental isolates). The MDR efflux pump genes *emrK* and *emrY* were beside *evgS* and *evgA*, in 6 *E. coli* genomes.

Another AMR TCS gene *baeR* was identified through Virsorter in one prophage from an animal *E. coli* isolate, flanked by the MDR efflux pump genes *mdtA*, *mdtB* and *mdtC*.

Regarding the MDR efflux pump gene *mdfA,* it was found inside prophage regions in 11 *E. coli* animal isolates. In 3 out of 11 cases PHASTEST could not recognized any prophage region, while Virsorter and Mobile-OG db yes. *mdfA* was also detected nearby prophages from *E. coli* animal isolates, in 8 cases for Virsorter and in 1 case considering PHASTEST.

This study highlights that TCSs and MDR efflux pumps’ genes, essential for bacterial persistence in specific niches where antibiotics are employed, like swine farms, can be present in or nearby prophages located in *E. coli* genome. Further studies are necessary to understand the role of prophages in fitness and evolution of AMR of potentially animal and human pathogens, such as *E. coli.* This is of particular concern, considering that prophages can potentially be mobilized, contributing to the AMR diffusion in contexts where humans and animals are in close contact, like animal farming system.




TCSs/MDR efflux pump genes nearby prophage*
* based on Virsorter or PHASTEST annotation data
evgsA, evgsS
Escherichia coli mdtA
emm49
emrY, emrK, evgA, evgS
emrY
E. coli acrAB-tolC with marR mutations
cpxA
0
1
2
3
4
5
6
7
8
9
10
Environment
Animal
N. of E. coli strains

Poster zone 3

Sardines

1693 – Towards a design framework for systems thinking in One Health education

Thomas-Julian IRABOR, Nicolas ANTOINE-MOUSSIAUX
University of Liège, Belgium

Background - One Health education increasingly calls for systems thinking, yet the term often carries broad ambition without clear guidance for educational design. In many teaching settings, systems thinking is presented as a topic to introduce or a mindset to encourage, while the learning conditions that help learners express it in visible, discussable ways remain fuzzy. A stronger educational foundation requires a clearer account of what should be designed into the learning environment so that learners can make system relations, constraints, responsibilities, and consequences explicit in collective work.

Methods - The framework was developed through a comparative interpretive synthesis of six educational studies examining serious games, simulations, and structured group activities in public health-related training. Cross-case analysis focused on how activity design and debrief conditions shaped the public expression of systems-oriented explanation, justification, and responsibility in recorded group discussion.

Results - Together these studies suggest a conceptual framework for designing systems thinking in One Health education as a form of publicly articulated reasoning. In this framing, systems thinking becomes visible when learners must explain how actions unfold across time, justify decisions under constraint, and connect immediate choices to wider effects in front of others. The central educational task is to create conditions that support this kind of explanation in a structured and inspectable form.

The framework defines five linked design conditions. Shared representations provide a common reference point, such as a map, board state, timeline, or written trace, that allows participants to examine relations, follow change, and test claims against visible evidence. Visible constraints, including time pressure, limited resources, partial information, and competing priorities, make trade-offs explicit and give decisions practical consequence. Organised responsibilities clarify who is expected to notice, decide, justify, and respond, making interdependence and accountability part of the learning situation. Reflection prompts focused on sequence, reasons, and expected consequences support explanation of persistence, delay, accumulation, and changing options over time. Implementation fit addresses whether these supports remain usable in routine teaching conditions, including clarity, visibility, audibility, and ease of use.

Conclusions - Together, these conditions define a configuration for learning environments that can support systems-oriented explanation in multidisciplinary settings. Serious games, simulations, mapping tasks, and other structured collaborative activities become educationally valuable when they help learners make their reasoning explicit through shared evidence, defined responsibilities, and time-linked consequences. The framework offers a basis for the design, study, and evaluation of One Health teaching activities by specifying the pedagogic conditions under which systems thinking becomes observable in group learning. It also supports clearer reporting of educational design, making it easier to judge when learners are being asked to engage with complexity in ways that are concrete, accountable, and open to collective scrutiny.

1700 – Does exposure to animals affect the infant gut microbiome? Case study of 6-18 month old children in Esmeraldas Province, Ecuador

Viviana ALBAN (1), Kelsey J. JESSER (1,2), April M. BALLARD (3), Caitlin HEMLOCK (1), Christine S. FAGNANT-SPERATI (1), Janet K. HATT (4), Erica R. FUHRMEISTER (1), Joan A. CASEY (1), Gwenyth O. LEE (5), Gabriel TRUEBA (6), Joseph N.S. EISENBERG (7), Konstantinos T. KONSTANTINIDIS (4), Karen LEVY (1)
1: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, Washington, United States of America; 2: Department of Environmental Health Sciences, University of Georgia, Athens, Georgia, United States of America; 3: Department of Population Health Sciences, Georgia State University School of Public Health, Atlanta, Georgia, United States of America; 4: School of Civil and Environmental Engineering and School of Biological Sciences, Georgia

Institute of Technology, Atlanta, Georgia, United States of America; 5: Rutgers Global Health Institute and Department of Biostatistics and Epidemiology, Rutgers University, New Brunswick, New Jersey, United States of America; 6: Instituto de Microbiología, Colegio de Ciencias Biológicas y Ambientales, Universidad San Francisco de Quito, Quito, Ecuador; 7: Department of Epidemiology, University of Michigan School of Public Health, Ann Arbor, Michigan, United States of America

Early-life exposure to animals represents an important pathway through which infants encounter environmental microbes that may influence their gut microbiome development. In many low- and middle-income countries (LMICs), domestic animals are closely integrated into household environments, increasing opportunities for microbial exchange between animals and household members, including infants. However, the influence of animal exposure on the infant gut microbiome in these settings has not been well-studied, particularly in early developmental stages. We analyzed data from a longitudinal birth cohort in Esmeraldas Province, Ecuador, to examine associations between animal exposure and infant gut microbiome outcomes during the first 18 months of life. Infant stool samples collected at 6, 12, and 18 months were characterized using 16S rRNA gene amplicon sequencing. Animal exposure was assessed using animal pathway-specific metrics, including animal ownership, number of animals owned, the presence of animals or animal feces in household environments, and maternal or infant contact with animals, as well as a composite score that integrated all metrics. We used regression models to evaluate both cross-sectional and 6-month lagged associations with within-host Shannon alpha diversity, between-host Bray-Curtis beta diversity, and differential taxonomic abundances. We found that higher animal exposure scores at 12 months were associated with greater gut microbial alpha diversity both cross-sectionally ($\beta = 0.18$; 95% CI: 0.01–0.37) and at 18 months ($\beta = 0.22$; 95% CI: 0.001–0.44). Exposures involving animals or animal feces inside the household and maternal–animal contact were most closely aligned with alpha diversity patterns in the same time windows (12 months animal exposure score and 12- and 18-months Shannon alpha diversity). Shifts in beta diversity with varying animal exposure score and pathway-specific metrics were not evident (PERMANOVA: $p > 0.05$), suggesting that animal exposure did not drive large-scale restructuring of the microbiome. Differential abundance analyses indicated changes in a few specific taxa associated with animal exposure metrics. Number of animals owned, a proxy for animal density, showed the strongest associations with microbiome taxa, including increased abundance of both potentially beneficial taxa (e.g., short-chain fatty acid (SCFA)-producing families like the *Oscillospiraceae* and *Ruminococcaceae*) and those associated with potential dysbiosis (e.g., the *Enterobacteriaceae*). Enrichment of SCFA-producing taxa with increased animal exposure was a consistent pattern across all time windows and multiple metrics of animal exposure. These findings suggest that animal exposures may shape infant gut microbiome development through both immediate and sustained effects, with exposures at 12 months associated with within-host microbial diversity patterns that persist into later developmental stages, while also introducing microbes with both potentially beneficial and detrimental functions.

1704 – A One Health approach to climate-driven malnutrition in the Koribari char, Gaibandha District, Bangladesh

Mouhamadou WILANE (1), Ramatoulaye SALANE (1), Mamy Navalona ANDRIAMIHAJARIVO (1), Mohammad Sakhawat HOSEN (2), **Nicolas ANTOINE-MOUSSIAUX** (1)

1: University of Liège, Belgium; 2: Friendship NGO, Bangladesh

Background

Bangladesh is one of the world's most climate-vulnerable countries, ranked 7th on the Global Climate Risk Index. The chars are riverine islands, harboring communities (5% of global population) that face compounded risks of flooding, drought, riverbank erosion, and geographic isolation. Public and non-governmental actors intervene in such disaster-stricken zones to assist communities, aiming to build resilience and robustness. This study investigates such a complex situation in the Char of Koribari to analyze those actors' actions and reflect on the need for a One Health approach in precarious environments.

Methods

A qualitative case study was conducted in the Koribari char, combining a review of scientific and grey literature (NGO reports), 14 semi-structured individual interviews with multisectoral professionals spanning human, animal, plant, and environmental health, 7 gender-stratified focus groups with

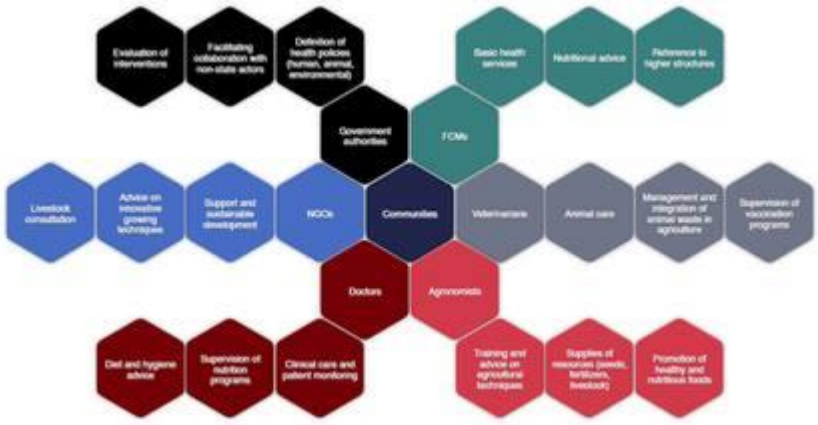
community stakeholders, and participant observation documented through field notes and photographic records. Data were analyzed using a thematic coding framework anchored in a framework of resilience, defined as an ability to restore an equilibrium after major disruptions of essential functions in the community, and robustness, defined as an ability to absorb shocks and adapt while maintaining essential functions in the community.

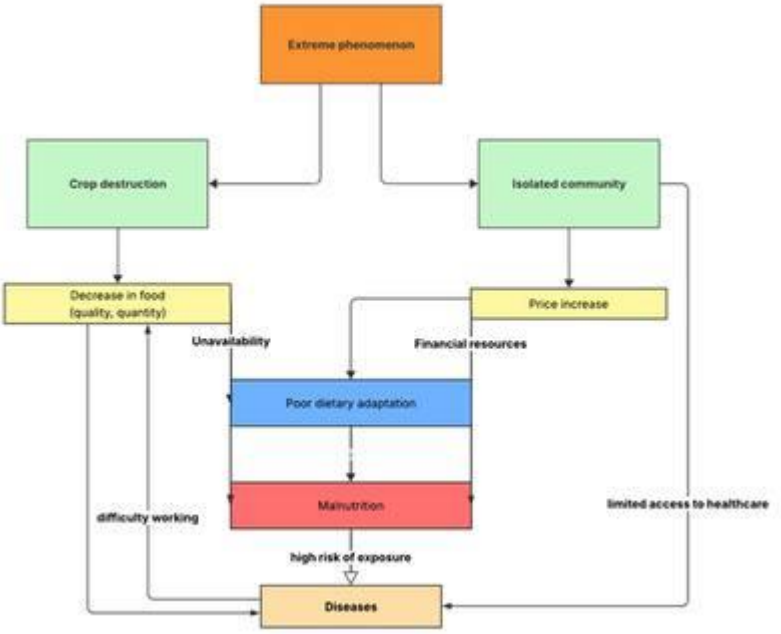
Results

Communities consistently described extreme climate disruptions of agricultural livelihoods (crops and livestock), limiting dietary diversity, increasing food prices, and impeding access to healthcare, particularly for pregnant women and children. A functional network of community actors trained by an NGO to serve as community health workers (FCMs), agronomists, veterinarians, NGO staff, and government extension services, provides complementary responses. An integrative approach has gradually emerged, mainly originating from the NGO actions, with a central role of FCMs and the development with communities of adaptation strategies facing extreme events. This integrative model is mainly characterized by interdisciplinarity within the NGO and transdisciplinarity by co-designing solutions with communities. However, these innovations remain fragile, relationship-dependent, and contingent on NGO continuity, mainly suffering from a lack of the multi-sectoral and multi-level action that define One Health. In particular, facing the dual burden of malnutrition and lack of access to health care, a priority appears in the set-up of intersectoral policies linking health and agriculture at national and district level, limiting the synergies needed for sustainable nutritional responses and undermining community resilience and robustness over time.

Conclusion

Formally adopting a One Health approach may significantly reinforce an already integrative action model that has been developed by NGO actors. Three structural reforms are necessary to sustain and scale these achievements: (i) national-level advocacy for a multisectoral nutrition-climate policy framework; (ii) the creation of formal intersectoral Technical Working Groups (TWGs) joining governmental and non-governmental actors; (iii) and the participatory co-development of culturally adapted integrated guides combining climate-smart agricultural practices and nutritional health messaging.





1707 – Characterizing the distribution patterns of pathogen nucleic acids and host antibodies on malaria rapid diagnostic test strips

Graham MATULIS (1,2,3), Nicole CHEN (1,3), Abigail A LILAK (1,2,3), Kellie GOODNIGHT (1,2,3), Ian PHSEA-SMITH (1,3,4), Modesto CRUZ (5), Alexandre EXISTE (6), Jacques BONCY (6), Bernard OKECH (7), Michael E VON FRICKEN (1,2,3)

1: One Health Center of Excellence, University of Florida, Gainesville, Florida, United States of America; 2: Department of Environmental and Global Health, University of Florida, Gainesville, Florida, United States of America; 3: Emerging Pathogens Institute, University of Florida, Gainesville, Florida, United States of America; 4: Spatial Epidemiology & Ecology Research Laboratory, Department of Geography, University of Florida, Gainesville, Florida, United States of America; 5: Institute of Microbiology and Parasitology (IMPA), Faculty of Science, Autonomous University of Santo Domingo (UASD), Santo Domingo, Dominican Republic; 6: Laboratoire National de la Sante Publique, Ministere de la Sant e Publique et de la Population, Port-au-Prince, Haiti ; 7: Department of Preventative Medicine and Biostatistics, Uniformed Services University, Bethesda, Maryland, United States of America

Background: The continual emergence and re-emergence of infectious diseases necessitates consistent surveillance activities to reduce public health impact. However, surveillance capacity in many countries is absent or has been interrupted due to sociopolitical unrest, resulting in significant knowledge gaps. Malaria rapid diagnostic tests (mRDTs), which are widely used in malaria-endemic regions, contain small amounts of blood that may be repurposed for surveillance. Here, we analyze the distribution of pathogen nucleic acids and host antibodies throughout the mRDT strip.

Methods: HRP2-positive mRDTs were collected from Haiti between 2023-2024 and were used to assess for the distribution of Plasmodium DNA. Commercially available HRP2-based mRDTs were purchased to characterize the distribution of dengue (DENV-4) or irradiated Marburg (MARV) RNA by applying blood spiked with either virus. Total nucleic acids were extracted from either the entire mRDT strip or subsections of the mRDT strip. The distribution of pathogen DNA or RNA throughout the strip was analyzed using real-time RT-qPCR. To assess the distribution of antibodies through the mRDT, we used both mRDTs from Haiti and commercially sourced mRDTs to which blood spiked with a pooled antibody solution was applied. Proteins were eluted from either the entire mRDT strip or subsections of the mRDT strip overnight in PBS. Antibody presence was assessed using the MagPix system.

Results: We confirmed the ability to obtain pathogen DNA, RNA, and human antibodies by processing the whole mRDT strip. Processing separate subsections of the mRDT demonstrated that Plasmodium DNA and MARV RNA were present throughout the strip, while DENV RNA was only present in the results window and the distal absorbent pad. Host antibodies were found exclusively in the distal absorbent pad. Further

mapping analyses of the distal absorbent pad demonstrated that while antibodies were present throughout the subsection, DENV and MARV RNA were only consistently detected in the first half of the distal absorbent pad.

Conclusions: Characterizing the distribution patterns of these surveillance molecules throughout mRDTs provides proof-of-concept evidence for their use as a viable, alternative sample source. Importantly, the ubiquitous use of mRDTs in healthcare centers within malaria-endemic countries represents a passive source for samples which, using this sample processing pipeline, can enhance pathogen surveillance efforts in under-characterized regions.

1710 – Evaluation of Integrated Kyasanur Forest Disease Surveillance System (Human, Animal, and Vector Surveillance) in Karnataka, India, 2025

Pooja JAYAPAL (1), Arushi GHAI (2), Padma M R (3), Ramesh CHANDRA (1)

1: National Centre for Disease Control, Delhi, India; 2: South Asian Field Epidemiology Network, India; 3: Department of Health and Family Welfare, Karnataka, India

Background:

Kyasanur Forest disease (KFD) is a viral, hemorrhagic, tick-borne zoonotic disease, transmitted by *Haemaphysalis spinigera* ticks with small-mammals and monkeys serving as hosts, and humans as dead-end hosts. KFD is only reported from India, and was first identified in 1956 in Karnataka, but is now endemic in five states along India's Western-coast. It presents with biphasic symptoms (haemorrhagic and neurotropic), and no approved antiviral treatments available. KFD is a neglected tropical disease and public health threat in India with expanding geographic range and recurring outbreaks. Monkey death acts as trigger-event for human, and vector surveillance. Annually 400-500 KFD human cases are reported under the Integrated Disease Surveillance Program (IDSP), a national digital platform. We evaluated the integrated KFD surveillance system (Human, Animal, Tick) with a One-Health approach to identify strengths and gaps.

Methods:

We conducted a mixed-methods study (July-August 2025) across all healthcare levels in two high-burden districts in Karnataka (Shivamogga and Chikmagaluru). Using the US Centers for Disease Control and Prevention (CDC) and Morbidity and Mortality Weekly Report (MMWR) guidelines, we evaluated the human surveillance system through stakeholder interviews, record reviews, and observational checklists. We conducted qualitative key informant interviews to evaluate animal and vector surveillance systems. Data was analyzed for frequencies and proportions, and key informant interviews were analyzed using a thematic framework.

Results

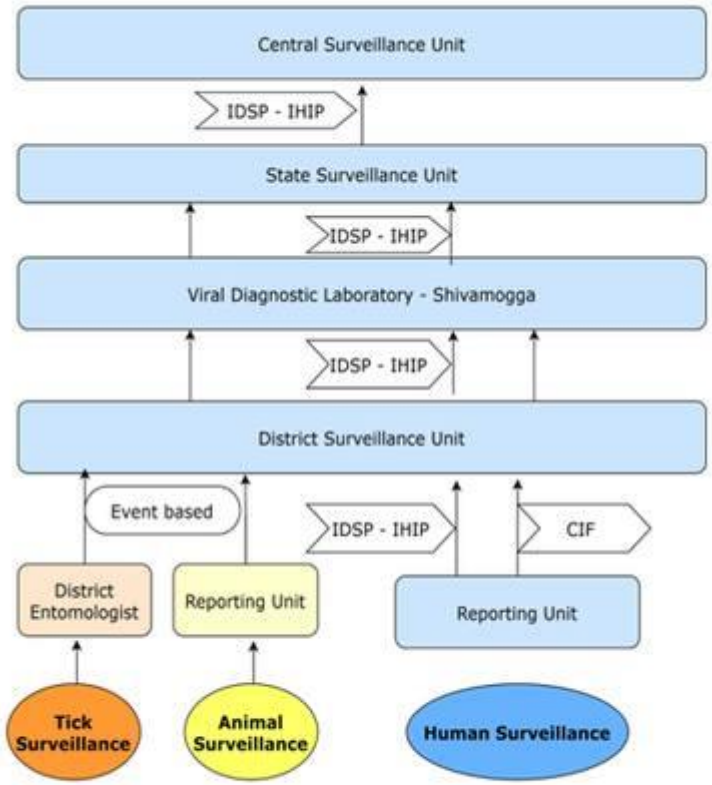
In human surveillance system, 75% healthcare-workers found case definition and reporting process simple. All (100%) cases from reporting units were reported on IDSP, but 43% units had complete human-surveillance registers, and all case-investigation forms were incomplete. We noted a lack of documentation on follow-up for disease progression and system-feedback, and 50% of staff were trained in KFD surveillance, prevention and control activities. Median delay from case detection to sample collection was 2 days (interquartile-range 1-3 days). Qualitative interviews indicated that surveillance system is mainly human-health driven with limited intersectoral-coordination and data-sharing within sectors across stakeholders and healthcare levels. There were no structured, standardized data collection and reporting formats with poor recordkeeping in animal and vector surveillance systems.

Conclusion:

The KFD human-surveillance system in Karnataka is simple, showed good reporting, with gaps in data quality and training. System lacked intersectoral-coordination and active stakeholder participation across levels. We recommend adopting a One-Health approach with shared ownership and equal participation by all stakeholders across healthcare levels, with clearly defined responsibilities, standard operating procedures (SOPs) for timely data sharing, and established data flows for digitalized vector and animal surveillance data. We integrated the event-alert system for monkey-death surveillance with the existing digital platform for animal patrolling (e-Gastu), revised the SOPs for routine tick collection, and

updated the reporting formats for human, animal, and tick surveillance, which were incorporated in the revised guidelines for integrated KFD surveillance.

Fig 1: Surveillance data flow in the KFD surveillance system



IDSP–IHIP - Integrated Disease Surveillance Program – Integrated Health Information Platform

CIF – Case Investigation Form

Table 1. KFD Human Surveillance System Evaluation in high-burden districts of Karnataka, India 2025 (using CDC MMWR guidelines)

S. No	Indicator	Observation
1.	Proportion of respondents with knowledge of case definition	75%
2.	Proportion of respondents aware of suspected case response	75%
3.	Proportion of health care workers finding the case-reporting process simple	85%
4.	Proportion of case reports included in the national surveillance platform	100%
5.	Proportion of staff trained in KFD prevention and control activities	62%
6.	Median between case detection and collection of samples	2 days
7.	Median time between sample collection and reporting results	1 day
8.	Proportion of outbreaks investigated	100%
9.	Proportion of duplicate case entries	3.6%
10.	Proportion of completed human surveillance registers	42.8%

Table 2: Themes and Key Findings of the Animal Surveillance System evaluation

S. No	Themes	Key findings
1.	Monkey death reporting	No intentional delay in reporting monkey death
2.	Barriers in animal surveillance	No structured animal surveillance data flow
3.	Intersectoral coordination	At the block and district levels, challenging and fragmented
4.	Standardised protocols	No standardized documentation for monkey deaths or sample collection.
5.	Community awareness	Good awareness, but gaps in understanding its transmission.

1714 – Mosquito Borne Disease Risk Assessment in Urban Water Buffers: A Field Study in Rotterdam, The Netherlands

Sille PELSER (1,2), Jordy VAN DER BEEK (3,4), Pauline A. DE BEST (1), Erley LIZARAZO FORERO (1), Marieta BRAKS (3,5), Marion KOOPMANS (1), **Maarten SCHRAMA** (3), **Gregorius J. SIPS** (2), **Reina S. SIKKEMA** (1)

1: Erasmus MC, Viroscience, Rotterdam, the Netherlands; 2: Public Health Service Rotterdam-Rijnmond, Rotterdam, the Netherlands; 3: Institute of Environmental Sciences, Leiden University, Leiden, the Netherlands; 4: Naturalis Biodiversity Center, Leiden, the Netherlands; 5: National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands

Introduction In response to climate change, climate adaptation measures are gaining momentum, leading to the rapid development of blue spaces such as urban water buffers. These blue infrastructures are designed to mitigate the impacts of extreme weather events. However, by creating (temporary) standing water, they may unintentionally provide breeding habitats for mosquitoes, which can be vectors of infectious diseases. Yet, little is known about the contribution of urban water buffers to mosquito abundance and related vector-borne disease risks. This study aims to assess mosquito presence and breeding in urban water buffers in the Rotterdam-Rijnmond region.

Methods A comparative longitudinal field study was conducted between June and October 2025. Seventeen water buffer locations in the Rotterdam-Rijnmond region were selected, including six above-ground systems (wadis and water squares) and eleven underground systems (water basins and infiltration crates, with subsurface areas ranging from 88-4450 m²). During three sampling rounds (16–17 June, 11–12 August and 6–7 October 2025; between 1-7 days after last day with >1mm precipitation), locations were inspected for the presence of water. Where present, sampling was performed at three manholes per system. Per manhole, adult mosquitoes and larvae were collected using an electric mosquito aspirator (60 s) and dipper (10 dips, total volume 3500 mL), respectively. In addition, 500 mL of water was collected for environmental DNA analysis. For each system, a nearby conventional storm drain was sampled as a reference site. Mosquito larvae and adults were morphologically identified and quantified in the laboratory. Water samples were filtered and tested for mosquito DNA using a mt-cox1 qPCR assay. Statistical analyses were performed in R.

Preliminary results None of the above-ground systems contained water at any of the three sampling rounds, whereas water was present in all underground water buffers (range 0-95 cm). Adult common house mosquitoes (*Culex pipiens*) were found in 9/11 underground locations (82%), with mosquito counts ranging from 1-104 individuals per manhole, and larvae in 6/11 locations (55%). However, the abundance of both larvae and adults was higher in the reference (conventional) storm drains. The current results are based on field observations; laboratory analyses will be available at the time of the congress.

Conclusion Underground, rather than above-ground, water buffers serve as breeding habitats for mosquitoes. Although larvae and adult mosquito abundance at sampled manholes are lower compared to the conventional stormwater network, the much larger subsurface area of these systems suggests their overall contribution may be underestimated. Future research is needed to assess whether these systems attract the tiger mosquito (*Aedes albopictus*), which, unlike the common house mosquito, may prefer

their relatively clean water. This potential risk highlights the importance of a One Health approach that integrates vector-borne disease risks into urban climate adaptation measures.

1719 – Unity Without Uniformity: Epistemic Pluralism and Knowledge Integration in One Health

Chikumbusko MTEGHA
Lilongwe University of Agriculture and Natural Resources, Malawi

Background

One Health is widely promoted as an integrated approach linking human, animal, and environmental health through multisectoral collaboration. However, many One Health initiatives struggle with interdisciplinary coordination despite strong institutional support. A key reason may lie in how knowledge integration itself is understood within global policy frameworks. While these frameworks emphasise shared data systems and coordination mechanisms, they rarely address how the different knowledge traditions involved in One Health—biomedical science, veterinary public health, ecology, and the social sciences—can be meaningfully integrated. This gap has implications for how One Health knowledge is produced, taught, and applied.

Methods

This study combines philosophy-of-science informed conceptual analysis with document analysis of core global One Health policy frameworks, including the One Health Joint Plan of Action (2022–2026) and the Tripartite Zoonoses Guide. Documents were examined using a directed qualitative coding framework derived from philosophy-of-science concepts: epistemic pluralism, incommensurability, evidence hierarchies, boundary objects, and systems epistemology. Passages referring to "integration," "evidence," "risk," and "knowledge" were coded to identify implicit assumptions about how disciplinary knowledge is expected to interact in One Health implementation.

Results

Analysis revealed a recurring epistemic pattern structured around three core assumptions: unity, commensurability, and neutrality. Policy texts describe One Health as an "integrated and unifying approach," implying that different knowledge systems can converge within a shared epistemic framework. They also assume commensurability—that evidence from different sectors can be combined within common decision processes. The Joint Plan of Action repeatedly emphasises "scientific evidence and risk assessment," implicitly privileging biomedical and epidemiological paradigms. A third assumption frames integration as technical coordination rather than epistemic negotiation. Social science and community knowledge, while acknowledged, are positioned to enable implementation rather than contribute equally to knowledge production.

Conclusions

Rather than pursuing epistemic uniformity, One Health may be more effective when understood as a framework for structured epistemic pluralism. An "epistemic charter" is proposed for interdisciplinary projects: a document specifying evidential standards, causal assumptions, and knowledge forms contributed by different disciplines and communities, with procedures for negotiating disagreements and synthesising evidence. Combined with interdisciplinary evidence portfolios and explicit training in evidential pluralism for One Health professionals and students, this approach can strengthen knowledge integration across disciplines and communities.

1723 – The first National Action Plan on antimicrobial resistance in Senegal: operationalisation and impacts on One Health governance capacity

Mouhamadou Moustapha SOW (1,2), Marion BORDIER (3), Mamadou CISS (2), Cécile AENISHAENSLIN (4)
1: Gaston Berger University, Senegal; 2: National Laboratory for Livestock and Veterinary Research, Senegalese Institute of Research in Agriculture, Senegal; 3: ASTRE, University of Montpellier, CIRAD, INRAE, Montpellier, France; 4: Department of Pathology and Microbiology, Faculty of Veterinary Medicine, University of Montreal, Canada

Background

Antimicrobial resistance (AMR) is a major global health challenge occurring at the human–animal–environment interface and disproportionately affecting sub-Saharan Africa. Addressing AMR therefore requires coordinated governance across sectors in line with the One Health (OH) approach. In response, many countries have adopted multisectoral national action plans (NAPs) aligned with the Global Action Plan on AMR. However, limited evidence exists on how these plans are operationalised and how they influence OH governance capacities. This study assessed, from a systemic perspective, the implementation of Senegal's first AMR NAP (2018–2022) and its effects on OH governance capacities.

Methods

A qualitative approach was used, combining 12 semi-structured interviews conducted between January 2023 and December 2025 and a participatory workshop held in February 2026, with stakeholders involved in NAP implementation. Workshop participants (14) identified and mapped factors acting as facilitators or barriers to NAP implementation and assessed the effects of the NAP on OH governance capacities using the Network for Evaluation of One Health (NEOH) framework. This framework evaluates six core dimensions of OH—systems thinking, planning, working, sharing, learning, and systemic organisation—on a five-point Likert scale. Interview data were used to deepen the analysis and characterise the overall level of NAP implementation.

Results

Overall, 45% of planned NAP activities were implemented, largely driven by the human health. Approximately 90% of funding originated from international partners, reflecting a strong external financial dependence. Territorial disparities were also observed, with only five of Senegal's fourteen regions benefiting from substantial interventions.

Workshop participants identified 10 factors facilitating implementation and 18 factors constraining it. Interactions among these factors generated three main feedback loops: two reinforcing loops linked to dependence on international partners and institutional fragmentation, and one balancing loop associated with the COVID-19 pandemic.

Regarding governance capacities, the highest scores were observed for *working* (3.2) and *systems thinking* (3.1), followed by *learning* (2.6), *planning* (2.5), *systemic organisation* (2.3), and *sharing* (1). Participants considered that the NAP contributed to improved collaboration and increased awareness of the OH approach in policymaking, particularly through the creation of a multisectoral institutional mechanism, the national One Health platform. However, progress in learning, planning, systemic organisation, and sharing remained limited due to institutional power dynamics, insufficient coordination within and between sectors, and constrained domestic financial resources.

Conclusion

The implementation of Senegal's first AMR NAP contributed to institutionalising the OH framework and strengthening certain collaborative practices. However, it did not produce a full systemic transformation of governance, largely due to persistent sectoral fragmentation, territorial inequalities, and strong reliance on external funding. Strengthening mechanisms for information sharing, intersectoral planning, and systemic organisation will be essential for the 2024–2028 NAP to support more sustainable and effective OH governance in a resource-constrained context.

1735 – Spatial Variation in Antimicrobial Resistance Among Human and Companion Animal Clinical Isolates, Washington State, USA

Hilary MCLELAND-WIESER (1), Hannah FENELON (1), Anna BAINES (1), Vickie RAMIREZ (1), Claire BURBICK (2), Scott J WEISSMAN (3), Erica FUHRMEISTER (1), **Peter RABINOWITZ** (1)

1: Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, USA; 2: Washington Animal Disease Diagnostic Laboratory, Washington State University, Pullman, USA; 3: Division of Infectious Disease, Seattle Children's Hospital, Seattle, USA

Background: Antimicrobial resistance (AMR) is a complex public health challenge, with human, animal, and environmental factors contributing to its emergence and spread. It is recognized as a growing health threat for both humans and animals, emphasizing the importance of understanding its emergence and spread in both human healthcare and veterinary care in order to inform effective antimicrobial

stewardship and prevent AMR spread. The Washington Integrated Surveillance for Antimicrobial Resistance (WISAR) database was developed to address the need for bringing together human, animal, and environmental AMR data. WISAR integrates antimicrobial data from human and animal clinical samples with environmental data to provide insight into AMR trends.

Methods: Data from human and veterinary diagnostic labs in Washington State, USA were integrated to analyze *E. coli* isolates from urine samples from 2015 to 2017. ECOFF values were used to define test results for 6 antibiotics as susceptible or resistant. The percentage of susceptible isolates and 95% confidence intervals for each antibiotic were mapped, aggregated to the level of the first 4 digits of zip codes. Regressions were run to assess regional variation in levels of susceptibility, controlling for species.

Results: Overall levels of susceptibility varied by antibiotic and source species (human, canine, or feline), ranging from less than 20% to more than 80%. In addition, there were notable differences in geospatial patterns of susceptibility, both between antibiotics and across source species within the same antibiotic.

Conclusions: This initial analysis suggests that there are differences in patterns of antimicrobial resistance among clinical *E. coli* isolates in Washington State. Though this data is not suitable for clinical decision making, it can be used as the starting point for additional targeted investigations of AMR trends in the state. In addition, it suggests that the inclusion of additional data sets may further clarify AMR patterns and allow for improved decision making among both human and veterinary public health practitioners.

1746 – Beyond the Label: Are Officially Clean Beaches Truly Safe Under Climate Change?

Adriano A. BORDALO

ICBAS - University of Porto, Portugal

A summer escape to the beach is in the imaginary of millions worldwide. However, are the beaches really safe according to the current European standards? The emergence of aquatic potential pathogens other than of fecal origin due to the increase of water temperature and decrease of sweater salinity poses an immediate risk that, so far, escaped the attention of the legislators.

The health of beachgoers may be at risk even if the beach water is considered safe by means of the two microbiological indicators currently used in Europe (*Escherichia coli* and Intestinal enterococci). The emergence of Vibrios and Aeromonas, native to the aquatic environment, for example, have been identified as potential human pathogens, thriving in marine coastal waters during the warmer summer months in temperate beaches. Besides screening indicators of fecal origin, recent research indicates the need to simultaneously run test on potential pathogenic non-fecal bacteria under the consequences of the current temperature rise worldwide. Indeed, the number of reported outbreaks of bacterial pathogens linked to recreational bathing is on the rise in the Northern Hemisphere. The World Health Organization guidelines on bathing water quality identify naturally occurring microorganisms of possible concern, and acknowledge the need for research to understand the associated microbial ecology. However, the current European Bathing Water Directive (2006/7/EC) only considers the above-mentioned fecal pollution indicators. A dedicates session on the subject will boost the awareness of the positive impact of screening other indicators than of fecal origin to ascertain the fitness for safe bathing of a given beach.

This session could contribute to raising public awareness of the impact that climate change is having on public health, and in this specific case, on beachgoers, and the need to alter the paradigm, including the legislative one, to adapt to this new reality.

Proposed talk titles:

1763 – Farming Practices Shape Rodent Communities and Sin Nombre Virus Risk in Agricultural Landscapes

Laura BUDD, Mathieu PRUVOT

Faculty of Veterinary Medicine, University of Calgary

Background:

Sin Nombre Virus (SNV) is a North American, rodent-borne zoonotic hantavirus, causes Hantavirus Cardiopulmonary Syndrome (HCPS) in humans. Most cases are acquired in peridomestic or agricultural settings. Deer mice (*Peromyscus maniculatus),* the primary reservoir, inhabit diverse environments, including anthropogenically disturbed habitats. While SNV prevalence and HCPS outbreaks can sometimes be predicted by climate and vegetation changes in natural systems, these relationships are poorly understood in agricultural settings. Farming practices, such as harvesting and grazing, alter vegetation structure, which impacts small mammal community composition, population dynamics, and movement, potentially altering SNV transmission risk. Our objective was to evaluate how agricultural land-use type and disturbance regime influence small mammal community composition, host abundance, and the subsequent impact on SNV prevalence and abundance of infected individuals.

Methods:

We conducted a multi-season capture-mark-recapture study from May to October (2024-2025) in Alberta, Canada. We compared three common field types with distinct disturbance regimes (Figure 1). Crop fields (barley and oats) experience severe, abrupt disturbance from harvesting in September. Hay fields (grasses and legumes) are harvested in July/August. Cattle pastures (grasses and legumes) undergo low-severity, longer-duration disturbance from grazing from July through August. Fields were sampled every six weeks for five nights from May to October. Blood samples were screened for SNV using ELISA and PCR.

Results:

We captured a total of 521 individuals from 1,273 capture events, with deer mice and meadow voles (*Microtus pennsylvanicus)* as the dominant species. Community composition differed by field type: crop fields were deer mouse dominated (90% ± 2%), pastures were meadow vole dominated (80% ± 4%), and hay fields showed a more even split. Across field types, deer mouse abundance peaked just prior to disturbance events, resulting in different timing of peak abundance according to harvest and grazing schedules (Figure 2). Overall deer mouse abundance was highest in crop fields. SNV prevalence was highest in crop fields, particularly in spring and fall, with moderate prevalence in hay fields in the fall. The abundance of infected individuals was highest on crop fields in the fall (Figure 3). Infected individuals were predominantly adult, male deer mice.

Conclusions:

Agricultural land use and disturbance regime are drivers of host community structure and SNV dynamics. Crop fields are seasonal SNV hotspots, with the highest risk occurring in fall. These findings demonstrate that specific farming practices shape zoonotic disease risk through their effects on rodent host ecology. This provides insights for targeted SNV surveillance and mitigation in agricultural landscapes and highlights the importance of linking agricultural management, host ecology, and pathogen surveillance in a One Health approach to zoonotic risk assessment.

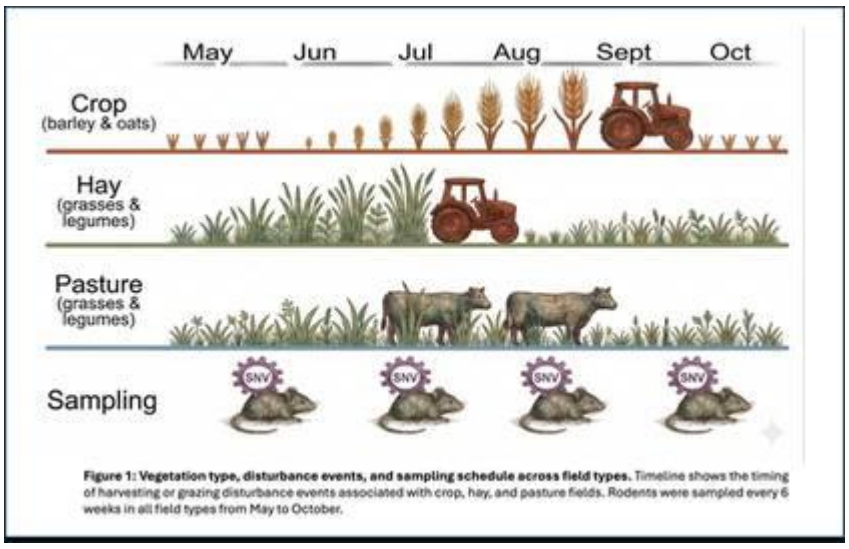


Figure 1: Vegetation type, disturbance events, and sampling schedule across field types. Timeline shows the timing of harvesting or grazing disturbance events associated with crop, hay, and pasture fields. Rodents were sampled every 6 weeks in all field types from May to October.

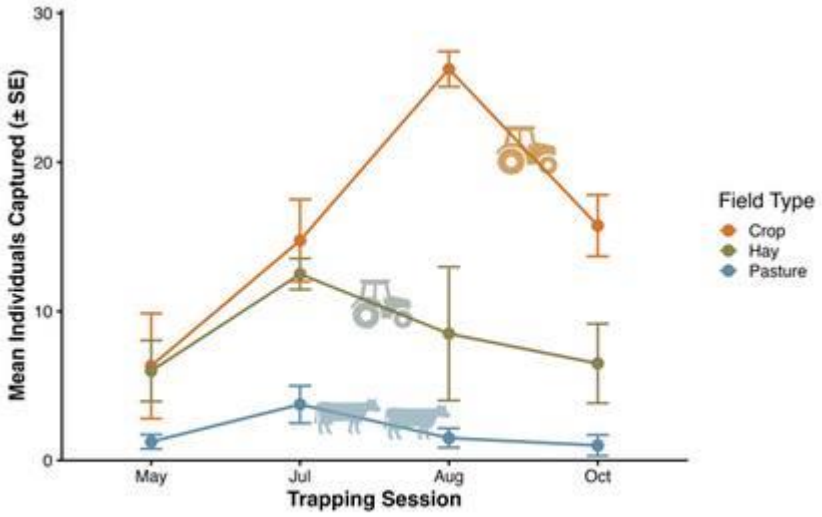


Figure 2: Seasonal deer mouse abundance across field type. Mean individuals (P. maniculatus) captured per session (± SE). Icons mark disturbance timing (tractors=harvest, cows=grazing).

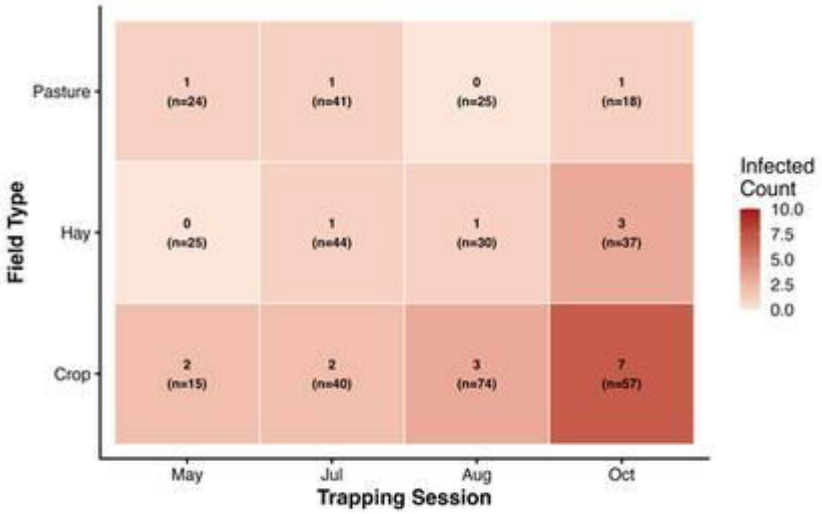


Figure 3: Spatiotemporal Abundance of SNV-Infected Rodents. Heatmap displays total positives detected by field type and trapping sessions.

1766 – From humans and animals to the environment: data sources, methodology, and cross-sector integration in leptospirosis surveillance.

Kellie LIBERA (1), Sarah ROBINSON (2), Katie CLOW (3), Lauren GRANT (3), Scott WEESE (1), Jane PARMLEY (1,4), Claire JARDINE (1,4)

1: Department of Pathobiology, Ontario Veterinary College, University of Guelph, Ontario, Canada; 2: Faculty of Health Sciences, Simon Fraser University, Burnaby, British Columbia, Canada; 3: Department of Population Medicine, Ontario Veterinary College, University of Guelph, Ontario, Canada; 4: Canadian Wildlife Health Cooperative, Ontario Veterinary College, University of Guelph, Ontario, Canada

Background: Leptospirosis is a globally important zoonotic disease affecting humans, domestic animals, and wildlife, with environmental drivers influencing pathogen persistence and transmission. Effective surveillance requires cross-sector integration to support early detection, risk assessment, and coordinated public health action. However, the extent to which leptospirosis surveillance efforts incorporate wildlife and environmental data within operational One Health frameworks remains unclear. This scoping review aimed to describe global leptospirosis surveillance approaches, characterize data types and sources, and assess cross-sectoral integration.

Methods: This scoping review followed a publicly available protocol published in the University of Guelph Atrium repository, Canada, and adhered to the PRISMA-ScR reporting guidelines. A systematic literature

search identified studies whose primary objective was leptospirosis surveillance or monitoring, as defined by the World Health Organization (WHO) and the World Organisation for Animal Health (WOAH). In total, 155 articles published between 2013 and 2023 met eligibility requirements and were included for full data extraction and analysis (Figure 1).

Results: Surveillance activities were frequently research-driven or embedded within established programs and were often initiated in response to human outbreaks. Using a predefined framework, 57% of studies were classified as proactive and 43% as reactive. Surveillance data were derived primarily from biological sampling of humans and animals. Studies focused exclusively on environmental sampling were rare (8%), with environmental information more commonly incorporated indirectly as risk factors. The microscopic agglutination test remained the most frequently reported diagnostic method, while molecular techniques such as polymerase chain reaction were increasingly reported. Humans were the sole focus of 31% of studies, and only 5% fully integrated data across human, animal, and environmental sectors (Figure 2).

Conclusions: This review synthesizes current global leptospirosis surveillance approaches and highlights both methodological diversity and variability in sectoral integration. Although One Health language is increasingly reflected in study design, analysis, and interpretation, operational implementation remains inconsistent across domains and regions. Better alignment between conceptual One Health framing and routine surveillance practice may strengthen cross-sector integration and may improve the consistency, comparability, and long-term effectiveness of leptospirosis surveillance.

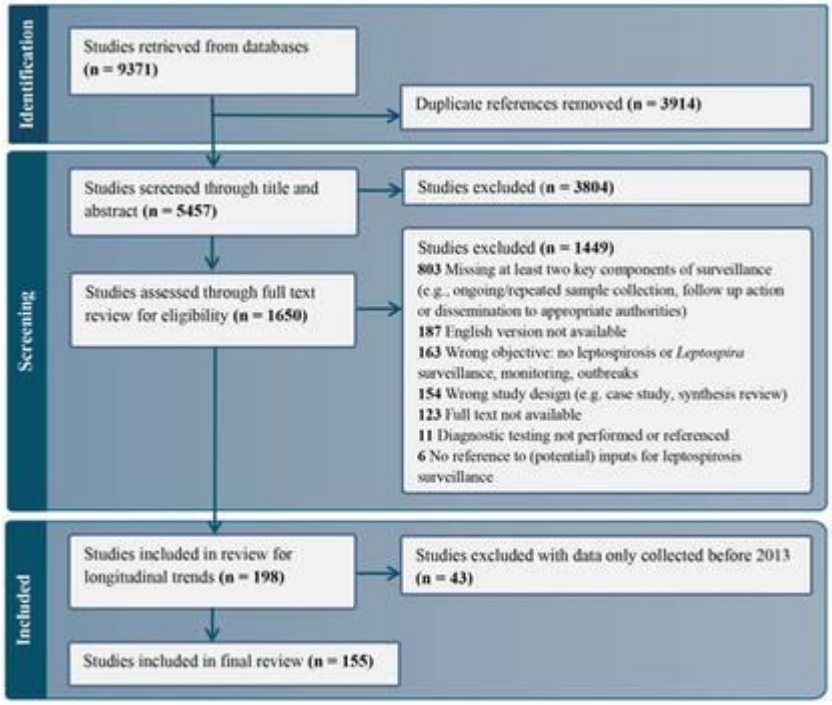


Figure 1: PRISMA flow diagram. Selection process for studies included in the scoping review of leptospirosis surveillance (2013-2023). Numbers correspond to records identified, screened, excluded, and retained for final analysis (n=155).

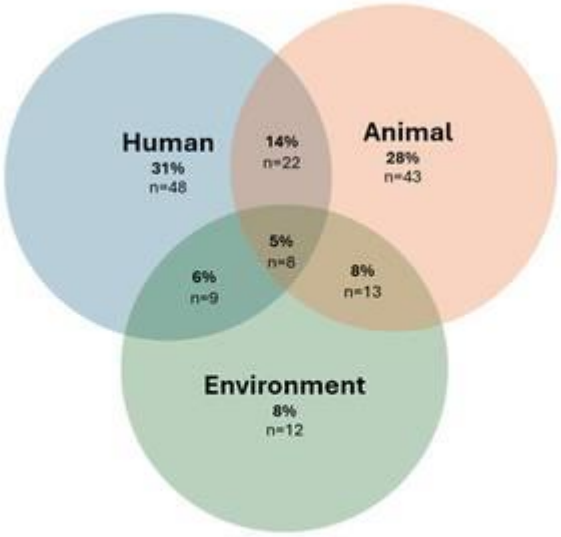


Figure 2: Integration across One Health sectors in leptospirosis surveillances studies from 2013 to 2023 (n=155), as defined by data collected and/or used in analysis. Percentages represent studies addressing each domain independently or in combination

1774 – Inside the Pig Gut: Molecular Detection of Intestinal Microeukaryotes in Farmed Sows from Cyprus

Ana Manuel FIGUEIREDO (1), Christina ZENIOU (2), Marios CHRISTOFOROU (2), Daphne MAVRIDES (2), Alejandro DASHTI (3), Pamela C. KÖSTER (3,4), Rita T. TORRES (1), Anastasios D. TSAOUSIS (5), Sergio SÁNCHEZ (3), David CARMENA (3,6), Eleni GENTEKAKI (2)

1: Department of Biology and CESAM, University of Aveiro, Aveiro, Portugal; 2: Department of Veterinary Medicine, University of Nicosia School of Veterinary Medicine, Nicosia, Cyprus; 3: Parasitology Reference and Research Laboratory, Spanish National Centre for Microbiology, Majadahonda, Madrid, Spain; 4: Faculty of Health Sciences, Alfonso X El Sabio University (UAX), Villanueva de la Cañada, Spain; 5: Laboratory of Molecular and Evolutionary Parasitology, University of Kent, Canterbury, UK; 6: CIBER Infectious Diseases (CIBERINFEC), Health Institute Carlos III, Madrid, Spain

BACKGROUND: Swine diseases can have significant economic impacts on farm production systems, leading to reduced growth rates, lower reproductive performance, and decreased meat quality. The lack of systematic faecal testing for parasitic diseases, along with the reliance on deworming protocols that primarily target helminth infections, results in insufficient monitoring and diagnosis of intestinal microeukaryotic parasites, which remain an ongoing challenge to swine health. Cyprus, an eastern Mediterranean island, depends on the livestock production sector both economically and socially; however, no information is currently available on the occurrence and diversity of intestinal microeukaryotic parasites in farm-raised pigs, which we propose to tackle in this study.

METHODS: The study focused on 15 pig farms in the Nicosia and Larnaca districts, where 100 faecal samples were collected directly from the rectum of sows in June and August 2024. Samples were processed for molecular detection and genotyping of intestinal microeukaryotes, including *Blastocystis*, *Balantioidescoli*, *Cryptosporidium* spp., *Giardia duodenalis*, and the microsporidia *Enterocytozoon bieneusi* and *Encephalitozoon* spp. combining PCR and Sanger sequencing methods.

RESULTS: A total of 92 samples (92.0%, 95% CI: 84.8–96.5) were infected with at least one intestinal microeukaryote. Overall, *Blastocystis* was the most frequently detected agent (68.0%, 95% CI: 57.9–78.0), followed by *B. coli* (60.0%, 95% CI: 49.7–69.7), and, less frequently, *E. bieneusi* (13.0%, 95% CI: 7.1–21.2), *G. duodenalis* (4.0%, 95% CI: 1.1–9.9), and *Cryptosporidium* spp. (3.0%, 95% CI: 0.6–8.5). *Encephalitozoon* spp. was not found in any of the analysed samples. Co-infections were common, occurring in 47.8% of the positive samples, with *Blastocystis* + *B. coli* as the most frequent combination (61.4%, 27/44). All 68 *Blastocystis*-positive samples were identified as potentially zoonotic, pig-adapted subtype ST5, whereas among *B. coli* infections, 49 samples belonged to genotype B and only two to genotype A. While *G. duodenalis* did not yield successful genotyping results, two zoonotic genotypes were identified for

Cryptosporidium: rodent-adapted *C. muris* (*n*=2) and pig-adapted *C. scrofarum* (*n*=1). For *E. bieneusi*, five genotypes belonging to zoonotic group 1were detected: EbpA (*n*=9), O (*n*=6), H (*n*=4), EbpD, and W (*n*=1, each), in both single and mixed infections. According to the sampling month, the sampled sows were more likely to harbour *Blastocystis* in June [χ2 (1, *n*=100) = 4.98, P 0.05] than in August.

CONCLUSIONS: This study represents the first molecular-based epidemiological survey of pig farms in Cyprus, revealing that sows harbour a high diversity and prevalence of potentially zoonotic intestinal microeukaryotes that may impact animal health, production systems, and the health of swine farm personnel. Further research is needed to understand the infection dynamics of these microorganisms within the sows' microbiota at different reproductive stages, including non-pregnant and gestating animals.

1786 – Genomic analysis and evolutionary insights of betacoronaviruses in wild Peromyscus mice and other terrestrial small mammals from southern Ontario, Canada

Jonathan D. KOTWA (1), **Simon P. JEEVES** (2), Lauren CRAWSHAW (3), Winfield YIM (1), Lily YIP (1), Kaela BEAUCLERC (3), Phuc TRAN (1), Will ZHANG (1), Albrecht I. SCHULTE-HOSTEDDE (4), Bradley S. PICKERING (5,6), David L. PEARL (7), Heather M. MURPHY (2), Finlay MAGUIRE (8,9,10), Jeff BOWMAN (3), Samira MUBAREKA (1,11), Claire M. JARDINE (2,12)

1: Sunnybrook Research Institute, Ontario, Canada; 2: Department of Pathobiology, University of Guelph, Ontario, Canada; 3: Wildlife Research and Monitoring Section, Ontario Ministry of Natural Resources, Ontario, Canada; 4: School of Natural Sciences, Laurentian University, Ontario, Canada; 5: National Centre for Foreign Animal Disease, Canadian Food Inspection Agency, Manitoba, Canada; 6: Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, Manitoba, Canada; 7: Department of Population Medicine, University of Guelph, Ontario, Canada; 8: Faculty of Computer Science, Dalhousie University, Nova Scotia, Canada; 9: Institute for Comparative Genomics, Dalhousie University, Nova Scotia, Canada; 10: Department of Community Health and Epidemiology, Dalhousie University, Nova Scotia, Canada; 11: Department for Laboratory Medicine and Pathobiology, University of Toronto, Ontario, Canada; 12: Canadian Wildlife Health Cooperative Ontario-Nunavut, Ontario, Canada

Introduction

Coronaviruses (CoVs) are diverse RNA viruses infecting a wide range of hosts; many are important pathogens of humans and domestic animals. Important human and livestock CoVs within the species *Betacoronavirus gravedinis* (e.g., human coronavirus OC43 [HCoV-OC43], bovine coronavirus [BCoV]) are thought to have rodent origins. However, surveillance and characterization of endemic CoVs infecting rodents and other terrestrial small mammals such as eulipotyphlans (e.g., shrews, moles) is limited in North America, particularly so in Canada.

Methods

Through the Wildlife Emerging Pathogens Initiative (Wild EPI), we surveyed wild rodents and eulipotyphlans in Ontario, Canada. Oral, rectal, or perianal swabs were collected from rodents and eulipotyphlans live-trapped across a gradient of human-modified environments. We used a nested real-time PCR to screen samples for CoVs. Positive samples were subject to partial RNA-dependent polymerase (RdRp) sequencing to identify CoVs, followed by attempted whole genome sequencing. Phylogenetic analyses were performed to characterize the evolutionary relatedness of the viruses identified to known CoVs including *B. gravedinis* viruses. Recovered genomes were assessed for recombination events, and we investigated predicted structural diversity and functional domains of spike proteins. Lastly, we used univariable multilevel logistic regression modelling to examine relationships between host demographics and CoV infection status.

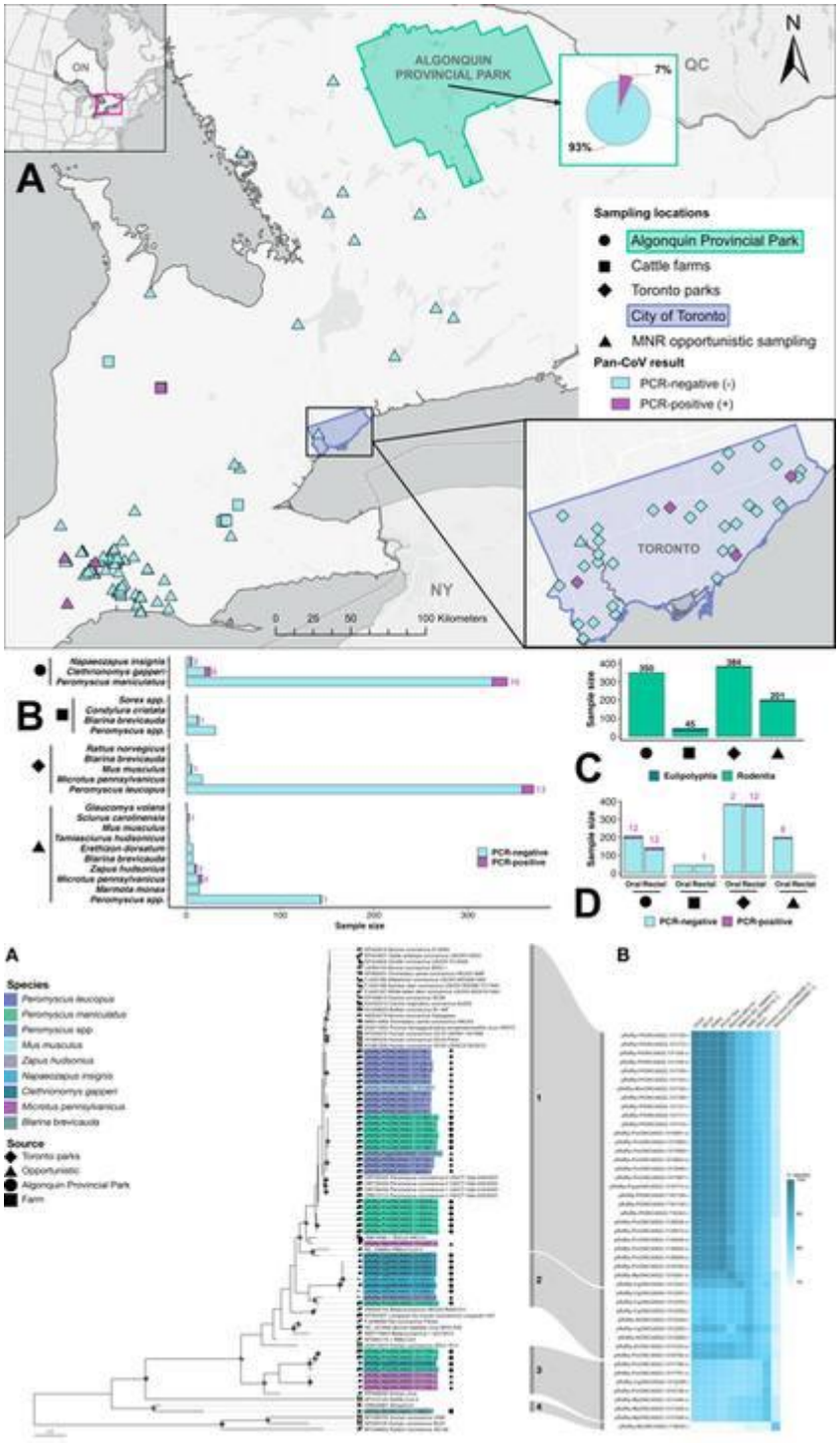
Results

Overall, 4.7% of sampled animals (46/980) were positive by pan-CoV real-time PCR, including 45 rodents (45/956; 4.7%) and one eulipotyphlan (1/24; 4.2%). Partial RdRp sequencing revealed at least four different clades of beta-CoVs spanning multiple host species and geographic locations. Our results suggest low barriers to cross-species transmission of the rodent CoVs identified. Whole *Peromyscus* CoV (PCoV) genomes were recovered from *Peromyscus* mice and were highly related to important human and livestock *Betacoronavirus gravedinis* viruses, including HCoV-OC43 and BCoV. We identified at least three PCoV genotypes resulting from recombination with other *B. gravedinis* viruses, suggesting the occurrence of previous cross-species transmission events. We found high similarity of predicted sialoglycan-binding

sites on the spike glycoprotein structure for PCoV, HCoV-OC43, and BCoV. Univariable regression modelling revealed that *Peromyscus* in Toronto, Ontario had elevated odds of CoV infection for those sampled in the first two years of collection (2021-2022 vs 2023-2024; OR=6.7; 95% CI:1.2 – 33.3; p=0.03) and for those sampled in the spring compared to summer (OR=5.9; 95% CI:1.3 – 25.0; p=0.02).

Conclusions

The present study is the first investigation of endemic CoVs infecting wild rodents and eulipotyphlans in Canada and establishes a baseline for these viruses in Ontario. The CoVs identified bear high similarity to known pathogens of consequence for both humans and other animals. Continued surveillance and viral genomic characterization are necessary to support investigation of the diversity, sylvatic transmission, and evolutionary history of these viruses – a critical step in assessing their risk for human and animal health.



1790 – Characterization of communication strategies in National Action Plans on Antimicrobial Resistance in the Region of the Americas

Augusto BARON CRUZ (1,2), Hafeez HAMZA (1), **Lia Esthefany LOREDO PAZ** (3), Paul Macaulay IZIOMO (4)

1: World Federation of Public Health Associations, Switzerland; 2: University of Washington, United States of America; 3: Universidad Tecnológica Centroamericana, Honduras; 4: Ajisefini Consulting, Nigeria

Background

Antimicrobial Resistance (AMR) has evolved beyond a clinical concern into a systemic risk intersecting climate change, pollution, and biodiversity loss. With 4.71 million deaths recorded in 2021, projections of 39 million by 2050, and USD 50 billion in annual productivity losses, AMR demands urgent, multi-sectoral governance. Effective communication is essential to foster a whole-of-society response, and national action plans (NAPs) are the primary mechanism countries use to guide their response. How NAPs operationalize communication in the Region of the Americas remains understudied. This study aims to describe how AMR NAPs embed vertical narratives across societal levels and horizontal ones across disciplines, empower youth and acknowledge AMR's socio-economic consequences.

Methods

A structured document review using quantitative content analysis was conducted on AMR NAPs from the Region of the Americas (published versions as of August 2024). A pre-defined codebook with closed and open-ended variables was applied independently to each NAP with absent information coded as "undefined".

Results

Fourteen NAPs from 14 countries were reviewed (median publication year: 2018; range 2015-2024). Communication strategies were present in 12 of 14 NAPs (85.7%), all of which had at least one relevant objective.

From those who had a strategy present, none operationalized objectives with measurable (SMART) indicators and no NAP included communication-specific budget details. For NAPs incorporating a monitoring and evaluation (M&E) plan, governmental sources (40%) and academic institutions (20%) were the only sectors identified to be engaged in feedback mechanisms and only 3 of 12 NAPs had evaluation indicators specific to communication. Human health, animal health and agricultural (crop and livestock farming) sectors were engaged in all NAPs, while environmental (75%), pharmaceutical (66.7%) and waste management (33.3%) featured less consistently. Civil society and NGOs engagement were absent in all NAPs. Communication-oriented objectives focused on awareness raising (91.7%) and education/capacity-building (66.7%). The general population was the most targeted audience (91.7%), followed by healthcare professionals (58.3%) such as pharmacists and medical doctors. Youth (13-24 years) were explicitly targeted in only 3 of 12 NAPs (25%). The most common dissemination channels were workshops (64.3%), social media (57.1%), internet portals (57.1%) and television (50.0%). Guidance on message framing, cultural sensitivity or misinformation risk management was absent across all plans.

Conclusions

AMR NAPs in the Americas broadly recognize communication as a strategic pillar of action, yet operationalization remains shallow. Gaps in measurable objectives, dedicated funding, M&E frameworks, youth engagement, and civil society inclusion reveal a disconnect between whole-of-society ambitions and the policy mechanisms in place. Future NAPs must embed accountability, inclusivity and strengthen One Health alignment into their communication frameworks to translate policy commitments into sustained action.

1800 – Understanding West Nile and Usutu infection patterns in African and European free-ranging birds: a systematic review and meta-analysis

Tijmen HARTUNG (1), Eldar N. RAKHIMBERDIEV (2), Frederic BARTUMEUS (3), Alex RICHTER-BOIX (3), Marion P. G. KOOPMANS (1), Reina S. SIKKEMA (1)

1: Erasmus Medical Center, Netherlands, The; 2: University of Amsterdam; 3: Centre for Advanced Studies of Blanes CSIC

West Nile and Usutu virus (WNV, USUV) emerged throughout Europe in recent decades. Wild birds serve as hosts, but host-range and reservoirs are not well understood, which is essential in understanding and predicting virus dynamics and designing targeted surveillance systems. Therefore, this systematic review aims to compile and analyze WNV and USV in free-ranging European and African bird populations.Literature on WNV and USUV surveillance in birds was retrieved from online databases, inclusion followed PRISMA guidelines. We fit phylogenetic multivariate generalized linear mixed models to species with minimal n=16 tested and n=1 positive in dead bird and serological studies. To understand if phylogenetic relatedness dictates infections, we calculated phylogenetic signals using Pagel's λ.

194 studies surveilled European birds and 21 African birds, most birds were sampled in the Netherlands, Italy and Germany, with undersampling in Eastern-Europe, the Balkans and Africa. 93.502 individuals (25 orders, 74 families, 375 species) were tested for WNV, 58.336 individuals (25 orders, 66 families, 272 species) for USUV. Waterfowl, Thrushes, Corvids and Warblers were sampled most often as live birds, Corvids, Thrushes and Doves as dead birds and samples from Corvids, Swallows, Doves, *Accipitridae* and Thrushes were most often tested serologically. Detected WNV prevalences were 0.84% in live birds, 6.80% in dead birds and seroprevalence 2.76%, infection was detected in 77 species across all methods. USUV prevalences were 0.63% in dead birds, 12.10% in dead birds and 6.76% seroprevalence, infection was detected in 46 species across all methods.

No significant WNV or USUV related mortality was detected in orders and families. USUV related mortality was detected in *Cyanistes caeruleus, Turdus merula, Turdus ilicaus, Turdus pilaris,* but not *Turdus philomelos,* near-significant mortality was detected in *Columba palumbus.* No WNV related mortality was detected when controlling for inter-study heterogeneity, when omitted, mortality was detected for *Accipiter genitilis* and *Garrulus glandarius* and near-significant mortality for *Corvus corone* and *Corvus cornnix*. Order and families had no significant deviations in WNV seroprevalences. The order *Accipitriformes* and its family *Accipitridae* showed a significant negative deviation in USUV seroprevalence, indicating infrequent infections. A range of *Accipitridae* and two species of coot showed significant positive deviation in WNV seroprevalence, suggesting frequent infection. *Turdus merula* experienced significant positive deviation in USUV seroprevalence and *Falco tinnunculus* significant negative deviation, respectively, indicating frequent and infrequent infections. Detected low phylogenetic signal for WNV (*order: λdead=0.0051 λserology=0.0054, family: λdead=0.0012 λserology=0.0075*), and USUV (*order: λdead= 0.0052, λserology= 0.0014, family: λdead= 0.0078, λserology= 0.0019*), indicate that phylogenic relatedness does not drive infection.WNV and USUV infections and mortality are likely species-specific rather than phylogenetically driven. Frequently infected birds within *Accipitridae* are undersampled for active infections in live and dead birds. Undersampled regions consist of Eastern-Europe, the Balkan and the African continent.

1802 – Bridging the One Health Education Gap: Academic and Non-Academic Training Pathways in Western Europe and the Western Balkans

Nedjeljko KARABASIL (1), Sara SAVIĆ (2), Olivera BJELIĆ-ČABRILO (3), Ivan VIĆIĆ (1), Aleksandar POTKONJAK (4)

1: University of Belgrade, Faculty of Veterinary Medicine, Belgrade, Serbia; 2: Scientific Veterinary Institute „Novi Sad54", Novi Sad, Serbia; 3: University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia; 4: University of Novi Sad, Faculty of Agriculture, Department of Veterinary Medicine, Novi Sad, Serbia

Background. The One Health (OH) approach has achieved significant global recognition as a key framework for addressing complex challenges at the intersection of human, animal, and environmental health. With the growing importance of interdisciplinary collaboration, education and capacity building have become central to effective OH implementation. In Western European countries, OH is increasingly integrated into formal education through university courses, interdisciplinary degree programmes, and in some cases early initiatives at the secondary school level. In contrast, Western Balkans countries often lack structured academic pathways for OH education. Knowledge dissemination in this region is therefore largely supported by non-academic initiatives, including short training workshops, project-based learning, professional seminars, webinars, conferences, and activities led by international organisations

and non-governmental institutions. Understanding these differences helps identifying gaps and opportunities to strengthen regional OH capacity.

Methods. The current landscape of OH education in Western Europe and the Western Balkans was examined through a comparative review of academic and non-academic educational initiatives. University curricula, publicly available programme descriptions, and OH related training activities were analysed to identify formal courses, degree programmes, and interdisciplinary modules that incorporate OH concept. Non-academic activities (e.g. workshops, professional training programs, and project-based capacity building initiatives) were mapped using institutional reports, project documentation, and other publicly available sources. The analysis focused on differences in educational structures, accessibility, and the sustainability of OH training pathways across the two regions.

Results. Western European countries increasingly incorporate OH principles into formal academic education, including interdisciplinary master's programmes, elective courses within veterinary, medical, and environmental science curricula, and dedicated research training opportunities. These structured programmes support systematic capacity building and foster early interdisciplinary collaboration among future professionals. In the Western Balkans, OH education remains fragmented and predominantly delivered through non-academic mechanisms. Capacity building is often driven by international projects, professional workshops, and short-term training that provide valuable knowledge exchange but may lack long-term institutional integration. While such activities raise awareness and build practical skills, the absence of stable academic programmes limits sustained OH expertise in the region. As a results, OH training is often introduced later in an expert's career, rather than during academic studies, with only occasional standalone university courses as exceptions.

Conclusions. Bridging the gap between academic and non-academic OH education is essential for strengthening regional capacity to address emerging health challenges. Although non-academic initiatives remain important for knowledge transfer and professional development, integrating OH concepts into formal academic curricula in the Western Balkans would support more sustainable interdisciplinary training. Strengthening collaboration between universities, research institutions, and international partners may help facilitate the institutionalisation of OH education and promote a more balanced and resilient educational framework across Europe.

1816 – Human Rift Valley Fever Seroprevalence and Risk Factors for Spillover in Tanzania: Community Epidemiological Findings Supporting Vaccine Preparedness Activities

Sonja MONTANUS (1), Grace MWANGOKA (2), Mwokozi MWANZALILA (2), Woutrina SMITH (1), Ally OLUTU (2), Maximillian MPINA (2), Cheryl MEEHAN (1), Ali HAMAD (2), Ali Mohamed ALI (2), Silas TEMU (2), Robinson MDEGELA (3), Sijali ZINKANKUBA (3), Ana PEROLA-BRANDOA (1), Mac FARNHAM (1), Tracy DRAZENOVICH (1), George MAKINGI (3), Latipha MOHAMED (2), Robert SUMAYE (2), Rosemarie SCHARF (1), Michael WILKES (1), Brian BIRD (1)

1: One Health Institute, University of California, Davis; 2: Ifakara Health Institute; 3: Department of Veterinary Medicine and Public Health, Sokoine University of Agriculture

Background Rift Valley fever virus (RVFV) is a mosquito-borne zoonotic pathogen affecting livestock and humans across Africa and parts of the Arabian Peninsula. Human infection occurs primarily through mosquito bites, but also through contact with infected animals or consumption of contaminated animal products. Large outbreaks, often following heavy rainfall and flooding, can cause severe disease in people and major economic losses due to livestock mortality and abortion storms. Despite these impacts, no licensed human vaccines and limited safe options for use in pregnant livestock currently exist.

The DDvax program is a long-standing One Health initiative to develop a safe and effective vaccine alongside integrated epidemiological research. In preparation for Phase I and II clinical trials in Tanzania, community-based studies have been conducted to better understand virus circulation and identify risk factors for human exposure during interepidemic periods. Complementary program activities include knowledge-attitudes-practices assessments, mosquito surveillance, and livestock sampling. Our study assessed human RVFV seroprevalence and risk factors to support surveillance and vaccine preparedness. Other aspects of the project addressed livestock as well as risk factors and modeling of One Health vaccine interventions in humans and animals.

Methods Community-based cross-sectional surveys were conducted during 2023–2024 across 13 wards in coastal (Pwani Region) and south-central (Iringa and Morogoro Regions) Tanzania. Eligible participants

were aged ≥12 years in coastal sites and ≥8 years in south-central sites and provided informed consent. Demographic characteristics, occupational activities, symptoms, and animal exposure information were collected through standardized questionnaires. Blood samples were tested for RVFV immunoglobulin G (IgG) antibodies using enzyme-linked immunosorbent assay. Occupations were categorized as crop farming, livestock contact, both exposures, or neither. Regional differences in seroprevalence were evaluated, and logistic regression identified geographic, demographic, and occupational risk factors.

Results Serological evidence of prior RVFV infection was identified in both study regions, with higher overall seroprevalence in south-central sites (16.6%) than coastal sites (5.2%). Among 2,349 human participants enrolled (1,503 coastal; 846 south-central), males had higher seroprevalence than females. Seroprevalence increased with age, and individuals engaged in livestock keeping or frequent animal contact had higher prevalence than those with neither exposure. Marked geographic heterogeneity was observed at the community level, including prevalence exceeding 40% in some south-central locations. Testing of livestock from these areas and human IgM serology results are pending.

Conclusions These findings demonstrate ongoing interepidemic circulation of RVFV in Tanzania and identify demographic, occupational, and geographic risk patterns relevant to outbreak preparedness. Higher seroprevalence in south-central regions and among males, older individuals, and those with livestock exposure suggests cumulative risk. Sub-regional variation indicates local ecological and behavioral influences on transmission. Strengthening interepidemic surveillance and targeted prevention in high-risk communities will be important to reduce infection risk and support evidence-based planning for future vaccine deployment.

1824 – From Ecosystems to Epidemics: Invasive Alien Plants Driving Mosquito Feeding Behavior and Disease Risk

Tasneem OSMAN (1,2), Tatenda CHIUYA (2,3), Eric FEVRE (3), Sandra JUNGLEN (4), Christian BORGEMEISTER (2)

1: University of Khartoum- Sudan; 2: Center for Development Research (ZEF) - University of Bonn ,Germany; 3: International Livestock Research Institute (ILRI) -.Kenya; 4: Charité -Universitätsmedizin Berlin ,Germany

Environmental change, including the spread of invasive alien plant species, is a major driver of vector-borne disease dynamics. Vegetation changes can influence mosquito ecology by altering sugar availability, habitat structure, and local microclimates. However, the role of plant-mosquito interactions in shaping mosquito populations and disease risk remains poorly understood.

This study investigated mosquito plant-feeding behavior in Baringo County in the Rift Valley region of Kenya, a semi-arid landscape experiencing rapid environmental change and expansion of the invasive plant *Parthenium hysterophorus*. Mosquitoes were collected from villages with contrasting vegetation compositions, including areas heavily invaded by this species. Specimens were morphologically identified to species level using standard taxonomic keys. Recent plant feeding was assessed using the anthrone assay to detect fructose as evidence of sugar intake. To identify plant sources, DNA was extracted from mosquito samples and chloroplast markers (*matK*, *rbcL*, and *ITS2*) were amplified using PCR and sequenced for plant species identification.

Mosquito sampling revealed a highly diverse community of 48 species representing the subfamilies *Anophelinae* and *Culicinae*. Molecular analysis showed that mosquitoes fed on a wide range of plant species present in the surrounding environment, with the invasive plant *Parthenium hysterophorus* frequently detected in mosquito plant meals. Villages heavily invadedby this plant also showed greater abundance of certain mosquito genera, particularly *Mansonia* and *Coquillettidia*. Mosquito abundance was notably higher during the dry season**,** especially in areas invaded by *P. hysterophorus*, suggesting that invasive vegetation may provide important sugar resources or favourable microhabitats for mosquitoes under arid conditions.

These findings indicate a potential ecological link between invasive vegetation and mosquito population dynamics. The results highlight how vegetation changes in Rift Valley ecosystems may influence mosquito ecology and potential disease risk. Integrating ecological factors such as plant resources into vector surveillance and integrated vector management may strengthen One Health strategies for controlling vector-borne diseases in rapidly changing environments, particularly by addressing how changes in vegetation can affect mosquito habitats and their role in disease transmission.

1833 – Wastewater-Based One Health Surveillance for Seasonal and Zoonotic Influenza A Viruses

Natalie PRYSTAJECKY (1,2), Adrian KENSE (2), Zohaib ANWAR (2), James KWAN (2), Kevin KUCHINSKI (3), John TYSON (1,2), James ZLOSNIK (1,2), Agatha JASSEM (1,2), David MCVEA (1,2), Sarah MANSOUR (1,2)

1: British Columbia Centre for Disease Control, Canada; 2: University of British Columbia; 3: British Columbia Ministry of Agriculture and Food

Background

Influenza A viruses circulate among humans, animals, and the environment, creating ongoing risks of seasonal epidemics and the emergence of new zoonotic strains such as highly pathogenic avian influenza (HPAI). Traditional surveillance relies mainly on clinical and animal health reporting, which may miss early signs of cross-species transmission. Wastewater surveillance provides a population-level approach and can be designed to capture influenza viruses from a broad range of hosts (One Health). In this study, we evaluated wastewater genomic surveillance to characterize circulating influenza A viruses in metropolitan areas and assess its ability to detect both human and animal strains.

MethodsWastewater samples were collected from municipal wastewater treatment plants (n=9) serving urban populations during the seasonal influenza period (6 months). Samples were concentrated, extracted and subjected to probe-based enrichment using a custom One Health influenza probe panel designed in-house using ProbeTools to capture the diversity of influenza A viruses circulating in both human and animal hosts (Kopetzky et al, 2026; Kuchinski et al, 2022). Enriched libraries were sequenced and analyzed to identify influenza A subtypes and genomic signatures present in wastewater samples.

ResultsInfluenza A viral sequences were consistently detected in wastewater during the surveillance period. Genomic characterization identified predominantly human seasonal influenza subtypes, primarily H1 and H3 lineages, with wastewater genomic signals peaking during the seasonal influenza period and corresponding with trends observed in clinical reporting. Limited sequences consistent with avian influenza were detected infrequently and at low abundance. Notably, H5N1 sequences were identified in wastewater from treatment plants serving catchments with H5-positive birds (wild birds and/or poultry farms), with sufficient coverage to recover key HA motif required for HPAI classification. The probe enrichment approach enabled recovery of influenza A genomic fragments sufficient for subtype identification and demonstrated the feasibility of wastewater-based surveillance for detecting diverse influenza A lineages in complex environmental samples.

ConclusionsWastewater genomic surveillance provides a scalable One Health tool for monitoring influenza A viruses in environmental samples and offers the potential to detect zoonotic influenza threats. In this study, we demonstrated that wastewater signals tracked seasonal influenza activity and captured the HPAI H5 sequences in catchment areas associated with locations reporting H5-positive birds. Therefore, probe-based enrichment sequencing can enhance detection, sensitivity, and broaden subtype coverage, supporting integrated surveillance strategies for seasonal influenza and emerging pathogens such as HPAI.

References

Kopetzky J et al. 2026. *J Virol Methods.*

Kuchinski KS et al. 2024. *Appl Environ Microbiol.*

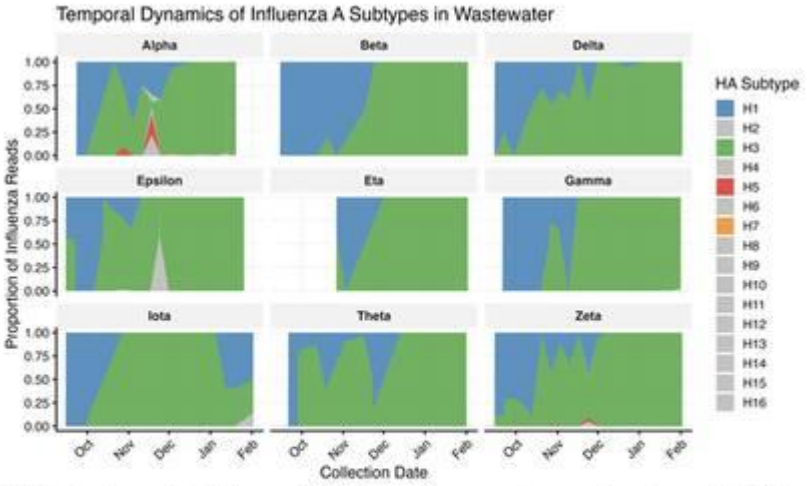


Fig1. Stacked area plot of Influenza A HA subtypes in wastewater over time. Seasonal H1/H3 dominate, with rare avian-origin H5/H7 signals, demonstrating wastewater-based One Health surveillance of seasonal and zoonotic influenza.

1840 – Ecological and Behavioral Drivers of Nipah Virus Spillover in Bangladesh

Ariful ISLAM (1,2), Shusmita Dutta CHOUDHURY (2), Emama AMIN (2), AKM Dawlat KHAN (2), Nabila Nujhat CHOWDHURY (2), Md. Arif KHAN (2), Monjurul ISLAM (1,2), Sarah MUNRO (3), Maryska KACZMAREK (4), Jade K FORWOOD (1), Tahmina SHIRIN (2), Jonathan H EPSTEIN (5)

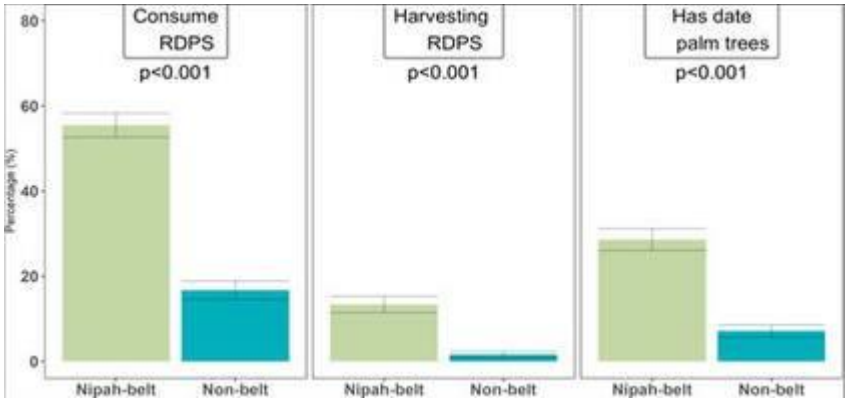
1: Gulbali Research Institute, Charles Sturt University, Wagga Wagga, NSW-2678, Australia; 2: Zoonotic Disease Research Program, Institute of Epidemiology, Disease Control and Research (IEDCR), Mohakhali, Dhaka, 1212, Bangladesh; 3: University of Arkansas, Fayetteville, AR72701, USA; 4: Department of Biology, The City College of New York, The City University of New York, NY USA; 5: One Health Science, Mt Kisco, New York, USA

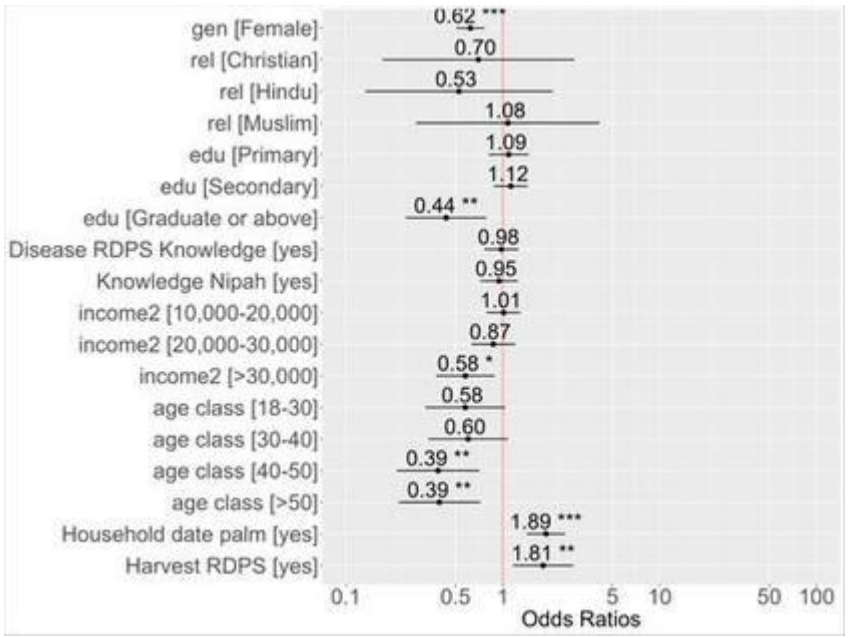
Background: Nipah virus (NiV) is an emerging bat-borne zoonosis causing repeated outbreaks in Bangladesh and India with >70% mortality. NiV spillover from bats into human populations is spatially clustered in Bangladesh's western "Nipah Belt," predominantly linked to consumption of bat-contaminated raw date palm sap (RDPS). However, NiV has been detected in Pteropus medius bats throughout the country, making the drivers of spatial outbreak patterns in human populations unclear. This One Health study aimed to determine how behavioral and ecological factors contribute to spatial differences in NiV exposure and outbreak risk.

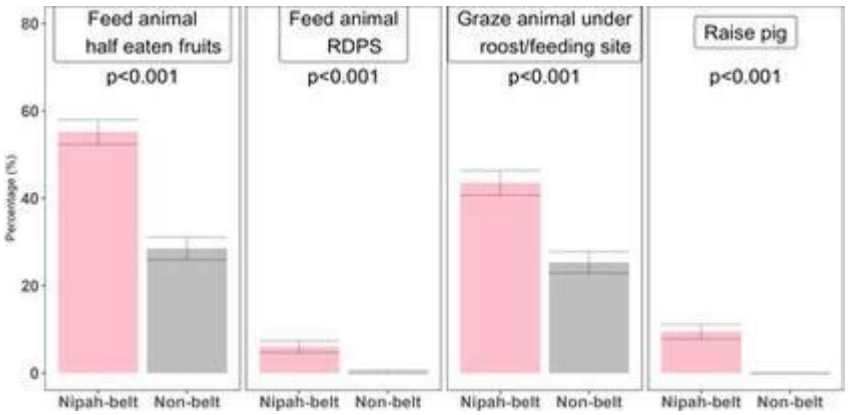
Methods: Between 2022-2023, we conducted a household survey to assess behavioral and ecological risk factors. We administered structured questionnaires from 2,400 individuals (400 per site) across six study districts: three within the Nipah Belt and three in eastern Bangladesh outside the Belt. Sampling was conducted at household level through randomization within communities. We enrolled one participant per selected household, contingent upon informed consent and satisfaction of inclusion criteria.

Results: Our study revealed distinct spatial patterns in human-bat interface behaviors between regions. Households within the Nipah Belt consistently exhibited elevated risk behaviors compared to eastern Bangladesh communities outside the Belt. The most pronounced difference was observed in RDPS consumption, with more than half of Nipah Belt households (55.5%) reporting consumption compared to less than one-fifth (16.8%) outside the Belt. This pattern extended to RDPS-related activities, where Nipah Belt communities showed substantially higher rates of sap harvesting (13.4% vs 1.6%) and date palm tree ownership (28.6% vs 7.2%). Beyond RDPS-related exposures, Nipah Belt households demonstrated significantly higher engagement in other high-risk human-bat interface behaviors. Over two-fifths (43.5%) reported grazing domestic animals under bat roosting sites compared to 15.3% in non-Belt areas. Similarly, consumption of bat-damaged fruits was more prevalent in the Nipah Belt (43.2% vs 29%). All observed differences between regions achieved statistical significance (p0.001). Generalized Linear Mixed Effect Model (GLMM) identified gender, education level, household income, active RDPS harvesting, and date palm tree ownership as significant determinants of consumption patterns.

Conclusions: Significantly higher consumption of RDPS in western regions could conceivably drive the spatial discrepancy in human NiV outbreaks in Bangladesh. However, this does not appear to explain the relationship in its entirety, given that RDPS consumption does occur outside of the Nipah Belt, albeit to a lesser extent. Higher consumption of contaminated fruits remains a plausible pathway for henipavirus and other bat-borne pathogen spillover to humans in Bangladesh. Additionally, the higher proportion of grazing animals under bat roosts and feeding of RDPS and half-eaten fruits to livestock might be key drivers of henipavirus spillover from bats to domestic animals in Bangladesh. These findings highlight the need for targeted One Health interventions addressing multiple human-bat interface behaviors beyond RDPS consumption alone.







1845 – Bushmeat Hunting, Extinction Risk, and Zoonotic Spillover: A One Health Assessment of Critically Endangered Primates in Kenya.

Stanislaus KIVAI, Pauline OTOLI, Samuel MOMANYI, Tonny WAMBUA, Mercy AKINYI
Kenya Institute of Primate Research (KIPRE), Kenya

Bushmeat hunting and consumption are increasingly recognized as major drivers of biodiversity loss and emerging infectious diseases of wildlife origin. Globally, most novel pathogens arise from zoonotic spillover at the human–animal–environment interface, particularly where hunting and wildlife exploitation increase direct contact between humans and wild animals. Non-human primates pose a particularly important risk because their close genetic and physiological similarity to humans facilitates cross-species pathogen transmission. Disease risk and hunting pressure accelerate extinction crisis affecting tropical biodiversity.The Lower Tana River gallery forest ecosystem in Kenya is a globally significant primate conservation hotspot supporting eight primate species, including two endemic and critically endangered monkeys: the Tana River red colobus (*Piliocolobus rufomitratus*) and the Tana River mangabey (*Cercocebus galeritus*). The floodplain forests function as critical ecological refuges for wildlife, livestock, and local communities during seasonal climatic stress, resulting in frequent interactions among humans, livestock, and wildlife.. Nonetheless, empirical evidence linking bushmeat hunting, primate population decline, and spillover risk in this landscape remains limited.This study examined the relationship between primate bushmeat hunting, primate population trends, and zoonotic exposure risks in the Lower Tana River ecosystem using a One Health framework. The study addressed three questions: (1) What are the scale and drivers of primate bushmeat hunting and consumption among communities adjacent to riparian forests? (2) How does hunting pressure influence the population status and spatial distribution of the Tana River red colobus and Tana River mangabey? A mixed-methods approach integrating ecological surveys, socio-economic assessments, and qualitative risk analysis was employed. Primate census survesy were done using quadrant method while household surveys to documented hunting practices, bushmeat consumption patterns and handling prcesses were evaluated using a structured questionnaire. Our results show that 66% of surveyed households reported human–wildlife conflict and it was highest in the mid–Lower Tana (70%). Primate hunting was highest in the mid–Lower Tana (40%). Direct exposure to primate tissues was common: 35% of respondents reported hunting and sharing primate bushmeat, while 5% reported consuming carcasses from injured or dead animals, increasing potential exposure to zoonotic pathogens. Population surveys reveal that, over the past two decades, the mangabey population has declined by approximately 25%. with an estimated remaining population of about 1,650 individuals. Within the mid lower Tana area the mangabey numbers declined from 912 to 105 individuals, while the red colobus declined from 1,075 to 288 individuals, indicating severe localized population collapse.These findings demonstrate that bushmeat hunting in the Lower Tana River ecosystem represents a converging biodiversity and public health crisis. Addressing this challenge requires integrated One Health interventions that combine endangered species conservation, climate-resilient livelihood diversification, improved food security, and strengthened wildlife and zoonotic disease surveillance.

1848 – Medical student impact on one health promotion: a five-year case study

Anna LIAKOPOULOU
International Federation of Medical Students' Assocations

Background:

The One Health approach recognizes the interconnection between human, animal, and environmental health, emphasizing interdisciplinary and community-based responses to complex global challenges. Climate change, environmental degradation, and biodiversity loss increasingly influence health outcomes, highlighting the need for innovative interventions. Youth engagement is recognized as a powerful driver of advocacy, awareness, and local implementation of health promotion initiatives. Medical students, in particular, are uniquely positioned to contribute to these efforts through education, outreach, and collaboration with stakeholders.

The International Federation of Medical Students' Associations (IFMSA) promotes student-led activities in One Health through its Standing Committee on Public Health (SCOPH) and the Environment and Health program. National Member Organizations (NMOs) implement initiatives at local, national, and

international levels addressing environmental determinants of health and Sustainable Development Goals (SDGs). A standardized activity enrollment system allows NMOs to document interventions, receive guidance, and share best practices worldwide. Despite this growing engagement, a comprehensive overview of the scope, thematic focus, and global reach of these initiatives is lacking.

Methods:

A descriptive cross-sectional analysis was conducted on activities enrolled in the IFMSA Environment and Health program between October 2021 and January 2026. Data were analyzed according to eight criteria: (1) thematic area, (2) level of implementation, (3) country or region, (4) duration, (5) methodology, (6) target population, (7) external partner involvement, and (8) alignment with the SDGs.

Results:

Seventy-six activities were implemented across 24 countries: 31 local, 34 national, 10 international, and one regional (Canada–Panama collaboration). In total, 38,853 individuals were directly engaged, primarily the general population and medical students. Most activities aligned with SDG 3 (Good Health and Well-being), with many also contributing to SDG 13 (Climate Action), SDG 4 (Quality Education), SDG 11 (Sustainable Cities and Communities), SDG 12 (Responsible Consumption and Production), SDG 6 (Clean Water and Sanitation), SDG 15 (Life on Land), and SDG 14 (Life Below Water).

Climate change was the most frequently addressed thematic area (53 activities), followed by Water and Sanitation (22), Air Pollution (20), Health Sustainability and Green Hospitals (19), Food Production and Security (9), and Fossil Fuel Divestment (8). Waste management was addressed in only one activity. Further details, including case studies and additional quantitative data, will be presented at the conference.

Conclusion:

Medical students demonstrate strong capacity to implement diverse One Health interventions with measurable community impact. The predominance of climate-focused activities reflects global priorities, while the limited number of regional and international collaborations highlights opportunities for scaling and cross-border partnerships. These findings provide evidence to support youth engagement in One Health policy and advocacy, inform strategies to strengthen student-led initiatives, and guide future efforts in planetary health promotion.

1859 – RIVIH–ROAM: a participatory One Health decision-support framework bridging transmission mapping and multisectoral action for priority diseases in the Democratic Republic of Congo

Justin MASUMU (1), Jean-Jacques MUYEMBE TAMFUM (1), Stéphanie MALTAIS (2)

1: Institut National de Recherche Biomédicale, Congo, Democratic Republic of the; 2: Department of Health Management, Evaluation and Policy, School of Public Health, University of Montréal, Canada

Context

The growing frequency of zoonotic, foodborne, waterborne and vector-borne diseases highlights persistent gaps between epidemiological risk analysis and operational decision-making within One Health systems. While the One Health approach is widely promoted globally, practical analytical tools capable of translating complex transmission dynamics into coordinated multisectoral interventions remain limited. To address this gap, we developed RIVIH–ROAM, an operational One Health decision-support framework that structures disease transmission along five components "**R**eservoir, *I*nterface, Vector/Amplifier/Vehicle, **I**nterface and Host (RIVIH)" and converts identified risk drivers into actionable multisectoral strategies through the ROAM operational matrix (Risk–Operational–Action–Management).

Methods

The framework was applied during a participatory multisectoral workshop conducted in Kinshasa, Democratic Republic of Congo, involving experts from public health, veterinary services, environmental authorities, agriculture, and community sectors. Using structured facilitation based on the "RIVIH model", participants mapped transmission pathways, identified key risk factors, and generated operational interventions for four priority diseases representing distinct epidemiological systems: cholera (waterborne), rabies (zoonotic), salmonellosis (foodborne zoonosis), and malaria (vector-borne). Risk

drivers were subsequently translated into a ROAM operational matrix linking transmission factors to prevention, surveillance, and response actions and responsible sectors.

Results

Across all four diseases, the “RIVIH framework” enabled stakeholders to systematically identify critical transmission interfaces and operational entry points for intervention. For cholera, the model highlighted contaminated water sources, food vehicles, and household hygiene practices as key drivers requiring water safety management, environmental sanitation, and food hygiene surveillance. Rabies analysis identified wildlife reservoirs and dog amplification dynamics as primary transmission pathways, leading to operational priorities including canine vaccination campaigns, management of stray dog populations, and strengthened veterinary biosafety. Salmonellosis analysis revealed complex transmission involving animal reservoirs and environmental amplifiers such as contaminated food, water, soil, and insects, emphasizing the need for improved food safety inspection systems and livestock biosecurity. For malaria, the framework clarified the human–vector–environment cycle and identified environmental management, vector control, and strengthened case management as critical intervention points. The approach consistently generated coordinated multisectoral operational actions spanning prevention, surveillance, and emergency response, demonstrating the practical utility of the “RIVIH–ROAM framework”.

Conclusions

The participatory application of “RIVIH–ROAM framework” demonstrates its potential as a scalable operational tool for bridging epidemiological risk analysis and multisectoral decision-making within One Health systems. By linking transmission pathway analysis with operational planning, the framework provides a structured approach for integrated surveillance, risk prioritization, and coordinated outbreak preparedness. The approach could support the development of national One Health strategies and strengthen decision-support systems for managing complex health threats at the human–animal–environment interface.

1866 – Building an Integrated Data Observatory for Animal Welfare and Wildlife Crime in Colombia: A One Health Analytical Approach

Catalina CRUZ, **Daniela ESTRADA**

ViAnimalis Foundation, Colombia

Background

Animal welfare, wildlife conservation, and environmental governance are critical components of the One Health framework. In Colombia, relevant information remains fragmented across multiple agencies: records on animal abuse, wildlife trafficking, environmental crimes, and biodiversity monitoring are produced independently by environmental authorities, law enforcement, judicial institutions, and research organisations, with no shared analytical infrastructure. This fragmentation limits the generation of evidence for decision-making. Existing legislation, including Law 1774/2016, which recognises animals as sentient beings, and Laws 2111/2021 and 2455/2025 on environmental crimes and animal protection, creates growing institutional mandates that cannot be monitored without cross-sectoral data integration.

Methods

This study employs a two-phase design. The first phase is a systematic regulatory mapping drawing on four source layers: (1) national legislation and executive regulations; (2) prioritised constitutional and administrative court rulings on animal sentience and environmental rights; (3) international instruments, including OMSA standards, the Convention on Biological Diversity, and the Escazú Agreement; and (4) subnational ordinances from Colombia's four largest cities: Bogotá, Medellín, Cali, and Barranquilla, to assess coherence between national frameworks and local implementation. Each gap is assessed across six dimensions: thematic category, affected population, normative basis, responsible actor, urgency, and proposed policy pathway. The second phase inventory existing official data sources, criminal records from the Attorney General's Office, wildlife registries from Regional Environmental Authorities (CAR), biodiversity monitoring systems, and judicial statistics, characterising their scope, format, and accessibility to inform the design of a national integrated observatory.

Results

The process has produced three outputs to date. First, a preliminary inventory of 11 critical normative gaps, including: absence of binding welfare standards for production animals, non-operationalisation of the Sistema Nacional de Protección y Bienestar Animal (SINAPYBA) under Law 2455/2025, lack of a unified companion animal registry, and regulatory ambiguity for aquatic and exotic species. Second, a classification framework systematising each gap by required action type: new legislation, executive regulation, or compliance enforcement. Third, a data source map identifying at least six institutional systems holding relevant records, and characterising key barriers to cross-sectoral analysis: incompatible formats, inconsistent geographic and species-level classification, and absent data-sharing protocols.

Conclusions

Colombia's animal welfare and wildlife governance face not an absence of legislation, but a structural gap between legal mandates, data production, and analytical capacity. The identified normative gaps and data fragmentation are measurable barriers to One Health implementation that civil society organisations are positioned to document and address. The proposed observatory, which harmonises administrative records into comparable indicators and enables geographic and trend analysis, offers a replicable model for countries facing similar fragmentation. This initiative demonstrates how analytical innovation can empower non-profit organisations to advance the One Health agenda, where official data remain dispersed and underutilised.

1872 – Co-Producing the Community-based One Health Network of Alaska (COHNA)

Michelle JOHANNSEN (1), Sara H. OLSON (1), Lucy KEATTS (1), Maya HOMSY KING (1), Martin ROBARDS (1), Chris WALZER (1), Raphaela STIMMELMAYR (2), Kimberlee BECKMEN (3), Cristina HANSEN (4), Alyssa LEARY (5)

1: Wildlife Conservation Society, United States of America; 2: North Slope Borough Wildlife Management Department; 3: Alaska Department of Fish and Game; 4: University of Alaska Fairbanks; 5: Yukon Kuskokwim Health Corporation

Developing sustainable food security and conservation strategies to support Arctic Indigenous Peoples requires One Health approaches that balance human, animal, and ecosystem health. The Arctic's climate is warming nearly four times faster than the global average, altering wildlife distributions, human access, and human-wildlife interactions. In this rapidly changing environment, where people depend heavily on healthy wildlife and ecosystems, effective communication systems and technical innovations capable of delivering near real-time health information are critical for strengthening community resilience. The Community-based One Health Network of Alaska (COHNA) aims to improve cross-sector communication, coordination, and collaboration through co-produced approaches to wildlife and environmental surveillance that center Indigenous lifeways, and wildlife stewardship. Central to this model is building on existing community strengths and priorities to support locally relevant, timely assessments of the health of people, animals, and the environment. The COHNA team conducted interviews, focus groups, and community meetings in three partner communities in Alaska to understand communication flows and coordination between institutions, governance structures, and **c**ommunity members regarding human, domestic animal, and wildlife health. The team also collected biological samples from wildlife, domestic animals, and wastewater to detect and characterize priority zoonotic pathogens and better understand their potential host range. Co-development with local and Indigenous partners led to the development of culturally grounded biological sampling kits and locally appropriate sampling protocols. Trust, community-based participation, relationship building, and respect for data sovereignty, including through establishing agreements, were prioritized throughout our efforts. Drawing on social science findings, we mapped existing health communication pathways, decision making structures, and information flows to strengthen a coordinated and effective One Health communication network with implications for food safety and conservation. Multi-sectoral, trans-disciplinary partnerships, spanning conservation organizations, academic research institutions, Indigenous and community partners, regional health organizations, and municipal and state wildlife management authorities, enabled the collection of over 1,400 biological samples from wildlife, domestic animals and human wastewater to investigate zoonotic pathogens with pandemic potential and/or food safety risk. Moving forward, COHNA will embed and operationalize these innovative approaches within routine practice, co-develop additional strategies, tools and technologies for community-led surveillance and advance supportive policy frameworks to sustain community-based One Health systems in the Alaskan Arctic.

1878 – One Health Water Africa (OHWA): A Retrospective Analysis of an International, Multidisciplinary and Collaborative Field School in a Rural Community (2022-2024)

Elise Stephanie MVODO MEYO EPSE ESSOMBA (1,7), Marie Noela ENYOE OLOUGOU (3), Christopher NGOSONG (3), Lila FERRAT (2), Jeanette WOGAING (6), Alessandra FALCHI (2), Frederic HUNEAU (2,10), Denis ZOFOU (5), Sylvie BELENGFE (4), Arouna NJAYOU (8,9)

1: Department of Agricultural Economics and Agribusiness, University University of Buea, Cameroon; 2: Risk and Natural Disaster Programme, University of Corsica Pascal Paoli, Grimaldi Campus, 20250, Corte, Corsica, France; 3: Rhizobiology Laboratory, Department of Agronomics and Applied Molecular Sciences, University of Buea, Po Box: 63, Buea, South West Region, Cameroon; 4: Department of Fisheries and Aquatic Resources Management, University of Buea, Po Box: 63, Buea, South West Region, Cameroon; 5: One Health in infectious Diseases and Antimicrobial Resistance Programme, Faculty of Health Sciences, University of Buea, South West Region, Cameroon; 6: Department of Anthropology, Faculty of Arts, Humanities and Letters, University of Douala, Littoral Region, Cameroon; 7: Foundation for Entrepreneurship, Research and Development (FERD), Akonolinga, Centre Region, Cameroon; 8: Department of Biomedical Sciences, Faculty of Sciences, University of Ngaoundéré, Adamawa Region, Cameroon; 9: School of Veterinary Medicine, Université des Montagnes, Bagangté, West Region, Cameroon; 10: Department of Hydrology, Faculty of Sciences, University of Douala, Littoral Region, Cameroon

Background:

The efficient training of next generation workforce implies putting together behavioral and societal determinants including indigenous complementarity of soft and hard skills. Recurrent pandemics oblige using multidisciplinary lenses to co-construct/co-implement measures for public health issues. One Health Water Africa (OHWA) Field school, the four-edition project, holding in Akonolinga, a Cameroon rural community, enabled masters' students from five North/South universities to investigate with a One Health approach water borne diseases.

Objectives:

Each annual edition of (OHWA) Field school organised an interdisciplinary, intercultural and multifaceted teams studying water borne issues in a rural community of Cameroon.

Methods:

A Memorandum of Understanding enabled the building of a North/South consortium of five universities and a plethora of research supporting institutions. Hosted by university of Buea, in Cameroon, other participating universities are: the University of Corsica Pascal Paoli (France), Universities of Douala, *des Montagnes* and Ngaoundéré. The 2022 edition had 29 members; from 4 cultural settings and 9 specialties. The team collected 134 households'data, testing quality of drinking water and restituted results to community leaders. The 2023 edition proposed to train 89 households in water purification using Moringa powder. It brought together 35 members from 12 specialties working for 12 days in villages. The 2024 edition had 31 members, 13 specialties. It enabled the investigation of epidemiological, soil and water from 94 households and nine villages. Results dissemination through sensitisation in two schools.

Results:

OHWA Has trained 64 students working interdependently in diversified health teams, 24 villages were visited and +3000 dwellers impacted. OHWA has trained +300 people in water purification. Inhabitants requested more training sessions. Participants have proposed +20 presentations in different Health research events. Subsequent projects were inspired: on sustainable agricultural entrepreneurship education (AGRICOM), One Health issues of stray animals, diseases transmission (TROHIKA) and Risk exposure to Arboviruses (Zoosanté). It has closed gaps between South/North youth. It has served as a case study and a success story in many training sessions. Two master's students in One Health and infectious disease and antimicrobial resistance completed research using OHWA results. Research Institutions hosting participants are pleased with teamwork and inclusiveness analytical skills acquired. OHWA field school has motivated the launching of an online collaborative Masters with five Universities: The University of Buea, The University of Ngaoundéré and Université des Montagnes (Cameroon) but also the University of Geneva (Switzerland) and the University of Corsica (France); Teams excited to implement the last edition.

Conclusions:

The OHWA Field School project enables community engagement to become a reality. Communities of knowledge are built and the One Health approach keeps providing more avenues to bring communities, and knowledge to be culminated for the building of a better world, our common good.

Samsung Quad Camera
Shot with my Galaxy A72

1890 – High-Resolution Epitope-Based Serosurveillance Reveals Evidence of Ebolavirus Exposure in Fruit Bats in Bangladesh

Sunil Kumar DUBEY (1), Ariful ISLAM (2), Sharmin SULTANA (3), Wenxin TIAN (1), Pronesh DUTTA (3), Arif KHAN (3), Ellen MURPHREE (4), James NG (1), Reed F. JOHNSON (4), Jade FORWOOD (2), W. Ian LIPKIN (1,5), Lisa E. HENSLEY (4), Tahmina SHIRIN (3), **Nischay MISHRA** (1,5)

1: Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, NY, United States; 2: Gulbali Institute, Charles Sturt University, Wagga Wagga, NSW, Australia; 3: Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh; 4: Zoonotic and Emerging Disease Research Unit (ZEDRU), National Bio and Agro-Defense Facility (NBAF), United States Department of Agriculture (USDA), Manhattan, KS, United States; 5: Department of Epidemiology, Mailman School of Public Health, Columbia University, New York, NY, United States

Background

Ebolaviruses (family *Filoviridae*) are zoonotic pathogens that cause severe hemorrhagic disease in humans, with case fatality rates ranging from 25–90%. Zoonotic spillover events represent a persistent threat, facilitating the emergence and re-emergence of both known and novel ebolaviruses at the human–wildlife interface. Although bats are implicated as natural reservoirs in Africa and parts of Southeast Asia, their broader geographic distribution and ecological range remain poorly characterized. Previous studies in Bangladesh have reported serological reactivity to Zaire ebolavirus (ZEBOV) and Reston ebolavirus (RESTV) in a wide range of bat species using whole-protein serological assays; however, these approaches are limited by antigenic homology and cross-reactivity among filoviruses. Epitope-resolved, multi-antigen serology offers improved sensitivity and specificity for detecting prior exposure and refining reservoir surveillance within a One Health framework.

Methods

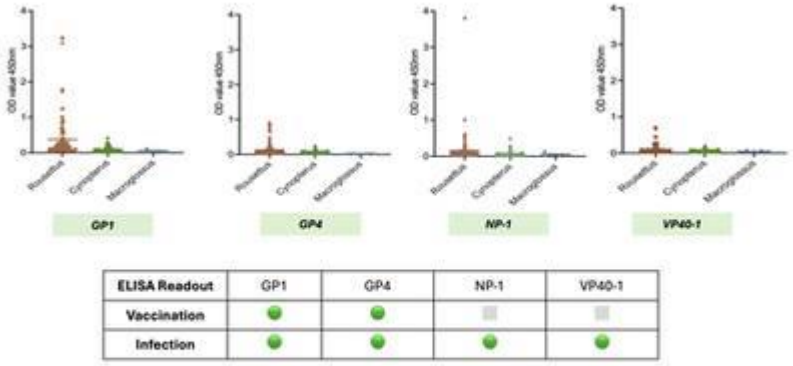
We conducted an epitope-based sero-epidemiological investigation of fruit bats from four districts in Bangladesh (Naogaon, Manikganj, Shariatpur, and Faridpur). Serum samples (n = 293) were collected from *Rousettus leschenaultii*(n = 100), *Cynopterus sphinx* (n = 188), and *Macroglossus sobrinus* (n = 5). Samples were screened using a multi-antigen IgG ELISA panel comprising four immunoreactive peptides derived from *Glycoprotein1,2* (two peptides: GP1 and GP4), *nucleoprotein* (NP-1), and *viral protein 40* (VP40-1) (**Figure**). The GP1 peptide corresponds to the glycan cap region and GP4 to the membrane-proximal external region (MPER); both peptides are located within highly conserved regions of *Glycoprotein1,2* across all orthoebolaviruses, supporting their utility as *pan*-orthoebolavirus serodiagnostic targets. These immunoreactive peptides were originally identified through enhanced proteome-wide epitope mapping using a high-density peptide microarray. All ELISA-positive *R. leschenaultii* samples (n = 29) and a subset of seronegative samples (n = 32) were further analyzed using high-throughput short-peptide phage-display immune-profiling. Phage libraries spanned the complete proteomes of representative filoviruses, including ZEBOV, RESTV, Sudan virus, Bundibugyo virus, Taï Forest virus, Bombali virus, Lloviu virus, and Lake Victoria marburgvirus.

Results

The peptide ELISA panel identified seroreactivity in 29% (29/100) of *R. leschenaultii* bats (21% GP1, 6% GP4, 6% NP-1, and 2% VP40-1) (**Figure**). All *C. sphinx* and *M. sobrinus* samples were seronegative. Phage-display immune-profiling revealed enrichment of cross-reactive epitopes across filovirus proteomes, with preferential identification of ZEBOV- and RESTV-associated epitopes in seropositive *R. leschenaultii* bats. Epitope-level signatures were consistent with prior exposure to ebolaviruses or antigenically related filoviruses among these bats in Bangladesh.

Conclusions

These findings provide high-resolution serological evidence of ebolavirus or ebolavirus-like exposure in fruit bats in Bangladesh, supporting a broader geographic distribution of filoviruses than previously recognized. GP1 and GP4 peptides have utility to recognize novel ebolaviruses. Integration of multiplex epitope-based serology with ecological surveillance enhances analytical specificity and offers a scalable platform for reservoir prioritization and zoonotic risk assessment within a One Health framework.



ELISA Readout	GP1	GP4	NP-1	VP40-1
Vaccination	●	●		
Infection	●	●	●	●

Figure. Multi-antigen peptide ELISA detection of filovirus-reactive antibodies in fruit bats. A multi-antigen peptide ELISA panel detected IgG antibodies targeting conserved domains of *Glycoprotein*$_{1,2}$ (GP1 and GP4), *nucleoprotein* (NP-1), and *viral protein 40* (VP40-1) in 29 of 100 (29%) *Rousettus leschenaulti* serum samples collected in Bangladesh, indicating prior exposure to ebolaviruses or antigenically related filoviruses.

1895 – Livestock Pathogen Spillover and Social–Ecological Impacts: African Swine Fever, Unregulated Trade and The Extinction Crisis for the Sulawesi Babirusa

Ahmad FAISAL (1), Lucy KEATTS (2), Dini RAHMANITA (3), **Christian WALZER** (4)

1: Wildlife Conservation Society Indonesia Program, Indonesia; 2: Wildlife Conservation Society; 3: Bogani Nani Wartabone National Park, Indonesia Ministry of Forestry; 4: Wildlife Conservation Society, United States of America

Background

The movement of pathogens across livestock–wildlife interfaces can generate downstream impacts across social–ecological systems. Sulawesi, Indonesia, is known for commercial trade of both domestic and wild meat, important for local economies and driven by strong traditions. However, unregulated wildlife and trade networks, including the long-distance transport of live animals and pork products under unhygienic conditions, create pathways for pathogen spillover with potential widespread One Health ramifications. In 2023, African Swine Fever (ASF), a transboundary disease with severe socio-economic consequences, reached North Sulawesi, raising urgent concerns about spillover into endemic wild pig species and the resulting ecological and livelihood impacts. Wild pigs play important roles as forest engineers through rooting and seed dispersal, and supporting ecological processes including regeneration and pollination pathways. Their decline triggers cascading impacts, affecting forest dynamics, reducing prey availability for large predators such as tigers, and increasing human–wildlife conflict, while also undermining local livelihoods and cultural practices linked to wildlife resources.

Methods

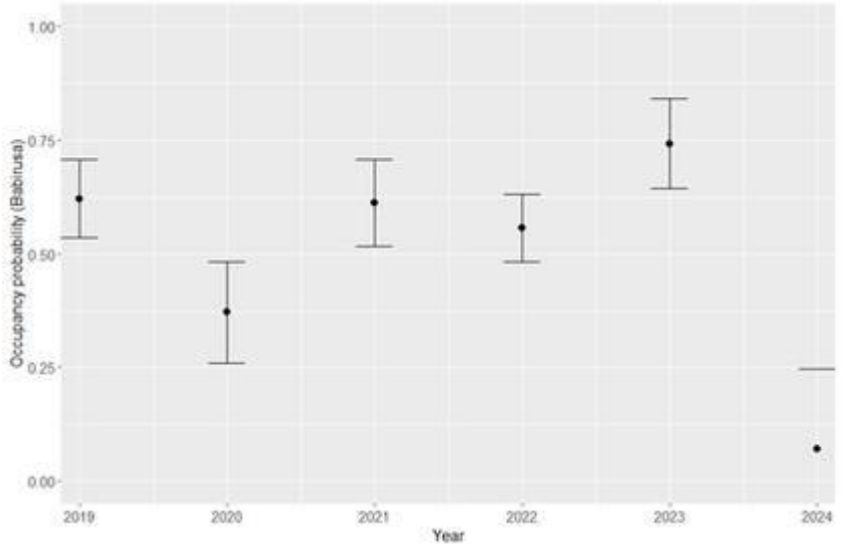
To assess risk and impacts, surveys were conducted with 135 residents (farmers, hunters, and collectors) in forest-edge communities around Bogani Nani Wartabone National Park (BNWNP). Biodiversity monitoring included the deployment of 50 camera traps within established wildlife monitoring grids to detect remnant wild pig population. Forest patrols were conducted to identify carcasses, and laboratory PCR testing was used to confirm the ASF virus.

Results

In October 2023, the first case of ASF in a Sulawesi babirusa (Babyrousa celebensis) within BNWNP was recorded. Between August 2023 and December 2024, 65 endemic wild pig carcasses (6 babirusa and 59 Sulawesi warty pigs) were found in the park. Alarmingly, camera trap surveys in 2024 recorded zero babirusa sightings, representing a catastrophic decline from the 40.2% average detection rate observed between 2020 and 2023. Social surveys identified the unregulated movement of live domestic pigs and pork products as the primary suspected transmission pathway. Among respondents, 79% of farmers reported selling sick pigs immediately to collectors, while 38% reported disposing of carcasses into the environment, including into 12 local rivers. Collectors handling live animals were found to have the highest occupational exposure, representing a transmission risk, as contaminated clothing and transport equipment can mechanically spread the virus between farms, markets, and wildlife habitats.

Conclusions

This case illustrates how livestock pathogen spillover, facilitated by unregulated meat trade and weak biosecurity can generate cascading impacts across biodiversity, livelihoods, and animal health systems. ASF transmission into endemic pig populations, poses an extinction-level threat to the Sulawesi babirusa and highlights a critical gap in One Health implementation at wildlife-livestock interfaces. Strengthening cross-sector coordination, regulating livestock and meat trade and integrating wildlife surveillance into animal health systems are urgently needed to prevent further biodiversity loss and reduce spillover risks within interconnected social–ecological systems.



1903 – From Biodiversity to Therapeutics: Antiparasitic Activity, Cytotoxicity and Hit Prioritization of Amazonian Snake Venom Fractions

Inês MORAIS (1,2), Paula MOREIRA (3), Milena SILVA (4), Paula GOMES (2), Juliana ZULIANI (4), Sofia CORTES (1), Sonia CHUDZINSKI (5), Fatima NOGUEIRA (1,2)

1: Global Health and Tropical Medicine, GHTM, LA-REAL, Instituto de Higiene e Medicina Tropical, IHMT, Universidade NOVA de Lisboa, Lisboa, Portugal; 2: LAQV-REQUIMTE, Department of Chemistry and Biochemistry, Faculty of Sciences, University of Porto, Porto, Portugal; 3: Development and Innovation Laboratory, Butantan Institute, São Paulo, Brazil; 4: Laboratory of Cellular Immunology Applied to Health, Oswaldo Cruz Foundation, FIOCRUZ Rondônia, Porto Velho-RO, Brazil; 5: Escola Superior do Instituto Butantan, Butantan Institute, São Paulo, Brazil

Background: Multidrug-resistant *Plasmodium falciparum* continues to threaten malaria control, reinforcing the need for new antimalarial leads. Natural products remain a key pipeline, and snake venoms (SVs) represent biodiversity-derived sources of bioactive molecules with translational potential. In a One Health perspective, responsible bioprospecting can link ecosystem stewardship with human

innovation, provided sourcing is ethical and scalable development routes (e.g., peptide synthesis) are considered.

This work aims to evaluate crude SVs and their fractions for (i) *in vitro* antiplasmodial activity against erythrocytic stages of *P. falciparum*, (ii) anti-*Leishmania* activity, (iii) cytotoxic and hemolytic effects, and (iv) molecular characterization and mechanisms of action investigation of prioritized active fractions.

Methods: Brazilian SVs and fraction panels were screened against erythrocytic stages of *P. falciparum* 3D7HT-GFP clone (MRA-1029). Fractions showing >70% inhibition in preliminary screening were selected for IC50 determination, and stage-specific assessment was performed using synchronized cultures. Safety profiling included cytotoxicity in mammalian cell lines (V79, HepG2, THP1, U937) and hemolysis assays. To evaluate broader antiparasitic potential, fractions were also tested against *Leishmania* spp. Chemical characterization and mechanism-of-action assays are ongoing for prioritized fractions.

Results: Fraction P1 and Pool inhibited parasite growth by >70% and showed IC50 values in the range of 400 and 200 µg/ml, respectively. In synchronized assays, P1 inhibitory profile was consistent with the predominant effect during schizont-to-merozoite transition and/or subsequently. Against the *Leishmania* clones tested, activity was observed only for crude venom. No fraction caused significant hemolysis (10%). P1 and Pool exhibited low cytotoxicity in V79 cells (≥70% viability within the tested range), whereas crude venom showed higher toxicity in THP-1 and HepG2 cells. Selective Index (SI) estimates are conservative because CC50 values were not reached within the tested concentration range.

Conclusions: These findings identify SVs fractions with selective *in vitro* antiplasmodial activity, supporting their potential as leads for antimalarial drug development. Ongoing chemical and mechanistic characterization will refine candidate selection and inform scalable development routes consistent with One Health principles.

1911 – Between Armadillos and Humans: Lack of Evidence for Zoonotic Transmission of Mycobacterium leprae.

Danilo KLUYBER (1), Patricia D. DEPS (2), Ciro M GOMES (3), Renata V. TIMBÓ (4), Michele SG GOUVÊA (5), Tomás MOUTINHO (6), Expedito J.A LUNA (7), Julio A BENAVIDES (8)

1: PhD (student) Programa de Pós-Graduação em Doenças Infecciosas e Saúde Global, IMT, FMUSP, Univ. de São Paulo, SP, Brasil/.IRD/Mivegec, Univ. de Montpellier, Montpellier, França. Naples Zoo, Florida, US/Inst. de Conservação de Animais Silvestres–ICAS, Campo Grande, MS,Brazil; 2: Dep. de Medicina Social e Prog. de Pós-Graduação em Doenças Infecciosas, Univ. Federal do Espírito Santo, Vitória, ES, Brasil.; 3: Fac.de Medicina, Lab. de Dermatomicologia, Univ. de Brasília, UNB, Brasília, Brasil; 4: Fac. de Medicina, Lab. de Dermatomicologia, Univ.de Brasília, UNB, Brasília, Brasil; 5: Lab.de Gastroenterologia e Hepatologia Tropical. Dep. de Gastroenterologia, Inst de Med. Tropical de São Paulo da FMUSP, SP, Brasil; 6: Dep. de Med. Preventiva, Univ. de São Paulo, SP, Brasil; 7: Prog. de Pós-Graduação em Doenças Infec. e Saúde Global, IMT, Fac. de Med., Univ. de São Paulo, SP, Brasil.; 8: MIVEGEC, Inst. de Recherche pour le Développement-IRD, Univ. de Montpellier, Montpellier, France

Background: Leprosy, caused by *Mycobacterium leprae*, remains an important public health problem in several tropical countries, particularly in Brazil, which ranks among the nations reporting the highest number of new cases annually. The disease affects the skin and peripheral nerves and may lead to permanent disabilities if not diagnosed and treated early. Although transmission is widely accepted to occur predominantly through prolonged respiratory contact between humans, evidence suggests that certain wildlife species may also play a role in the ecology of the pathogen. In the Americas, armadillos have been identified as potential natural hosts of *M. leprae*, raising concerns about possible zoonotic transmission. However, few studies have investigated the epidemiological relevance of these animals or quantified their contribution to the transmission cycle of the disease in natural environments. Environmental changes, habitat fragmentation, and increasing overlap between human populations and wildlife habitats in biomes such as the Pantanal and Cerrado may influence pathogen circulation. Within the One Health framework, which recognizes the interconnection between human, animal, and environmental health, this study investigated the presence of *M. leprae* in humans and armadillos sharing the same landscape to assess potential transmission risks at the human–wildlife interface. **Methods:** The study was conducted in three areas located within the Pantanal wetland and Cerrado savanna in the state of Mato Grosso do Sul, Brazil. Biological samples were collected from captured free-living armadillos and from individuals killed by vehicle collisions. Samples from live animals included blood and ear biopsies, while tissues collected from road-killed animals included ear fragments, liver, and spleen. Residents from

nearby rural communities voluntarily participated and underwent epidemiological interviews, clinical examination, and blood collection. Samples were analyzed using serological testing for anti-PGL-1 antibodies and polymerase chain reaction (PCR) assays for detection of *M. leprae* DNA. **Results:** A total of 62 free-living armadillos, 71 samples from road-killed animals, and 158 human participants were evaluated. Among the live armadillos, 6.4% tested seropositive for anti-PGL-1 antibodies.Only one individual collected after a vehicle collision (1.4%) tested positive for *M. leprae* by PCR. None of the examined animals presented clinical signs compatible with leprosy. Among human participants, 6.3% presented clinical signs suggestive of the disease and 28.9% were seropositive for anti-PGL-1 antibodies. **Conclusions:** The findings confirm the persistence of leprosy endemicity in the human populations studied. The low detection of *Mycobacterium leprae* in armadillos suggests limited circulation of the bacillus in these wildlife hosts, indicating that person-to-person transmission likely remains the dominant epidemiological pathway in the region. Nevertheless, integrated surveillance strategies encompassing human health, wildlife monitoring, and environmental assessment remain essential. Strengthening early diagnosis, contact tracing, and epidemiological surveillance in rural communities and at the human–wildlife interface is critical for improving disease control and preventing potential zoonotic transmission.

1913 – Drought Incidence, Humidity Dynamics, and Chikungunya in Brazilian Municipalities

Mattheus RODRIGUES DA SILVA (1), **Noêmia TEIXEIRA DE SIQUEIRA FILHA** (2), **Tatiane ALMEIDA DE MENEZES** (1), **Celina Maria TURCHI MARTELLI** (3)

1: Universidade Federal de Pernambuco, Brasil; 2: Universidade de York, Reino Unido; 3: Fundação Oswaldo Cruz (Fiocruz), Brasil

BackgroundChikungunya is an increasing public health concern in the Americas. Because Aedes mosquitoes require standing water for larval development, moisture conditions influence transmission. However, the temporal scale at which moisture affects disease risk has received limited attention (Morin et al., 2013). The Standardised Precipitation Evapotranspiration Index (SPEI) measures moisture anomalies at multiple timescales, from short-term rainfall variability (SPEI 1) to longer climatic regimes (SPEI 12) (Vicente Serrano et al., 2010). We examine whether different SPEI timescales are associated with chikungunya incidence through distinct mechanisms and whether the relationship is nonlinear, as heavy rainfall may reduce transmission by flushing larvae from breeding containers (Benedum et al., 2018).

MethodsWe constructed a quarterly panel of 5,556 Brazilian municipalities from 2015 to 2020 (122,016 observations). Confirmed chikungunya cases were obtained from the national surveillance system (SINAN). Gridded climate data were aggregated to municipal quarters, and SPEI was calculated at 1, 3, 6, and 12-month timescales (Begueria et al., 2014). We estimated Poisson pseudo maximum likelihood models (Silva and Tenreyro, 2006) with municipality and quarter fixed effects. Models included one-quarter lagged climate controls (temperature, humidity, and thermal amplitude), a population offset, and standard errors clustered at the municipality level. Linear, quadratic, interaction (SPEI and temperature), and inclusive specifications, including all four SPEI scales, were estimated.

ResultsShort-term moisture (SPEI 1) showed the strongest statistically significant association with chikungunya incidence. A one-unit increase in SPEI 1 was associated with 53 per cent higher expected case counts (IRR 1.53, p = 0.016). SPEI 3 and SPEI 6 showed weaker associations that were not statistically significant. SPEI 12 showed a negative association with incidence (IRR = 0.86), but this association was not significant when estimated alone.

When all four SPEI scales were included simultaneously, SPEI 1 remained positively associated with incidence (beta 0.64, p = 0.002) while SPEI 12 became significantly negative (beta -0.28, p = 0.041). The four SPEI scales were jointly significant (Wald p 0.001).

Quadratic terms were negative and significant across all scales (p 0.01), indicating an inverted U relationship between moisture and incidence. Interactions between SPEI and temperature were significant for longer timescales (SPEI 6 p = 0.036; SPEI 12 p = 0.026) but not for SPEI 1 (p = 0.638). Results were similar after adjusting for the Premises Infestation Index.

ConclusionsShort and long-term moisture conditions are associated with chikungunya incidence in opposite directions. Recent rainfall appears to increase transmission by creating breeding sites, whereas sustained moisture at longer timescales may reflect environmental conditions that reduce vulnerability.

The inverted U relationship supports the role of larval flushing during extreme rainfall. Multi-scale climate indicators may improve early warning systems for arboviral diseases because single-scale analyses can mask opposing temporal dynamics.

1919 – Exploring biodiversity and associated pathogens with the help of flies: refining the iDNA approach

Simon KRÜCKEMEIER (1), Mueena JAHAN (2), Alix ARMERO (3), Tomke BÜTOW (4), Nikolai GUSEV (3), Fabian LEENDERTZ (1), Jan F. GOGARTEN (3), Sébastien CALVIGNAC-SPENCER (4), Lorenzo LAGOSTINA (1)

1: Department of Ecology and Emergence of Zoonotic Diseases, Helmholtz Institute for One Health, Helmholtz-Centre for Infection Research (HZI), Greifswald, Germany; 2: Department of Microbiology and Public Health, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh; 3: Evolutionary Community Ecology Research Group, Helmholtz Institute for One Health, Helmholtz-Centre for Infection Research (HZI), Greifswald, Germany; 4: Department of Pathogen Evolution, Helmholtz Institute for One Health, Helmholtz-Centre for Infection Research (HZI), Greifswald, Germany

We are currently experiencing a dramatic decline in biodiversity on a local and global scale. The tragic, ongoing disappearance of many plant and animal species, often referred to as the Holocene or sixth mass extinction, is largely due to anthropogenic disturbance. Although the dilution effect remains controversially discussed, scientific evidence seems to indicate that biodiversity loss is linked to the emergence of infectious diseases, threatening human and animal health alike. The tropical rainforest of Taï National Park in the Ivory Coast is a biodiversity hotspot in decline due to human activity and a major location for the emergence of novel pathogens with zoonotic potential. In the area of the national park, *Bacillus cereus* biovar *anthracis* (Bcbva), an agent causing anthrax, is known to be responsible for a significant amount of the wildlife mortality. Increasing anthropogenic pressure, combined with climate change, underscore the need for tools to study these dynamic human-wildlife interfaces. Metabarcoding of invertebrate-derived DNA (iDNA) has proven to be useful for describing vertebrate diversity, and intriguingly can be combined with the detection of pathogens from these same flies, to explore their host range and contribute to the understanding of the ecology and distribution of emerging infectious diseases.

A past study aimed at assessing biodiversity and simultaneously monitoring the presence of Bcbva in Taï national park, at the edges of the forest and close to villages surrounding the forest with the help of fly iDNA. While the biodiversity around the villages was well characterized, only a fraction of the mammal community could be reconstructed in the two other habitats. In the framework of BCOMING, our research project investigated the number of flies required to accurately describe the mammal communities and to explore the possibility to assess relative abundance of the detected species using a pooled fly extraction approach (5776 total flies in 144 pools). Furthermore, we wanted to determine whether the absence of Bcbva around villages could be confirmed. Flies were captured over a period of four years, in the same three habitats as in the previous study. Metabarcoding techniques enabled us to well characterize the mammal communities in the all three habitats. In addition, Bcbva could be detected in the forest (3/48 pools) and in the village (1/48 pools). Our results underline the use of fly iDNA as a cost-effective and efficient method for measuring biodiversity and studying disease ecology of selected pathogens. At the same time, our study aims to expand its range of biomonitoring applications.

1947 – The Network for Ecohealth and One Health (NEOH): Strengthening One Health Education, Collaboration and Community Building for Integrated Health Approaches

Barbara HAESLER (1), Evan GRIFFITH (2), Simon RUEGG (3), Hans KEUNE (4), Gabrielle LAING (5), Nicolas ANTOINE-MOUSSIAUX (6), Margarida SIMOES (7), Asta TVARIJONAVICIUTE (8), Sara SAVIC (9)

1: 1 Royal Veterinary College, London, UK; 2: 2 Cummings School of Veterinary Medicine, Tufts University; 3: 3 University of Zurich, Switzerland; 4: 4 University of Antwerp, Belgium; 5: 5 Unlimit Health, London, UK; 6: 6 University of Liege, Belgium; 7: 7 Univesidade De Evora, Portugal; 8: 8 University of Murcia, Spain; 9: Scientific Veterinary Institute "Novi Sad", Serbia

Background

Complex global challenges such as emerging zoonotic diseases, biodiversity loss, climate change, and antimicrobial resistance highlight the need for integrated approaches that recognize the interconnections

between human, animal, and environmental health. The Network for Ecohealth and One Health (NEOH) was formed to promote collaboration, education, and capacity building in support of integrated approaches. NEOH originates from the COST Action “Network for Evaluation of One Health” (2014–2018), which initially focused on strengthening the evidence base for One Health by developing methods for evaluating the added value of integrated health initiatives. Building on this foundation, the network has evolved into a broader platform that supports interdisciplinary collaboration, education, and community development within the One Health and Ecohealth fields.

Methods

NEOH exists and works as an international, transdisciplinary network connecting researchers, educators, practitioners, and policy stakeholders from disciplines including public health, veterinary medicine, environmental sciences, social sciences, etc. The network facilitates collaboration and learning through webinars, workshops, working groups, books and joint publications. Particular emphasis is placed on supporting education and workforce development by sharing methodological tools, training resources, and educational materials that help strengthen One Health competencies and systems thinking among students, early-career researchers, and professionals.

Results

Key outputs of the network include the development and dissemination of the NEOH One Health evaluation framework and handbook, which provide assessment for One Health evaluation of different initiatives. NEOH members have also contributed to collaborative publications and learning resources, including the book Principles of One Health for a Better Planet, which highlights conceptual foundations and practical applications of integrated health approaches. Through these activities, the network has fostered international collaboration, implemented differences, gender and social inclusion, supported knowledge exchange, and contributed to strengthening the One Health community.

Conclusions

NEOH provides a collaborative platform that supports education, knowledge exchange, and community building across disciplines relevant to One Health and Ecohealth. By promoting systems thinking and interdisciplinary learning, the network contributes to developing a skilled and connected international One Health approach and workforce capable of addressing complex global health challenges.

2337 – Got it — reframing the abstract as a case study grounded at the Dourados Reserve, with the broader argument about indigenous peoples in Brazil emerging from that empirical anchor.

Maria BELDI ALCANTARA (1,3,4), **Herintha COETO NEITZKE-ABREU** (2), Marcia DALASTRA LAURENTI (1), **Sheila REGINA LOPES DUTRA** (1)

1: Faculdade de Medicina, Universidade de São Paulo (FMUSP/USP), São Paulo, Brazil; 2: Universidade Federal da Grande Dourados (UFGD), Dourados, Brazil; 3: Associação dos Jovens Indígenas de Dourados (AJI), Dourados, Brazil; 4: International Work Group for Indigenous Affairs (IWGIA), Copenhagen, Denmark

BACKGROUND

Brazil’s Dourados Indigenous Reserve concentrates approximately 18,000 Guarani Kaiowá, Ñandewa, and Aruak Terena people in 3,539 hectares — one of the highest indigenous demographic densities in the country. Territorial confinement, structural violence, and suicide rates that far exceed national averages make this site an empirical laboratory for examining whether dominant health frameworks can accommodate indigenous healing systems. One Health, Global Health, and Brazil’s Unified Health System (SUS) each claim inclusive governance over health at human-animal-environment interfaces. Yet the Dourados Reserve reveals a structural contradiction: the same conditions of confinement that produce collective illness simultaneously undermine the ontological foundations of indigenous healing processes. This study asks whether the onto-epistemic premises of these three frameworks permit symmetrical dialogue with the autonomous health systems operating at Dourados — or whether their architecture structurally precludes it.

METHODS

Case study employing onto-epistemic analysis of three institutional health frameworks against the healing systems of Guarani Kaiowá, Ñandewa, and Aruak Terena peoples at the Dourados Indigenous Reserve. Analysis is organized across four axes: theories of the health subject, disease causality, knowledge legitimacy, and relation to coloniality. The theoretical framework articulates Latin American decolonial theory (Quijano, Segato, Viveiros de Castro, Krenak) with postcolonial theory (Said, Bhabha). Empirical grounding draws on over two decades of dialogical field research conducted through FMUSP/USP, the Association of Indigenous Youth of Dourados (AJI), and the LEICH project (UFGD/FMUSP/USP), which investigates leishmaniasis at the interface between biomedical protocols and Guarani Kaiowá ontologies of human-animal relations in the Reserve.

RESULTS

At Dourados, One Health reduces human-animal interdependence — ontologically constitutive of Guarani Kaiowá life through ñangareko (reciprocal care) — to biosecurity risk, as demonstrated by euthanasia protocols that treat dogs as zoonotic vectors rather than beings of the tekohá. Global Health renders the Reserve's populations as deficit groups measurable in DALYs, erasing their status as knowledge-bearing subjects. The SUS, through its Indigenous Health Subsystem, performs colonial mimicry: Indigenous Health Agents operate in a Third Space between biomedical protocols and their own cosmological knowledge that the system neither registers nor remunerates. The suicide crisis among young Guarani Kaiowá and Ñandewa emerges as double therapeutic refraction — confinement destroys both the conditions of ñande reko (the Guarani way of being) and the efficacy of ñemoñare (the collective healing process). The LEICH project demonstrates viable knowledge co-production from this contested space.

CONCLUSIONS

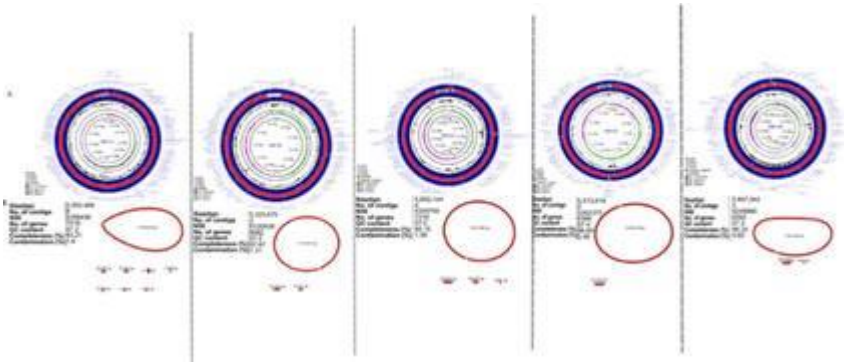
The Dourados case reveals that the exclusion of indigenous healing systems from dominant health frameworks is not a gap to be filled by cultural sensitivity training but a structural onto-epistemic feature. For indigenous peoples in Brazil, a health pluriverse requires institutional architectures capable of recognizing autonomous therapeutic systems without requiring biomedical validation.

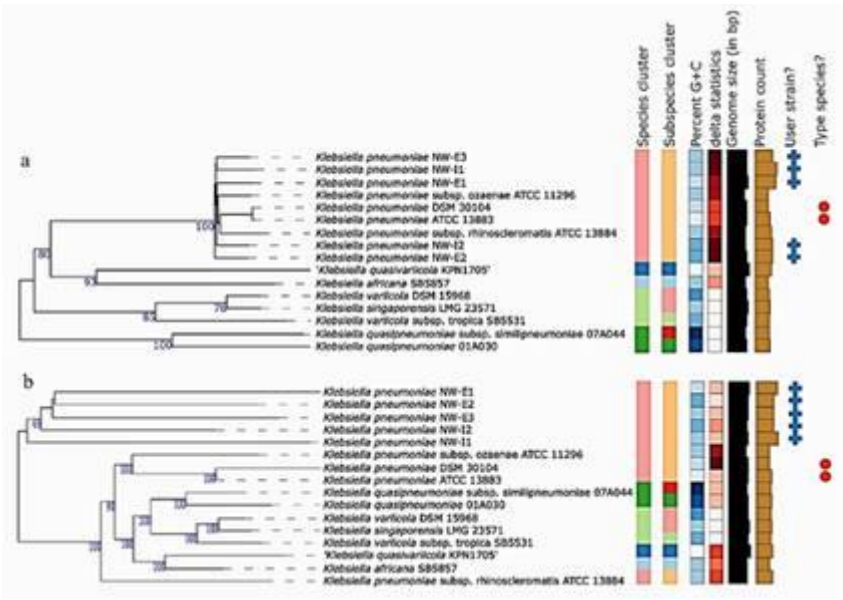
2365 – Comprehensive genome analysis of MDR Klebsiella pneumoniae in influent and effluent of a selected wastewater treatment plant

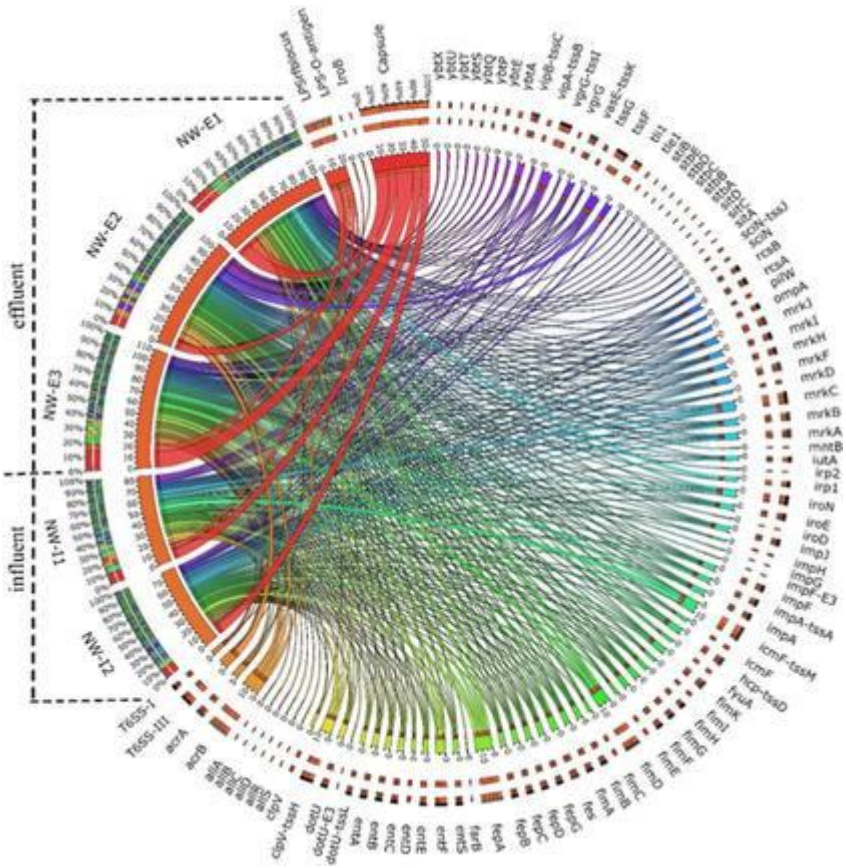
Onalenna Refilwe MABEO, Oluwaseyi Samuel OLANREWAJU, Cornelius Carlos BEZUIDENHOUT, Lesego Gertrude MOLALE-TOM

North West University, Potchefstroom Campus, South Africa

This study investigates the antibiotic resistance profiles, virulence factors and genomic characteristics, of Klebsiella pneumoniae isolates obtained from influent and effluent samples of a wastewater treatment plant. Data generated sheds light on the dissemination and persistence of antibiotic resistance in compartments in a wastewater treatment plant (WWTP). Given the increasing concern regarding the role of wastewater in the dissemination of antibiotic-resistant bacteria, this research focused on K. pneumoniae populations using culture-based and genomics approaches. The culture-based approach showed that antibiotic resistance to β-lactam antibiotics was corroborated by PCR detection of the genes. Whole Genome Sequencing (WGS) analysis revealed a diverse array of Antibiotic-Resistant Genes (ARGs), including those encoding extended-spectrum β-lactamases (ESBLs) and resistance to other clinically relevant antibiotics. Plasmid analysis unveiled various replicon types indicative of horizontal gene transfer mechanisms. Moreover, the identification of virulence genes implicated in adhesion, biofilm formation, and iron acquisition underscores the pathogenic potential of K. pneumoniae isolates in wastewater. In addition, the genomics comparison between K. pneumoniae strains from the influent and effluent of the WWTPs ecosystem reveal that "core" genome is shared. However, unique genomic clusters in the environmental strains suggests niche-specific adaptations, shedding light on the genomic plasticity of K. pneumoniae in response to environmental cues. This may have implications for antibiotic resistance dissemination and ecological interactions within wastewater ecosystems. Data presented here highlights the urgent need for enhanced surveillance and management strategies to mitigate the spread of antibiotic resistance through wastewater treatment plants ecosystems.




a
b
Species cluster
Subspecies cluster
Percent G+C
delta statistics
Genome size (in bp)
Protein count
User strain?
Type species?
Klebsiella pneumoniae NW-E3
Klebsiella pneumoniae NW-I1
Klebsiella pneumoniae NW-E1
Klebsiella pneumoniae subsp. ozaenae ATCC 11296
Klebsiella pneumoniae DSM 30104
Klebsiella pneumoniae ATCC 13883
Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884
Klebsiella pneumoniae NW-I2
Klebsiella pneumoniae NW-E2
'Klebsiella quasivaricola KPN1705'
Klebsiella africana 585857
Klebsiella varricola DSM 15968
Klebsiella singaporensis LMG 23571
Klebsiella varricola subsp. tropica 585531
Klebsiella quasipneumoniae subsp. similignеumoniae 07A044
Klebsiella quasipneumoniae 01A030


effluent
influent
NW-E1
NW-E2
NW-E3
NW-I1
NW-I2
T6SS-I
T6SS-III
LPS-O-antigen
Capsule
ybtX
ybtU
ybtT
ybtS
ybtQ
ybtP
ybtE
ybtA
irp6
iroB
iroC
iroD
iroE
iroN
irp1
irp2
iutA
mrkA
mrkB
mrkC
mrkD
mrkF
mrkH
mrkI
mrkJ
ompA
pilW
rcsA
rcsB
scdN
scdN-tssJ
tssK
tssL
tssM
tssF
tssG
tssE
vgrG
vipA-tssB
vipB-tssC
icmF
icmF-tssM
impA
impA-tssA
impF-E3
impG
impH
impJ
hcp-tssD
fyuA

2372 – Comparison of ESKAPE Pathogen Levels in Wastewater and Receiving Water Bodies Using Agar-Based Enumeration and Real-Time PCR

Lesego MOLALE TOM, **Onalenna Refilwe MABEO**, **Karabo TSHOLO**, **Carlos BEZUIDENHOUT**

Unit for Environmental Sciences and Management, Potchefstroom Campus, North-West University, Private Bag X6001, 2520 Potchefstroom, South Africa

The ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) are key multidrug-resistant organisms increasingly recognized outside clinical settings. Their persistence in wastewater raises concerns regarding the efficacy of conventional treatment processes and the dissemination of antimicrobial resistance. This study aimed to detect and quantify ESKAPE pathogens in wastewater treatment plants (WWTPs) and downstream environments using agar-based enumeration and real-time PCR (RT-PCR). Culture methods detected all targeted species, with Enterobacter spp. being most abundant and A. baumannii least prevalent. RT-PCR quantified four species (E. faecium, S. aureus, K. pneumoniae, and A. baumannii), identifying K. pneumoniae as dominant. Both approaches revealed higher concentrations in influents that declined after treatment, although RT-PCR indicated elevated downstream levels, suggesting incomplete removal. The highest removal efficiency (100%) was observed for S. aureus and A. baumannii in WWTPs B and J, and the lowest (54.1%) for S. aureus in WWTP K. Integrating culture and molecular methods improved detection sensitivity and provided complementary insights. These results demonstrate that conventional treatment may not fully eliminate ESKAPE pathogens and underscore the need to include them in wastewater-based surveillance for antimicrobial resistance monitoring.

2391 – Quantifying Human Risk from H5N1 in Canada Using a Multi-Species Spillover Model

Victoria D'ALESSANDRO (1,2), Dimitra V POULIOPOULOU (1,2), Nicole BILLIAS (1,2), Joy C MACDERMID (1), Erin MILLER (1), Heather MCCLINCHEY (3), Kieran QUINN (4), Saverio STRANGES (5), Scott WEESE (6), Elena BOUTSIKARI (7), Tiago V PEREIRA (8), Jennie JOHNSTONE (9), Lauren E CIPRIANO (5,10,11), Jessica P HOPKINS (12,13), Elena CINI (14), Jessica J WONG (1,5), Pavlos BOBOS (1,5)

1: School of Physical Therapy, University of Western Ontario, London, Ontario, Canada; 2: Collaborative Specialization in Musculoskeletal Health Research, Bone and Joint Institute, University of Western Ontario, Canada; 3: Ontario Ministry of Health, Toronto, Ontario, Canada; 4: Department of Medicine, Sinai Health, Dalla Lana School of Public Health, Institute of Health Policy, Management and Evaluation, University of Toronto, Toronto, Ontario, Canada; 5: Department of Epidemiology and Biostatistics, Schulich School of Medicine and Dentistry, University of Western Ontario, London, Ontario, Canada; 6: Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada; 7: Department of Epidemiology and Biostatistics, Faculty of Medicine, National and Kapodistrian University of Athens, Athens, Greece; 8: Nuffield Department of Population Health, University of Oxford, Oxford, United Kingdom; 9: Department of Medicine, University of Toronto, Toronto, Ontario, Canada; 10: Ivey Business School, University of Western Ontario, London, Ontario, Canada; 11: Department of Medicine, Schulich School of Medicine and Dentistry, University of Western Ontario, London, Ontario, Canada; 12: Public Health Ontario, Toronto, Ontario, Canada; 13: Department of Health Research Methods, Evidence, and Impact, McMaster University, Hamilton, Ontario, Canada; 14: Global Sustainability Institute, Faculty of Science and Engineering, Anglia Ruskin University, Cambridge, England, UK

Background:

Highly pathogenic avian influenza A(H5N1) continues to circulate among avian and mammalian hosts in Canada during the 2021-2026 epizootic period. Canada has reported one domestically acquired human infection, while more than 650 infected domestic-bird premises and approximately 17.5 million impacted birds have been reported since December 2021. Sporadic detections in Canadian mammals further motivate risk assessment under current ecological and virological conditions.

Methods:

We developed a multi-species SEIR(D) model combining deterministic and stochastic components to simulate cross-species H5N1 transmission in Canada. Populations included wild birds, backyard and commercial poultry (large- and small-scale), reassortment hosts, poultry workers, and the general population, linked through an environmental reservoir. We calibrated uncertain parameters through

Bayesian inference and Markov chain Monte Carlo using synthetic Canada-scale weekly reported case-targets. We evaluated five non-pharmaceutical interventions (NPIs) that reflect plausible or existing response levers: accelerated depopulation of infected commercial poultry, enhanced worker PPE and hygiene, enhanced commercial biosecurity, reduced backyard poultry exposure, and environmental management.

Results:

Over the 15-week post-outbreak detection window, the model estimated 393 reported human cases (0.936 per 100 000), corresponding to 760 modelled human infections after accounting for the reporting probability (95% CrI [484–1,400]; 1.809 per 100 000). The deterministic final epidemic size was ≈ 2,877total human infections (6.85 per 100 000). Human-to-human transmission was negligible with R_0 approximately zero (95% CrI 3x10-5), indicating that sustained human transmission was unlikely under modelled assumptions. Source attribution identified large commercial poultry-to-worker exposure as the largest attributed pathway, followed by environmental, wild-bird, and backyard-poultry pathways. Short-term intervention effects were heterogeneous but generally modest, with occupational and environmental interventions producing the largest median reductions. Under the 52-week stochastic extension, projected annual modelled human infections increased to ≈ 3,658 (8.709 per 100,000), with enhanced biosecurity and accelerated depopulation producing the largest long-term reductions.

Conclusions:

Under the Canadian ecological and virological conditions represented in the model, human H5N1 risk arises from repeated animal-to-human spillover rather than sustained human transmission. Layered interventions targeting occupational exposure, environmental persistence, commercial poultry control, and community-level poultry contact can reduce human infection risk and support evidence-based preparedness and cross-sector policy coordination.

2399 – Strengthening subnational emergency preparedness in Kazakhstan through simulation-based multisectoral training

Assem SULEIMENOVA (1), Anna DERYABINA (1), Zaure AKHMETOVA (2)

1: ICAP at Columbia University, Kazakhstan; 2: National Center for Public Health

Background

Public health emergencies are often first detected and managed locally, yet professionals expected to respond may have limited opportunities to practice working together before a crisis occurs. Kazakhstan faces a complex risk environment shaped by recurrent floods, infectious disease threats, zoonotic risks, and technological hazards associated with industrial and extractive sectors. The severe floods of 2024 highlighted the need for stronger local preparedness and better coordination across sectors. This work aimed to implement and evaluate a simulation-based Public Health Emergency Management (PHEM) training program designed to strengthen practical, multisectoral preparedness at the subnational level. A key objective was to bring together stakeholders from public health, veterinary, emergency response, healthcare, and industry sectors to improve coordination relevant to emergency preparedness, including zoonotic and environmentally linked risks.

Methods

Between September 2025 and February 2026, a hybrid training program was delivered across five priority oblasts in Kazakhstan: Aktobe, Atyrau, Mangystau, West Kazakhstan, and North Kazakhstan. The program combined self-paced online learning, live virtual sessions, in-person teaching, and simulation exercises based on locally relevant hazards, including floods, infectious disease outbreaks, anthrax-related scenarios, and chemical or technological incidents. A total of 165 multidisciplinary participants took part, including representatives of sanitary and epidemiological services, health departments, emergency response authorities, veterinary services, and industrial partners. The RE-AIM framework was used to assess reach, effectiveness, adoption, implementation, and early maintenance. Evaluation data included pre- and post-training knowledge assessments, participant evaluation forms, end-of-workshop discussions, facilitator observations, and a three-month follow-up survey.

Results

The program achieved broad multisectoral reach across all five oblasts and was well accepted by participants and partner institutions. Mean knowledge scores on core PHEM topics increased from 61% before training to 74% after training. Simulation exercises were consistently identified as the most valuable component, particularly for strengthening practical skills in emergency planning, Incident Management System activation, intersectoral coordination, and risk communication. Participants valued the realistic scenarios and the opportunity to work across sectors in a setting that reflected real-world emergency response. Iterative adaptations during rollout, including greater emphasis on in-person delivery and contextualization of scenarios, improved engagement and perceived usefulness. Follow-up findings suggested continued relevance of the training to participants' work and early application of knowledge and tools in practice.

Conclusions

Simulation-based, multisectoral training is a feasible and adaptable approach for strengthening subnational preparedness in settings where human, animal, environmental, and technological risks intersect. In addition to participant learning, the program generated a scalable model to support continued capacity building and coordination in Kazakhstan and comparable settings.

2424 – Confirmed Rift Valley fever virus seroconversions from cohort study reveals limitations of ELISA-based endpoints for countermeasure trials in endemic settings

Keli GERKEN (1,2,3), Richard Rasto OLUBOWA (2), Alice KIYONG'A (2), Abraham REREU (2), Andrew STRINGER (3), Matthew BAYLIS (3), Christine MUTISYA (2), David TCHOUASSI (4), Faith CHEROP (4), Esra BUYUKCANGAZ (5), Desiree LABEAUD (5), Anna LACASTA (2), Sarah CLEAVELAND (6), Eric FEVRE (2,3)

1: Wageningen University, The Netherlands; 2: International Livestock Research Institute (ILRI), Kenya; 3: University of Liverpool, United Kingdom; 4: International Centre of Insect Physiology and Ecology (ICIPE), Kenya; 5: Stanford University, U.S.A; 6: University of Glasgow, United Kingdom

Background

Rift Valley fever virus (RVFV) is a priority zoonotic arbovirus that impacts communities through human disease and disruption of livestock-based livelihoods. Most human infections are mild or asymptomatic, though severe manifestations can occur. Consequently, endemic human infections remain poorly understood as surveillance systems largely focus on clinically apparent outbreak-associated cases, and there are limited longitudinal studies using serological assays over time. This limits our understanding of RVFV burdens and intervention strategies.

RVFV has been prioritized by the Coalition for Epidemic Preparedness Innovations (CEPI) for development of countermeasures, and seroconversion is increasingly being considered as a practical trial endpoint in endemic settings.

Methods

To improve detection of endemic infections and characterize endemic exposure risk, we established a high-risk human cohort in Loitokitok sub-county, southern Kenya, where extensive livestock keeping continues within a rapidly changing semi-pastoral landscape. Individuals involved in routine livestock contact, including those that milk, slaughter, and herd animals, were followed quarterly over one year. Serum samples were tested using two anti-RVFV IgG ELISAs, with all positive samples and a subset of negative samples undergoing plaque reduction neutralization testing (PRNT) confirmation. Sensitivity and specificity of ELISAs were assessed individually and for both assays in parallel. Seropositivity was defined as having one PRNT positive result in a participants' series. Baseline seropositivity, incidence, exposure behaviours, and clinical symptoms were assessed across 783 serum samples collected from 354 participants.

Results

Individual RVFV seropositivity was 6.2%, while 18.7% of enrolled homesteads had at least one seropositive participant. Two PRNT-confirmed seroconversions were identified, corresponding to an incidence of 2.26 per 100 person-years. These infections were associated with recall of increased mosquito exposure and recent contact with livestock abortion material and home slaughter activities. Neither participant recalled clinical signs consistent with RVF illness.

With PRNT confirmation as the gold-standard, ELISAs demonstrated low specificity and specificity, which was improved when adopting results of both ELISAs carried out in parallel (Table 1). Reliance on ELISA results alone would have identified 13 false positive seroconversions. .

Conclusions

Our findings haveimmediate relevance for ongoing RVFV vaccine trials using seroconversion endpoints. We demonstrate a low-level endemic exposure of RVFV in high-risk people outside of recognized outbreaks. Seroconversion endpoints are appealing for RVFV intervention studies in endemic settings because clinical disease is uncommon and outbreak timing and location can be hard to predict. However, substantial misclassification can occur. Our results suggest that current ELISA assays may have limited utility for confirming seroconversion in human cohort studies in endemic settings but may may have screening value when followed by confirmatory testing. RVF cohort studies in endemic settings are feasible but require careful attention to diagnostic confirmation, retention, ethics, and the overlapping ecological and behavioural pathways shaping risk.

	ELISA assays and paired ELISA parallel testing rules			
	ID Vet (%) [95% CI]	MP-12 (%) [95% CI]	"and" rule for both positive (%) [95% CI]	"or" rule for either positive (%) [95% CI]
Sensitivity	80.8 [60.6–93.4]	84.6 [65.1–95.6]	65.4 [44.3-82.8]	100.0 [86.8-100.0]
Specificity	84.8 [75.0–91.9]	87.3 [78.0–93.8]	96.2 [89.3-99.2]	75.9 [65.0-84.9]
PPV	63.6 [45.1–79.6]	68.8 [50.0–83.9]	85.0 [62.1-96.8]	57.8 [42.2-72.3]
NPV	93.1 [84.5–97.7]	94.5 [86.6–98.5]	89.4 [80.8-95.0]	100.0 [94.0-100.0]

2445 – Strengthening Governance for Antimicrobial Resistance through Legislation: Insights from the Updated Global Action Plan on AMR 2026-2036 and the Quadripartite One Health Legislative Assessment Tool for AMR

Carmen BULLON CARO (1), Camille LOI (4), Jorge MATHEU (3), Angelique MUHAVANI (2), Aitziber ECHEVERRIA (2)
1: FAO, Italy; 2: UNEP; 3: WHO; 4: WOAH

Background The updated Global Action Plan on antimicrobial resistance for 2026-2036 issued on 26 May 2026 places urgency on multisectoral governance as a core strategic objective to achieve the Plan's goal. The Plan highlights persistent constraints including fragmented institutional arrangements, weak accountability and limited integration into broader development systems. At the same time, experience from the Quadripartite One Health Legislative Assessment Tool for AMR (OHLAT-AMR) and analysis of national frameworks in AMR-Lex provide new evidence on how governance arrangements are structured in practice. This study examines how these developments inform a shift towards more integrated and operational governance for antimicrobial resistance, as a model for broader One Health governance.

Methods Through the lens of the priorities for multisectoral governance outlined in the updated Global Action Plan, the study analyses evidence from the development and country level application of the OHLAT-AMR and comparative analysis of national frameworks captured in AMR Lex. It focuses on governance functions, including coordination mechanisms, institutional mandates, surveillance systems, and accountability arrangements across sectors.

Results The updated Global Action Plan advances a governance centred approach built on four interrelated elements: formal multisectoral multi-tier coordination with sufficiently robust political support, integration of the antimicrobial lifecycle including environmental dimensions, integrated surveillance across sectors, and the alignment of governance with financing and accountability mechanisms.

Evidence from country applications of the OHLAT-AMR and AMR Lex shows that these elements are inconsistently operationalised. Governance arrangements are often fragmented across sectors, coordination mechanisms lack authority or sustainability, and surveillance systems remain only partially integrated. Environmental and agrifood dimensions are frequently insufficiently embedded within governance structures.

The findings of the study demonstrate that effective governance structures benefit from legally constituted] mandates across institutions, mechanisms and processes to facilitate intersectoral and multi-tier governmental coordination for a whole-of-society approach, and oversight and decision-making mechanisms that span cross-sectoral surveillance and implementation.

Conclusions The updated Global Action Plan's emphasis on governance, as the foundation of effective antimicrobial resistance response, sharpens discourse on multisectoral and multi-tier governance mechanisms that are anchored in legislation. Evidence from OHLAT-AMR and AMR Lex supports the focus on strengthening governance systems to translate One Health approaches into practice. Legal frameworks are a key enabling tool; their impact depends on how well they underpin integrated, accountable and adequately resourced governance structures in their design.

2466 – Kounis Syndrome and Scombroid-Associated Acute Coronary Syndrome at the Human-Animal Interface: Addressing Global Underreporting of Histamine-Mediated Cardiac Emergencies in Human and Veterinary Medicine

Aileen MARTY
Elsevier Publishing, United States of America

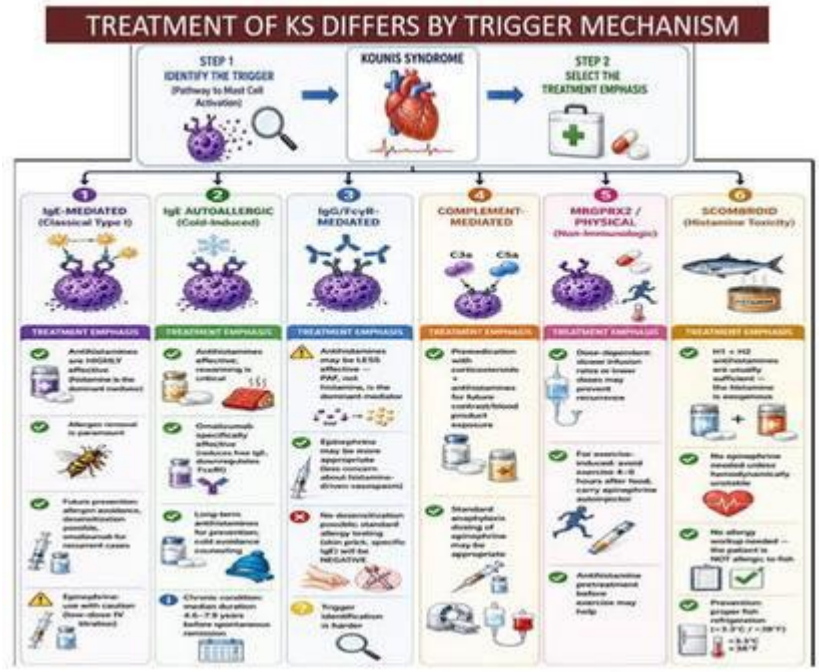
Background: Histamine-mediated acute coronary syndrome (ACS) is an underrecognized and potentially fatal condition affecting humans and other mammals through conserved pathophysiologic mechanisms. Cardiac mast cells and histamine-responsive coronary vasculature are present across species. Yet, analogous disease in companion animals is rarely recognized despite shared exposures to insect stings, drugs, venoms, and spoiled fish. Two distinct but convergent mechanisms produce histamine-mediated ACS: Kounis syndrome (KS), in which endogenous mast cell degranulation during allergic reactions triggers coronary vasospasm, plaque destabilization, or stent thrombosis; and scombroid-associated ACS, in which exogenous histamine generated by bacterial decomposition in fish causes pharmacologic coronary vasospasm and myocardial ischemia. Although differing in origin, both conditions converge on histamine-mediated coronary injury and create similar diagnostic and therapeutic challenges. Recent systematic reviews and emerging evidence demonstrate profound global underrecognition of the

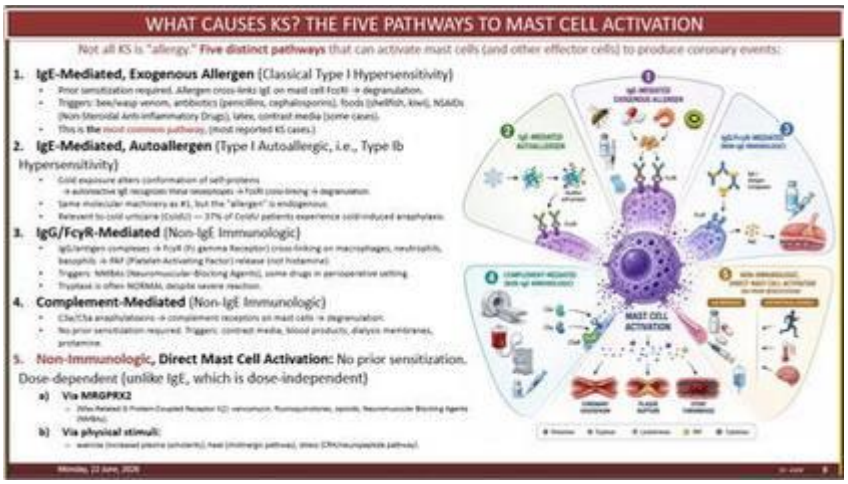
condition despite substantial mortality, and suggest that comparable cases in veterinary medicine are too often overlooked. This convergence of comparative cardiology, food safety, allergy, toxicology, and emergency medicine makes histamine-mediated ACS a timely late-breaking topic for the emergency, food safety, and One Health communities.

Methods and Objectives: This presentation synthesizes newly integrated evidence from human clinical reports, epidemiologic studies, pharmacovigilance data, comparative physiology, and veterinary literature to: (1) distinguish immune-mediated KS from toxic scombroid-associated ACS while emphasizing their shared histamine-driven pathway; (2) quantify likely underreporting and missed diagnosis; (3) examine diamine oxidase deficiency as a potential cross-species susceptibility factor; (4) identify conserved mechanisms and shared environmental exposures across humans and companion animals; and (5) propose a practical One Health framework for recognition, research, and emergency management.

Key findings: Histamine-mediated coronary injury represents a common final pathway linking allergy, foodborne intoxication, drugs, insect stings, venoms, and contaminated seafood. KS may produce coronary vasospasm, plaque destabilization, or stent thrombosis, whereas scombroid-associated ACS typically causes transient vasospasm but may also trigger secondary mast cell activation. Cardiac mast cells and histamine-responsive coronary vasculature are conserved across mammalian species, suggesting that companion animals are vulnerable to analogous diseases despite an almost complete absence of recognition in the veterinary literature. Diagnostic limitations, species-specific shock responses, and infrequent use of cardiac biomarkers likely contribute to substantial underdiagnosis. Management presents a therapeutic dilemma because interventions routinely used for anaphylaxis or ACS may aggravate the opposing pathology, requiring simultaneous treatment of both the histaminergic and cardiac processes.

Conclusions: Histamine-mediated ACS exemplifies a neglected One Health problem at the intersection of allergy, toxicology, cardiology, emergency medicine, veterinary medicine, and food safety. Increasing global seafood distribution, climate-associated bacterial proliferation, and growing use of raw-fish diets for companion animals may expand exposure risks. Improved interdisciplinary awareness, standardized diagnostic approaches, and coordinated human-veterinary surveillance could reduce preventable morbidity and mortality from these frequently missed but potentially reversible cardiac emergencies.





2535 – Strengthening Community Engagement and Risk Communication for Avian Influenza Preparedness in Guinea: Lessons from a One Health Implementation Project

Kadia DOUMBOUYA (1), Alpha Mahmoud BARRY (1), Claire STANDLEY (2), Maciré SYLLA (1), Sona SIDIBE (1), Kouramoudou BERETE (3), Mamadou bhoye KEITA (4)

1: Santé Plus Organisation, Guinea; 2: University Georgetown; 3: Laboratoire central vétérinaire de diagnostic; 4: institut nationale de santé publique

Background

Highly Pathogenic Avian Influenza (HPAI) H5N1 continues to threaten human, animal and economic health worldwide. Following the 2022 outbreak in Guinea, strengthening community preparedness became a national priority. This study assessed how community engagement and risk communication contributed to H5N1 preparedness within a One Health implementation project.

Methods

A cross-sectional mixed-methods study was conducted in Coyah, Forécariah and Boké. The project included 179 poultry farms, biological sampling of poultry and other domestic animals, and interviews with 399 poultry workers. Community surveys documented farming practices, previous exposure to avian influenza, access to veterinary services and perceptions of disease prevention. Risk communication

activities engaged local authorities, veterinary services and poultry associations through participatory discussions and awareness sessions.

Results

A total of 1,825 animals were sampled across 179 farms. Although no evidence of H5 infection was detected among poultry workers, seasonal influenza circulated widely among participants. The study identified several communication challenges, including farmers' reluctance to participate because of previous outbreak experiences, limited trust in surveillance activities and gaps in biosecurity practices. Active involvement of local authorities, producer associations and technical partners strengthened stakeholder participation and facilitated implementation of One Health surveillance activities.

Conclusion

Community engagement and risk communication are essential components of preparedness for zoonotic influenza. Integrating communities into surveillance systems and strengthening collaboration between human, animal and environmental health sectors can improve trust, early detection and outbreak preparedness in Guinea.

2539 – Environmental occurrence of Acinetobacter baumannii in a protected marine ecosystem: characterization of a rare ST848 isolate

Carlos Henrique CAMARGO (1), Amanda Yaeko YAMADA (2), Anna Luiza Bauer CANELLAS (3), Mauro de Medeiros OLIVEIRA (3), Pedro Smith Pereira FERRARO (2), Daniel de Sena MIRANDA (1), Matheus de Oliveira Nithack MARQUES (3), Guilherme MURICY (3), Marinella Silva LAPORT (3)

1: Instituto Adolfo Lutz, São Paulo, Brazil; 2: Universidade de São Paulo, São Paulo, Brazil; 3: Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil

Background:

Acinetobacter baumannii is a major opportunistic pathogen frequently associated with healthcare settings and antimicrobial resistance. However, the ecology and genomic diversity of environmental populations remain poorly understood. Fernando de Noronha is a protected oceanic archipelago located off the northeastern coast of Brazil, characterized by regulate human visitation and relatively low anthropogenic impact.

Methods:

In 2022, an *A. baumannii* isolate was recovered from a marine sponge collected in Fernando de Noronha, Pernambuco State, Brazil. Antimicrobial susceptibility testing was conducted using standard BrCAST method. Whole-genome sequencing was performed using Illumina NextSeq. Assembly was used to define sequence typing by MLST (Pasteur/Oxford scheme) and acquired antimicrobial resistance genes were identified using ResFinder.

Results:

Phenotypic testing revealed resistance to amikacin and tobramycin, while susceptibility was observed for ciprofloxacin, gentamicin, levofloxacin, imipenem, meropenem, trimethoprim-sulfamethoxazole, and polymyxin B. The isolate was assigned to ST848Pas/novelOxf, a rarely reported lineage not associated with the globally disseminated carbapenem-resistant *A. baumannii* (CRAB) clones. This clone lacks clinically relevant acquired antimicrobial resistance genes, supporting its distinction from typical hospital-associated populations. To our knowledge, ST848 has previously been described only from a bloodstream isolate recovered in Norway in 2017. Our isolate has *bla*OXA-64 (as *bla*OXA-51-like) even though the presence of this variant indicates association with IC7/CC25, the isolate was classified as a singleton (13-3-2-3-7-1-16). Whole-genome analysis did not identify aminoglycoside-modifying enzymes genes, 16S rRNA methylase genes, or other clinically relevant acquired antimicrobial resistance determinant, even after lowering the identity and coverage tool thresholds; efflux pumps were inhibited by PaβN, indicating.

Conclusions:

This study reports the recovery of a rare *A. baumannii* ST848 isolate from a marine sponge in the protected Fernando de Noronha archipelago, with resistance to amikacin and tobramycin, representing, to our knowledge, the first report of this lineage in South America and the first environmental record of ST848. The detection of clinically relevant *in vitro* resistance highlights the importance of environmental surveillance for understanding the diversity, evolution, and ecological distribution of *A. baumannii* and to investigate natural reservoirs of antimicrobial resistance beyond healthcare-associated environments.

Processo Fapesp 2025/10643-3

2543 – NAPAHPI in Practice: Operationalizing the North American Preparedness for Animal and Human Pandemics Initiative for the FIFA World Cup 2026 – A One Health Approach

Iris SHURDHI

Office of Global Affairs, Office of the Secretary, U.S. Department of Health and Human Services, United States of America

Background

The North American Preparedness for Animal and Human Pandemics Initiative (NAPAHPI) is a standing trilateral health security platform that facilitates collaboration among Canada, Mexico, and the United States using a One Health approach to strengthen regional prevention, preparedness for, and response to shared health security threats. This One Health approach recognizes the interconnection between human, animal, plant, and environmental health and is implemented according to national contexts and laws, as relevant. The 2026 FIFA World Cup—the first men's tournament co-hosted by the three countries—provided the first major opportunity to operationalize this platform during a multinational mass gathering. While many One Health-relevant frameworks define governance arrangements, fewer describe how they are implemented during multinational public health emergencies. We describe how NAPAHPI was operationalized to support cross-border information sharing and operational coordination among the three countries while preserving each country's national preparedness and response systems without creating a new event-specific structure.

Methods

We conducted a descriptive implementation case study of NAPAHPI activation for the FIFA World Cup 2026. The setting comprised the trilateral preparedness and response system spanning Canada, Mexico, and the United States. Data sources included governance documents, work plan records, the Communications Hub Standard Operating Procedure (SOP), pre-tournament trilateral Emergency Operations Centre (EOC) coordination meeting, and operational preparedness activities conducted before and during the tournament. We characterized governance architecture, activation processes, multisector participation, and operational coordination mechanisms used to support cross-border preparedness while preserving national decision-making authority.

Results

For the tournament, NAPAHPI functioned as an operational, exercised, multisector platform supporting trilateral preparedness rather than relying on a newly created event-specific mechanism. Twenty-two government organizations participated across public health, agriculture, animal health, environmental, foreign affairs, public safety, and emergency management sectors. Preparedness activities included 11 trilateral governance meetings, six trilateral measles coordination meetings, and two multinational exercises validating the Communications Hub SOP, including a FIFA scenario. Before kickoff, all three countries completed a trilateral EOC coordination call and communications check, confirming the coordination and escalation process with continuously staffed 24/7 EOCs as the primary communication pathway. During the tournament, the three countries coordinated border health measures related to the concurrent Ebola outbreak, with no suspected North American cases identified. In response to the measles outbreak in Jalisco, Mexico established measles vaccination sites at airports and transportation hubs. The Senior Coordinating Body endorsed continued collaboration and a post-tournament after-action review.

Conclusions

This case study demonstrates how a standing trilateral health security platform taking a One Health approach can be operationalized to support multinational public health emergencies while preserving

national sovereignty and decision-making authority. By leveraging an existing platform rather than creating a new one, NAPAHPI provided a scalable approach for future cross-border mass gatherings and regional health security initiatives.

2549 – Veterinary Behavioral Health Issues Associated with Disaster Response

Gary VROEGINDEWEY

Lincoln Memorial University, United States of America

Emergencies and disasters create stressful situations that can exacerbate ongoing behavioural health issues. Veterinarians have been identified as a professional group at elevated risk for behavioural health issues when they are involved with an emergency response. Prior studies looking at transboundary animal disease disaster management demonstrate the significant and long-lasting mental health effects experienced by veterinary responders. To examine the scale and scope of behavioural health issues exhibited by veterinary responders, an online and anonymous survey was conducted with veterinarians who had participated in events in the Asia-Pacific, Africa, Europe, Latin America and North America regions. The results of the survey showed that behavioural health issues were reported by 51 per cent of respondents during and up to 6 months after the disaster. Behavioural health issues reported included loss of sleep, anxiety, difficulty with personal and professional relationships, mood swings, depression, nightmares and flashbacks and suicidal thoughts. Being involved in more than 1 disaster event was associated with higher anxiety and/or depression, difficulty with relationships, and a greater prevalence of sleep problems. Veterinarians deployed longer than 2 months had the highest prevalence of anxiety and/or depression and sleep problems. Veterinarians that received behavioral health training before deployment had lower rates of anxiety and/or depression. Respondents involved with depopulation had the highest rates of anxiety and/or depression and sleep problems. The scope and magnitude of veterinarians with behavioural health issues associated with disasters underscores the need for guidelines, standards, education, training and further research in this area

2562 – Establishing a National One Health Sentinel Surveillance System for Early Detection of Respiratory Threats in Georgia

Giorgi CHAKHUNASHVILI (1), Olga TARKHAN-MOURAVI (1), Irakli KARSELADZE (1), Ana TATULASHVILI (1), Ana GULBANI (2), Tengiz CHALIGAVA (3), David PUTKARADZE (1), David CHAKHUNASHVILI (1)

1: National Center for Disease Control and Public Health, Georgia; 2: State Laboratory of Agriculture of Georgia, Georgia; 3: National Food Agency, Georgia

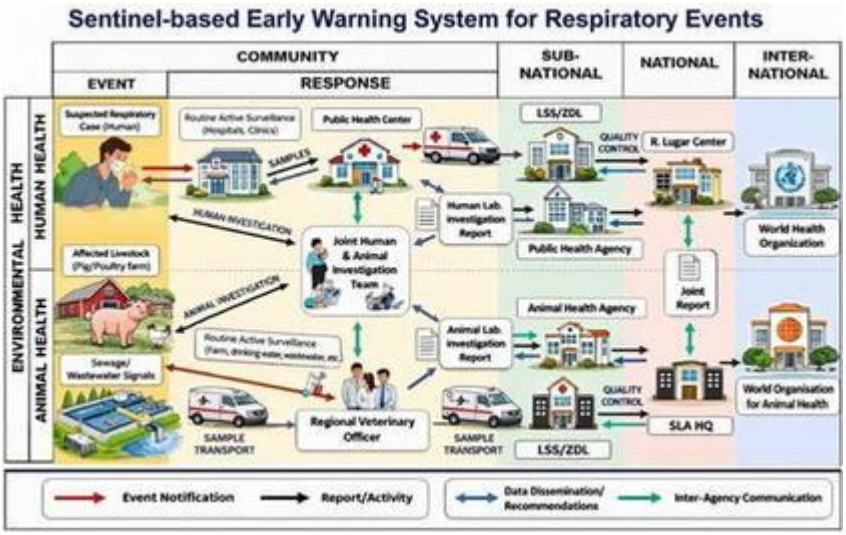
BackgroundEmerging respiratory pathogens pose substantial threats to global health security, underscoring the need for integrated surveillance systems that detect signals across human, animal, and environmental interfaces. In 2025, Georgia launched a Pandemic Fund–supported initiative to establish a national One Health Sentinel Surveillance System integrating human, animal, and genomic surveillance, with wastewater monitoring as an additional environmental data stream, to strengthen early warning for respiratory threats. As of July 2026, enrollment of all eight planned animal sentinel sites has been completed, marking a key milestone toward a fully functional national surveillance network.

MethodsA One Health surveillance framework was developed through collaboration between public health, veterinary, and laboratory stakeholders. Sentinel sites were selected using predefined epidemiological and operational criteria, with priority given to locations along Georgia's major migratory bird corridors, including the Black Sea coastal corridor and the inland wetland corridor. The network comprises one industrial swine farm, two backyard poultry farms, and five industrial poultry farms (four layer farms and one broiler farm), distributed across western (3), central (3), and eastern (2) Georgia. Standard operating procedures (SOPs) for respiratory specimen collection, wastewater surveillance, and surveillance data management are being adapted from international guidance and tailored to the Georgian context, with sampling scheduled to begin in September 2026.

ResultsEnrollment of all eight planned animal sentinel sites has been completed, up from three sites at initial project reporting, establishing the full geographic and production-system footprint of the network. Sites span industrial swine and poultry production (layer and broiler) as well as backyard poultry, and are

positioned along the Black Sea coastal corridor and the inland wetland corridor to capture wild-domestic interface risk. Draft SOPs for respiratory specimen collection, wastewater surveillance, and data management have been developed and are undergoing field-level adaptation ahead of sampling, planned for September 2026. Site assessments and stakeholder consultations across veterinary, public health, and laboratory sectors have shaped sampling strategies and reporting workflows, and surfaced early operational lessons on coordinating backyard and industrial production settings within a single national framework.

ConclusionsCompletion of enrollment across all eight planned sentinel sites, strategically located along the Black Sea coastal and inland wetland migratory corridors and spanning both industrial and backyard production systems, marks a significant step toward operationalizing Georgia's first national-scale One Health surveillance system for respiratory threats. Early implementation experience (spanning site selection, SOP adaptation, and multisectoral coordination) offers practical, immediately relevant lessons for other resource-constrained countries currently establishing similar sentinel networks ahead of sampling launch.



2571 – The U.S. International Health Regulations (IHR) National Focal Point: A Whole-of-Government Approach to One Health Event Assessment

Angela MONAHAN

U.S. Department of Health and Human Services, Office of Global Affairs, United States of America

BACKGROUND

The International Health Regulations (2005) require each State Party to maintain a National Focal Point (NFP) responsible for communicating with international health authorities on potential Public Health Emergencies of International Concern (PHEIC) within 24 hours of assessment. Given that three out of every four new or emerging infectious diseases in humans come from animals, NFP functions require rapid coordination across One Health sectors. This One Health approach recognizes the interconnection between human, animal, plant, and environmental health and is implemented according to national contexts and laws, as relevant. The U.S. IHR NFP integrates three core functions: a 24/7 watch and communications hub, a policy and programmatic coordination arm, and a senior Message Authorizing Official (MAO), supported by a government-wide stakeholder network spanning 35 departments and agencies across nine sectors. This abstract describes the U.S. IHR NFP's One Health operationalization, using the highly pathogenic avian influenza (HPAI) H5N1 outbreak as a case study.

METHODS

This descriptive analysis draws on coordination records and IHR Article 6 notification data since 2007. For potential PHEIC events, the U.S. IHR NFP follows a standard operating procedure: a 48-hour technical assessment, a two-hour multisector interagency review, a two-hour MAO review, and formal notification to the Pan American Health Organization (PAHO). The interagency network spans nine sectors: Energy,

Food Safety, Human Health, Animals/Agriculture, Environment, Travel/Trade, Transportation, Security, and Defense. The HPAI H5N1 outbreak illustrates coordination across this network and a Unified Coordination Group (UCG) co-led by human and animal health authorities. Records were reviewed to characterize One Health engagement, UCG activation, and process adaptations.

RESULTS

Since 2007, the U.S. has submitted 183 IHR Article 6 notifications to PAHO spanning respiratory, zoonotic, foodborne, vaccine-preventable, and other categories. Between April 2024-November 2025, the U.S. submitted 35 notifications related to HPAI H5N1 human cases across multiple states. Consistent with a One Health approach, UCG coordination spanned human, animal, plant, and environmental health authorities throughout the outbreak. Analysis shows that the UCG was activated for elevated interagency review during the most complex clusters, including the early dairy cattle cases and the Colorado poultry worker cluster. Consistent with a One Health approach, the outbreak required sustained multisector engagement across human, animal, plant, and environmental health authorities – a broader response than the largely human-health-focused coordination typical of prior Article 6 notifications.

CONCLUSIONS

The HPAI H5N1 outbreak – spanning nearly two years, 35 IHR Article 6 notifications, and sustained coordination across human, animal, plant, and environmental health authorities — demonstrates the capacity of the U.S. IHR NFP's whole-of-government structure to operationalize One Health. The elevated UCG process, cross-sector engagement, and reporting refinements illustrate how a standing NFP mechanism operationalizes One Health, offering a transferable framework for fellow State Parties implementing IHR (2005).

2573 – Estimating future vaccine manufacturing capacity requirements using discrete event simulation to support Africa's 2040 ambition, tailored by local vector borne and environmental settings

Nico VANDAELE

KU Leuven, Access-To-Medicines Research Centre, Belgium

Background: The African CDC's New Public Health Order aims to improve health, greater regional self-reliance and security by boosting local vaccine manufacturing capacity from 1% to 60% by 2040. Although multiple studies have examined vaccine manufacturing capacity in Africa, none quantified vaccine manufacturing capacity requirements. Africa wants to become more self-reliant as it addresses its vaccination needs, thereby supporting more equitable access. Our research constructs decision support models that enable to define the manufacturing systems needed to realize a particular manufacturing system throughput. In particular, some of the vaccines most viable and sustainable to be produced in Africa are vector borne (e.g. malaria) or related to environmental conditions (e.g. cholera).

Methods: The study is scoped on the African continent taking local characteristics into account. We integrate deterministic approach and discrete event simulation (DES) to estimate vaccine manufacturing capacity and assess the impact of process variability and uncertainty on manufacturing capacity. We model PCV, Pentavalent, Measles-Rubella, Malaria, BCG, HIV/AIDS & Covid-19. Data became available on July 7th.

Results:

Besides the necessary physical capacity to meet the required volumes, we estimated that about 3,737 drug substance and drug product technical staffs are required in Africa, and yet only about 1,600 vaccine manufacturing staffs are available in Africa according to African CDC. This shows that considerable investments towards training, recruiting and retaining future vaccine manufacturing experts in the continent is needed.

Conclusions: This study demonstrates the need for substantial investments in vaccine manufacturing in Africa in order to realize the 2040 ambitions for a local and sustainable vaccine supply. Those investments must be coordinated and extended across different vaccines, vaccine manufacturing platforms and technologies in the continent to avoid overcapacity in a few vaccine technologies and platform as witnessed with the massive investments in mRNA technology post-COVID-19 and

undercapacity in others. Our capacity estimation approach can provide valuable evidence to support the coordination of manufacturing infrastructure establishment and expansion, workforce development, assess the feasibility of future manufacturing capacity before major investments are made, and align manufacturing capacity with market demand. The study departed from local demand needs combined with the long term viable local production volumes to ensure sustainable equitable access and concluded on the gaps between current and future needed manufacturing capabilities. Current steps are to construct synergetic vaccine manufacturing networks and identify local producers. At this point manufacturer specific data refinement comes in. However, this is just a necessary condition, not a sufficient one: the manufacturing subsystem needs to be embedded in the broader eco-system, where it touches several one-health aspects: important and promising vaccines to be produced locally are vector borne and environmentally determined. This opens a totally new view on the typically more narrowly defined local vaccine production ambition.

2617 – BACI analysis demonstrates no effect of sanitation interventions in synanthropic small mammals from Salvador, Brazil

Leonela BAZAN (1), Ana Maria BARRETO (2), Roberta COUTINHO DO NASCIMENTO (3), Maria Luiza VIEIRA DE JESUS (4), Hernán Dario ARGIBAY (2), George GONÇALVES MACHADO (5), Eduardo MENDES DA SILVA (1), Samilly MIRANDA (2), Federico COSTA (2,3), Caio GRACO ZEPPELINI (2), Hussein KHALIL (6)

1: Institute of Biology, Federal University of Bahia, Salvador, BA, Brazil; 2: Institute of Collective Health, Federal University of Bahia, Salvador, BA, Brazil; 3: Gonçalo Moniz Institute, Oswaldo Cruz Foundation (FIOCRUZ), Salvador, BA, Brazil; 4: University Salvador (UNIFACS), Salvador, BA, Brazil; 5: Institute of Geosciences, Universidade Federal da Bahia, Salvador, BA, Brazil; 6: Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, Umeå, Sweden

Background: Urban infrastructure interventions, including the expansion of basic sanitation, are essential measures for health promotion and infectious disease prevention. In vulnerable communities shaped by unplanned urbanization, inadequate sanitation, poor waste management, and environmental degradation may increase exposure of humans, domestic animals, and wildlife to contaminated environments and zoonotic pathogens. Sanitary sewerage interventions that remove domestic sewage from rivers and open drainage systems may reduce environmental contamination and alter habitat conditions for synanthropic mammals, such as brown rats (*Rattus norvegicus*) and opossums (*Didelphis aurita*). However, the ecological effects of sanitation interventions on small mammal populations remain poorly understood. We evaluated the effects of a simplified sewerage intervention on brown rat and opossum occurrence in vulnerable communities in Salvador, Brazil.

Methods: The study was conducted in two vulnerable urban communities in Salvador, Brazil, from 2024 to 2026: Nova Sussuarana (NS; intervention area) and Calabetão (CAL; control area). Three trapping campaigns were conducted before and after implementation of a simplified sewerage intervention in NS. During each campaign, 30–40 sampling points were randomly selected, and two Tomahawk traps were installed per point for four consecutive nights. We used a Before–After Control–Impact (BACI) approach, generalized linear mixed models, and multi-species occupancy models to evaluate intervention effects on rat and opossum occurrence, species interactions, and associations with environmental characteristics.

Results: Rat captures decreased in the control area (CAL), whereas rat and opossum captures remained relatively stable in the intervention area (NS). BACI analyses detected no significant effect of the sewerage intervention on rat, opossum, or overall capture occurrence. Opossums were more frequently associated with sites containing greater vegetation cover and open sewers, while rat occurrence differed mainly between study areas. Multi-species occupancy models and GLMMs found no evidence that opossum presence reduced rat occupancy or capture probability.

Conclusions: The sewerage intervention was insufficient to promote detectable short-term changes in rat or opossum occurrence. The reduction in rat captures in CAL may have been influenced by an unplanned chemical rodent-control action, limiting attribution of observed changes solely to temporal or intervention-related effects. Small mammal occurrence is likely influenced by multiple factors, including food and shelter availability, solid-waste management, urban landscape characteristics, and climatic conditions. Therefore, reducing zoonotic reservoirs and environmental exposure to pathogens may require integrated strategies combining sanitation improvements, environmental management, waste control, and reservoir surveillance within a One Health framework.

2636 – Strengthening Points of Entry for Cross-Border Health Facility Readiness in Bangladesh using Existing Institutional Facilities

Nitish Chandra DEBNATH, Ayan Shankar SEAL, Md. Zakiul HASAN, Zubair SHAMS, Samina CHOUDHURY, Abid HASAN, Sharif Hossen SAIMUM, Paul DARU
FHI360, Bangladesh, People's Republic of

Background: Bangladesh faces persistent threats from infectious diseases that can spread across borders through the movement of people, animals, and goods. As a country with extensive land, air, and sea travel and trade, points of entry (PoE) serve as the frontline defense for preventing, detecting, and responding to human and animal health risks. In collaboration with the Directorate General of Health Services (DGHS), the Department of Livestock Services (DLS), and the Port Authorities of Bangladesh, the U.S. Government-funded Meeting Targets and Maintaining Epidemic Control (EpiC) project is working to strengthen systems and capacities at four PoEs in its geographic scope to prevent, detect, and respond to cross-border transmission of infectious diseases.

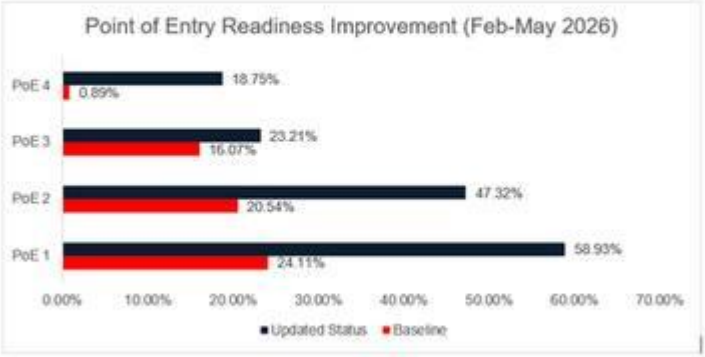
Methods: EpiC conducted a comprehensive assessment of four PoEs in February 2026, focusing on strategic directives, infrastructure, coordination, surveillance, communication, cross-border collaboration, budgeting, and quarantine. The assessment was conducted by trained field staff using a standardized questionnaire aligned with Joint External Evaluation (JEE) priorities and World Organization of Animal Health (WOAH) standards. EpiC, working with in-country human and animal health professionals and the port authority, used the assessment findings to improve health screening through on-the-job coaching and resource mobilization. This work included improving record keeping, reporting to relevant health authorities, providing electric connection for display boards and a water supply for hand washing stations, ensuring space for health screenings, and assisting the government in issuing instructions from the International Health Regulation (IHR) focal point to reinforce the health screening practices at PoEs. EpiC monitored to track improvements in the PoEs' functionality after taking all those initiatives.

Results: The assessment revealed critically low levels of readiness, with an average baseline score of 15.40%. Preparedness scores were 24.11%, 20.54%, and 16.07% in three PoEs, while one PoE was nearly nonfunctional, scoring only 0.89%.

The EpiC team worked closely with government authorities involved in PoE governance, including the IHR focal point, port authorities, and local PoE authorities, to strengthen understanding of the critical role of PoEs in preventing the spread of zoonotic infections. Through government resource mobilization and targeted technical support, PoE readiness increased significantly from 15.40% to 37.05% by May 2026. Further improvement in the infrastructure of facilities in the PoEs will be necessary to establish full compliance with international requirements. Significant imprvoment measured during last four months.

Conclusions: These results demonstrate significant progress in strengthening PoE preparedness and response capacities. This approach will be institutionalized for maintaining the PoE capacities in line with global health security (GHS) priorities. By addressing operational and coordination gaps, the country can significantly strengthen its ability to detect emerging threats early, contain outbreaks at their source, and safeguard both national and regional health security in line with GHS goals without requiring substantial external support.

Figure 1. Point of entry readiness scores status, February - May 2026



2638 – Is the One Health an asset for Health Security? Insights from the International Workshop "Strengthening capacities to adopt One Health to enhance Health Security" (Rome, 13-15 April 2026)

Maham HABIB (1), Asma SAIDOUNI (2), Alessia RANGHIASCI (1), Gloria NACCA (1), Cosima ZINGARIELLO (2), Maria Grazia DENTE (1)

1: Istituto Superiore di Sanità, Italy; 2: World Health Organization, Libya

Background:

One Health (OH) is considered essential for global health security, yet its operationalization within integrated national systems remains uneven across sectors. While policy-level recognition has grown, practical implementation is hindered by sectoral silos, fragmented data exchange, and weak institutional governance. Essential health security drivers including technical networking and community engagement also remain underutilized. International multisectoral workshops can help bridge these gaps by translating cross-country dialogue into sustainable, system-based actions that reinforce regional health security pillars.

Methods:

The Istituto Superiore di Sanità (ISS), Rome, in collaboration with the World Health Organization (WHO) Libya, organized an international multisectoral workshop on 13 –15 April 2026 under a joint OH capacity-strengthening initiative focused on arboviral and zoonotic disease threats in Libya. The event convened experts from European and Mediterranean countries across human, animal, environmental, and entomological sectors, representing over 25 institutions. The workshop included a keynote lecture on OH sustainability, sessions on networking and national OH strategies, multidisciplinary working groups, and a final roundtable on international governance. Using a structured template, working groups mapped collaborations, national challenges, and data gaps. Findings were thematically synthesized to generate priority recommendations for a sustainable OH implementation.

Results:

The workshop generated a comprehensive understanding of OH operationalization across diverse national contexts and what is needed to move from policy recognition to routine, system-based implementation.

Country presentations highlighted varying stages of national OH strategy development, including implementation status, primary focus areas, and key operational challenges, as summarized in Table 1.Building on country presentations, working groups used a structured template to examine cross-country OH collaboration, including existing mechanisms, gaps, resources and priority actions, as summarized in Table 2.

Concurrently, the session on Networking and final roundtable with Food and Agriculture Organization of the United Nations, WHO, World Organisation for Animal Health, European Centre for Disease Prevention and Control and European Food Safety Authority reinforced the need to move from activity-driven collaboration to system-based OH implementation. To support long-term sustainability, agreed priorities included stronger legal and coordination frameworks, routine intersectoral data exchange, sustained capacity building, and recognition of community engagement as a relevant component of health security oriented OH implementation.

Conclusion

The workshop established a practical blueprint to guide the progressive operationalization of OH over the coming years. To strengthen health security, OH implementation should shift from informal and project-driven cooperation to formal governance supported by sustainable financing and cross-country coordination. This requires clear legal frameworks, regular cross-sectoral data sharing, stronger multi-agency networking, and community engagement in national and regional strategies.

This work was supported by the Italian Ministry of Foreign Affairs and International Cooperation through the Agency for Development Cooperation, with technical and financial support from the National Institute for Public Health and the Environment, the Netherlands.

Country	Strategy Status	Primary Focus Pillar	Main Operational Challenges
Spain	Formally Adopted	Vector-borne diseases	No permanent coordination structures
Armenia	Under Development	Integrated Surveillance	Limited formal coordination
Egypt	Formally Adopted	Integrated Surveillance	Cross-sectoral data sharing
Netherlands	Fully Operational	Integrated Data Systems	Complex coordination
Türkiye	Formally Adopted	Zoonoses & AMR surveillance	Fragmented governance
Tunisia	Under Development	Integrated Surveillance	Reliance on external funding
Georgia	Formally Adopted	Integrated Surveillance	System interoperability
Serbia	Not Formally Adopted	Policy Alignment	Policy-to-practice gaps
Libya	Under Development	Governance and Capacity Building	Siloed surveillance
Lebanon	Under Development	Multisectoral coordination	Data exchange gaps

Table 1. Status, focus areas and operational challenges of national One Health strategies

Working group finding	Consolidated message
Existing collaborations	Bilateral, regional, project-based mechanisms exist
Current functioning	Primarily ad-hoc, informal, and project-driven
System gaps	Limited formalization, fragmented data, and poor interoperability
Operational gaps	Limited multisectoral response capacity
Available resources	Workforce, surveillance capacities, technical networks
Priority needs	Legal frameworks, data harmonization, sustainable financing

Table 2. Consolidated findings on cross-country One Health collaboration

Poster zone 4

Olive Tree

2658 – Indigenous-Led Wildlife Health Monitoring: Strengthening One Health through Indigenous Knowledge, Food Security, and Collaborative Governance

Brenda PARLEE (1), **Kevin AHKIMNACHIE** (2), **Kacey YELLOWBIRD** (3), Hannah CUNNINGHAM (4)

1: McGill University, Canada; 2: Treaty 8 First Nations of Alberta; 3: Samson Cree Nation, University of Alberta; 4: University of Alberta

Background: Emerging wildlife diseases present complex One Health challenges that cannot be addressed through biomedical surveillance alone. Chronic wasting disease (CWD), a fatal prion disease affecting deer, elk, moose, and caribou, is spreading across western Canada and carries profound implications for Indigenous Peoples whose food systems, cultures, and well-being depend on healthy wildlife populations. While One Health recognizes the interconnectedness of human, animal, and environmental health, Indigenous Knowledge systems remain underrepresented in wildlife disease research and monitoring. This study examines how Indigenous-led wildlife monitoring strengthens One Health practice by expanding surveillance capacity and producing health and well-being outcomes that go beyond — but are consistent with — the aims of conventional One Health frameworks.

Methods: This research draws on more than a decade of collaborative, community-based research involving Treaty 6 and Treaty 8 First Nations in Alberta, Canada, and university researchers. Data were synthesized from over 320 surveys with Indigenous hunters conducted between 2008 and 2026, community workshops, Elder dialogues, youth engagement activities, collaborative meetings with wildlife health researchers, and the co-development of culturally appropriate monitoring tools and educational resources. Research design and implementation were guided by Indigenous leadership and cultural protocols, with a sustained focus on community participation and youth training. All outcomes were used and shared in accordance with the principles of Free, Prior and Informed Consent (FPIC).

Results: Indigenous-led monitoring produced four complementary outcomes that strengthen One Health research and practice. First, Indigenous Knowledge contributed new, place-based observations of cervid health, behaviour, habitat conditions, and harvesting and consumption patterns that complemented conventional wildlife surveillance. Second, active participation in monitoring and knowledge-sharing improved community understanding of CWD, reducing uncertainty and anxiety surrounding wildlife health risks and the safety of country foods while increasing confidence in evidence-informed harvesting decisions. Third, integrating Indigenous Knowledge with scientific monitoring expanded the scope of wildlife health assessment beyond disease prevalence to encompass food security, cultural continuity, stewardship responsibilities, and heath and well-being. Finally, Indigenous leadership in the whole research process improved the relevance of research outcomes to communities while at the same time creating other opportunities for knowledge braiding with scientific research.

Conclusions: Indigenous-led monitoring should be recognized as a core component of One Health research, not merely a source of supplementary local knowledge. By generating new ecological observations, broadening community participation, reducing health-related uncertainty, and integrating the cultural and social dimensions of wildlife health into surveillance systems, Indigenous-led monitoring produces more comprehensive and actionable evidence for wildlife disease management. Future One Health initiatives addressing emerging wildlife and zoonotic diseases must embed Indigenous leadership, knowledge systems, and governance throughout research design, implementation, and decision-making — not as an afterthought, but as a foundation for both scientific rigour and equitable community health outcomes.

2661 – Advancing One Health research in the Canadian Arctic through infrastructure, partnerships, and community-driven science

Alexandra KANTERS, **Alexandra TAYLOR**

Polar Knowledge Canada, Canada

Background: One Health recognizes the interconnectedness of environmental, animal, and human health. In the Canadian Arctic, rapid environmental change is affecting ecosystems, wildlife populations, food systems, and community wellbeing. Polar Knowledge Canada (POLAR) is a Canadian federal agency that advances an integrated One Health approach to Arctic research through funding, infrastructure, partnerships, and knowledge mobilization activities that support northern and Indigenous priorities. POLAR's work spans all three One Health domains, with particular emphasis on the intersections between climate change, wildlife health, and community resilience.

Methods: We present a portfolio analysis of POLAR's research, funding, and partnership activities. Initiatives were categorized according to their alignment with environmental, animal, and human health, and their intersections within a One Health framework. Considered activities include research conducted through the Canadian High Arctic Research Station (CHARS), internal research, projects funded through POLAR's grants and contributions program, knowledge mobilization, and collaborations/partnerships.

Results: POLAR's activities demonstrate engagement across all One Health domains. Environmental health activities include ecosystem monitoring, climate change research, and studies of Arctic terrestrial, freshwater, and marine systems. Animal health activities include wildlife health surveillance and community-based monitoring. Human health and wellbeing are supported through research related to food security, community resilience, climate adaptation, youth programming, and knowledge co-production. At the intersections of these domains, POLAR supports projects and partnerships addressing zoonotic disease risks, country food systems, environmental determinants of health, and climate-driven changes affecting wildlife and people. In March 2026, POLAR released its updated Science and Technology Framework (2026-2029), which identifies "One Health" as a key research priority for the agency. In April 2026, POLAR opened a targeted One Health funding call, announcing $3.8M for food security research related to the health, availability, and sustainability of country foods (locally harvested plants, animals and fish) in the Arctic.

Conclusions: POLAR's integrated approach to funding, infrastructure, partnerships, community engagement, and knowledge mobilization advances One Health, enabling research that addresses complex challenges in a rapidly changing Arctic.

2672 – i-Tafaray: an integrated and interoperable national One Health surveillance system in Madagascar

Veronique CHEVALIER (1), Bénédicte RAZAFINJATO (2), Florian GIROND (1), Rufin ANDRIANDAZA (2), Hary RASEHENO (3), Zo ANDRIANASANDRATRA (4), Olitina RATOVO (5), Andres GARCHITORENA (6), Katerina ALBRECHTOVA (1), Haja ANDRIAMAROFARA (7), Vaoary RAZAFIMBIA (3)

1: CIRAD, Madagascar; 2: ONG PIVOT; 3: Ministry of Public Health, Madagascar; 4: Ministry of Livestock, Madagascar; 5: Ministry of Environment and Sutainable Development; 6: IRD, FRance; 7: World Bank

Background

While the One Health approach, linking human, animal, and environmental health, is widely recognized as essential to address emerging threats, translating it into operational surveillance systems remains challenging, especially in low-income settings. Madagascar is particularly vulnerable to zoonotic disease emergence, driven by ongoing deforestation, biodiversity loss and a resource-limited health system. In this context, Malagasy human, animal and environmental health authorities, the French Development Agency (Africam Madagascar project), the World Bank (Pandemic Preparedness and Basic Health Services project), NGO PIVOT, IRD and CIRAD joined efforts to develop and operationalize a multisectoral, interoperable surveillance system compliant with the national and International Health Regulations (IHR).

Methodology

The system builds on a community-based, human event-based surveillance system implemented by the NGO PIVOT in Ifanadiana district (south-eastern Madagascar) using the CommCare platform. Representatives of the Ministries of Public Health, of Environment and Sustainable Development, and of Livestock co-defined a list of 18 abnormal events (e.g. rodent mortality, sudden rise in human respiratory syndromes); a dedicated reporting module was integrated into CommCare. A training-of-trainers program was held for community health workers, veterinarians, vaccinators and rangers to strengthen adoption of integrated One Health surveillance. An interoperability layer was then developed to connect CommCare

with existing systems (MadSur for livestock, SMART for wildlife morbidity/mortality) and to integrate notifications into a national platform, i-Tafaray, through: (1) validation of the target architecture and technical standards; (2) a common data dictionary and definition of intersectoral data flows; (3) configuration of notifications, alerts, dashboards, a risk-analysis framework and automated reports. User guides were developed and validated with stakeholders.

Results

The solution automates and centralizes community field-event notifications via smartphones and basic phones (SMS). It is connected to the secure national X-Road gateway, feeding real-time data automatically into the platform, and incorporates local climate and SMART environmental data, going beyond health indicators alone. i-Tafaray links signals from different sectors occurring in the same location and assesses the risk of disease onset in real time. By clustering cross-sector signals around each alert, the platform estimates the detection lead time gained between the first non-human signal and the first human case, while improving both sensitivity, capturing events a single sector would miss and specificity, since cross-sector corroboration filters out false alarms. The platform was deployed and configured in line with the recommended architecture for health information systems (OpenHIE) and the interoperability standards adopted by Madagascar's Digital Governance Unit (UGD).

Conclusions

i-Tafaray complies with the national interoperability framework based on international and national standards. It has been officially endorsed by the Secretary-General of the Malagasy Government as the system to be reinforced locally and then scaled up nationally — demonstrating a replicable path from the One Health concept to operational, interoperable surveillance.

2693 – Multiomic analysis of microbiome and resistome with chemical pollutants in the indoor environment: a CELSPAC:TNG cohort study

Petra BORILOVA LINHARTOVA, Jan BOHM, Barbora ZWINSOVA, Jaroslav JANOSEK, Eva KLVANOVA, Vojtech BARTON, Paula MARCINEKOVA, Simona Rozarka JILKOVA, Petr KUKUCKA, Petr SENK, Jakub MARTINIK, Petra BRENEROVA, Eva BUDINSKA, Pavel PILER, Lenka ANDRYSKOVA, Petra PRIBYLOVA, Lisa MELYMUK, Jana KLANOVA

RECETOX, Faculty of Science, Masaryk University, Brno, Czech Republic

Background

Indoor environments are a reservoir of microorganisms, mobile genetic elements, and chemical pollutants that can significantly affect the overall well-being of users of a given space, particularly children. Based on the results of our pilot metagenomic studies of samples collected from a maternity hospital, a children's hospital, households with children, and parents' workplaces, this study analyzed interactions between the microbiome, the resistome, and chemical pollutants in dust samples from households – spaces where children spend a large part of their lives and which, therefore, represent one of the most significant risks to children's health.

Methods

Dust samples were collected from households of children from the CELSPAC:TNG cohort study. Selected chemical pollutants in dust samples were analyzed by GC/MS or LC/MS, as appropriate. DNA from dust samples was isolated and both 16S rRNA amplicon sequencing and whole metagenomic sequencing were performed for analysis of microbiome and resistome. The DIABLO framework from the mixOmics package was employed to integrate the multi-omics datasets and identify the key variables driving the differences between households.

Results

Environmental and opportunistic genera such as *Moraxella, Acinetobacter, Sphingomonas, Pseudomonas,* and *Methylobacterium* were frequently detected in household dust samples. As expected, the core microbiome across households was dominated by commensal and skin-associated taxa, including *Staphylococcus*, *Corynebacterium*, *Cutibacterium*, *Streptococcus*, and *Micrococcus*. These bacteria were often linked to some classes of antimicrobial resistance genes (ARG) including macrolide/lincosamide/streptogramin, phenicol, and aminoglycoside. Significant correlations were observed between byproducts of combustion and ARG classes such as phenicol and

lincosamide/macrolide/streptogramin. Importantly, integrated cross-class correlation analyses revealed structured associations between bacterial taxa, ARG classes, and chemical features, indicating a tightly interconnected indoor ecological system.

Conclusions

These pilot data highlight the importance of a multiomic approach due to the complexity of relationships within the indoor environment. To this date, the metagenomic and chemical patterns of households have gone relatively unexplored and their impact on children's health and development needs to be considered. To further explore associations between such patterns and actual human health, we are investigating microbiome and chemical exposure in samples from children enrolled in the CELSPAC:TNG 4MI cohort and intend to analyze associations between the exposome and their health.

Acknowledgements

This work was carried out with the support of RECETOX Research Infrastructure (ID LM2023069). This project has received funding from the EU's H2020 research and innovation programme under GA No 857560 and from the Horizon Europe programme under GA No 101136566. The views expressed are those of the author(s) only and do not necessarily reflect those of the EU or HADEA. Neither the EU nor the granting authority is responsible for any use of the information. The authors acknowledge funding from the Czech Science Foundation (GAČR, grant no. GA22-32743S).

2703 – Guidebook and Toolbox to Investigate Novel Diseases

Shiyong WANG (1), Roger MORRIS (2)

1: World Bank; 2: EpiSoft International Ltd., Consultancy and software for global disease control

Background

New diseases are frequently emerging from wildlife, and diseases are constantly evolving. Most of these developments occur in regions of the world where access to the latest information and resources to investigate such events is limited. This slows down the investigation and can reduce the effectiveness of the response. Yet there are no readily available guides to help investigators around the world apply a one health approach to investigate novel diseases which may involve people, domestic animals and wildlife, and are likely to be epidemiologically complex.

The Book

To provide this missing guide, a book has been completed and is about to be launched - "How to Solve a Mystery Disease – Methods for investigating emerging and evolving diseases". There are forty authors, from all parts of the world. They have been chosen both for their expertise in the methods they describe, and their experience in undertaking disease investigation in regions where disease emergence may occur.

The book first describes the investigation strategy to be used, then there are ten chapters describing all of the essential methods available for use, ranging across all necessary fields from genomics to spatio-temporal analysis, climate effects and wildlife disease investigation.

It then provides tools to implement the investigational approach, including how to involve all the various stakeholders in taking action. Four case studies describe successful implementation of a one health approach to investigation of important new disease developments. Finally, a guide is provided on how global, regional and national resources can be brought together in a disease response.

The Disease Investigation Toolbox

Although diseases evolve constantly, a book cannot evolve until a new edition appears. To overcome this limitation, the book is accompanied by an open access Disease Investigation Toolbox www.disease-investigation-toolbox.org which allows the information available to users to be kept up to date. It initially contains over 3,000 scientific papers and other documents which are cited as references in the chapters of the book, and it is organized in the same chapter structure as the book. It also includes two complete books on epidemiological analysis methods. It has a Forum for people to ask questions and discuss current issues.

The toolbox will be kept up to date by the addition of new material, as each of the investigation methods advances in the future. It can therefore ensure that users are kept completely up to date on how to use each of the methods.

Conclusion

The book and toolbox will jointly provide enhanced support to investigators undertaking a one health approach to novel disease events.

2705 – Uncovering the dynamics and socio-ecological drivers of Rift Valley fever across an endemicity gradient in Uganda.

Elise RINGWALDT (1), Charity A. NASSUNA (2), Nackson BABI (2), Phiona KATUSHABE (2), Naomi FULLER (1), Gladys K. NAKANJAKO (2,3), Swaib LULE (1), George BALDRY (1), Laura FERGUSON (4), Janet SEELEY (5), Mercy HAUMBA (2), Teddy NAMAGGA (2), Joseph MUTYABA (2), Wilber SSEMBAJWE (2), Deo NTEZA (2), Dennison KIZITO (2), Julius LUTWAMA (2), Nigel FIELD (1), Rory GIBB (1)

1: University College London, United Kingdom; 2: Uganda Virus Research Institute, Uganda; 3: National Animal Disease Diagnostics and Epidemiology Centre (NADDEC), Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Uganda; 4: University of Southern California, United States of America; 5: London School of Hygiene & Tropical Medicine (LSHTM), University in London, United Kingdom

Background:

Rift Valley fever (RVF) is a mosquito-borne, multi-host viral zoonosis, which causes significant outbreaks in animal and human populations across Africa. Human transmission dynamics are shaped by interactions between environment, vectors, and animals. Although historically considered to arise in periodic large outbreaks, an epidemiological continuum is increasingly recognised, with some landscapes sustaining endemic transmission, and others experiencing more sporadic outbreaks. Understanding the social-ecological and climatic factors that shape RVF endemicity has been challenging because research has rarely taken a comparative lens across different transmission settings. Here, we combine multi-host serology with vector, behaviour, climate and environmental data, collected across a gradient of transmission settings within Uganda. We aimed to identify area-level characteristics for RVF transmission and understand the relative importance of socio-ecological and livestock-related factors in patterns of human and livestock infection.

Methods:

A large, multispecies, age-structured serology dataset was collected by the Collaborative One Health Research Initiative on Epidemics (COHRIE - Uganda) to investigate RVF at the human-livestock-wildlife interface, in 90 communities interfacing six diverse conservation areas. We used catalytic and spatial statistical models to: (1) estimate and map regional differences in the force of infection (FOI) in people (n= 2852) and livestock (n = 4043; 2175 cattle, 1548 goats and 320 sheep); (2) investigate the importance of livestock in RVF transmission to humans; and (3) identify individual-level social, demographic, and environmental risk factors.

Results:

Overall, 12.1% of people, 11.6% of cattle, 10.5% goats, and 21.6% sheep were seropositive for RVF. Geographical patterns of RVF seropositivity were broadly similar across humans and cattle, although seroprevalence was only weakly correlated at village-level. We found that RVF dynamics in humans grouped into settings with high population exposure (represented by Pian-Upe, Murchison Falls, and Lake Mburo-Nakivale; average seroprevalence = 20.4% (SD ±4.2%)), or low population exposure (represented by Queen Elizabeth National Park, Kidepo Valley and Bwindi-Mgahinga; average seroprevalence 3.5% (SD ±1.9%)). Using catalytic models, we estimated an annual FOI of 0.4% (95% CI: 0.35-0.44) of susceptible people becoming infected, 3.0% (95% CI: 2.6-3.3) of cattle, 3.4% (95% CI: 2.9-4.0) of goats and 7.0% (95% CI: 5.5-8.7) of sheep; with greater FOI in high-transmission areas. Using spatial models, we observed that exposure risk in humans was strongly associated with time spent in outdoor environments, including occupations such as animal herding and crop farming, which is culturally determined in geographically-specific ways.

Conclusions:

Our results demonstrate a clear gradient of RVF across different settings in Uganda, and provide strong evidence for hyperendemic foci at the margins of conservation areas, especially in the cattle corridor. Together, our findings provide an integrative understanding of the drivers and pathways of RVF exposure, and will support geographically targeted public health surveillance and community-based interventions for RVF.

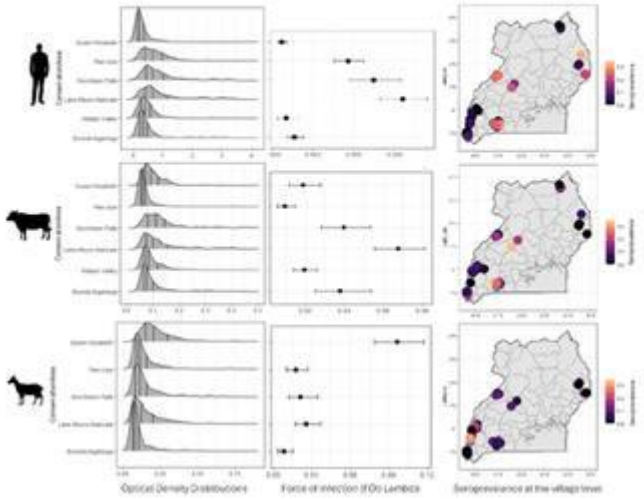


Figure 1: Rift Valley Fever (RVF) serology and force of infection (FOI) for humans, cattle and goats.. Left column: the distribution of RVF IgG ELISA assay optical density values are shown for each conservation area, with the median and 95% intervals (solid-black lines) for humans (n=2852), cattle (n=2175), and goats (n=1548). Middle column: Points and error-bars show the median and 95% confidence intervals for the force of infection per year for each conservation area. Right column: Maps of Uganda showing the seroprevalence per village (n=90), with lighter colours indicating higher seroprevalence.

2715 – Occurrence of Per- and Polyfluoroalkyl Substances (PFAS) in Avian, Bovine and Porcine Muscle from Sicily: A One Health Surveillance Study

Elisa Maria Domenica MESSINA, Francesco Giuseppe GALLUZZO, Gaetano CAMMILLERI, Licia PANTANO, Maria Drussilla BUSCEMI, Calogero ALFANO, Pietro RIOLO, Claudia AMANTE, Gianluigi Maria LO DICO, Andrea MACALUSO, Vincenzo FERRANTELLI

Istituto Zooprofilattico Sperimentale della Sicilia, Italy

Background

Per- and polyfluoroalkyl substances (PFAS) are persistent environmental contaminants with high bioaccumulation potential and long biological half-lives. Food-producing animals may be chronically exposed through contaminated water, feed and soil, creating a potential pathway for human dietary

exposure. Although muscle is widely consumed, information on PFAS occurrence in Mediterranean livestock remains limited. This study evaluated PFAS in muscle samples from animals reared in Sicilian areas characterised by different environmental contamination scenarios.

Methods

Forty-six muscle samples, comprising 20 avian, 11 bovine and 15 porcine samples, were collected from industrialised and rural areas of Sicily (Southern Italy). Sampling included potentially impacted areas (Milazzo, Priolo and Gela) and reference areas (Agrigento, Palermo and Termini Imerese). Homogenised samples stored at −20 ± 3 °C were extracted using a QuEChERS procedure and analysed by liquid chromatography–tandem mass spectrometry with a triple-quadrupole analyser and an electrospray ionisation source operated in negative mode. $^{13}C_8$-PFOA and $^{13}C_8$-PFOS were used as internal standards.

Results

At least one PFAS was quantified in 16/46 muscle samples (34.8%), including 14/20 avian samples (70.0%) and 2/11 bovine samples (18.2%); no PFAS was quantified in porcine muscle. PFOA was the most frequently quantified compound (10/46; 21.7%) and occurred exclusively in avian muscle (10/20; 50.0%), with a mean concentration of 0.045 ± 0.010 µg kg^{-1} and a maximum of 0.069 µg kg^{-1}. PFHxS was quantified in 4/46 samples (8.7%), all of avian origin (4/20; 20.0%), with a mean concentration of 0.109 ± 0.048 µg kg^{-1} and a maximum of 0.155 µg kg^{-1}. PFOS was quantified in 2/46 samples (4.3%), both bovine (2/11; 18.2%), with a mean concentration of 0.037 ± 0.009 µg kg^{-1} and a maximum of 0.044 µg kg^{-1}. PFNA was not quantified in any sample.

Conclusions

PFAS occurrence in muscle was strongly matrix- and species-dependent and was predominantly associated with avian samples. PFOA showed the highest quantification frequency, whereas PFHxS reached the highest mean and maximum concentrations. PFOS was quantified only in bovine muscle, and none of the target PFAS was quantified in porcine muscle. These findings support continued food-chain surveillance and the application of a One Health framework to identify environmental contamination pathways and protect consumers.

2721 – Occurrence of Per- and Polyfluoroalkyl Substances in Eggs from Different Environmental Areas of Sicily

Licia PANTANO, Francesco Giuseppe GALLUZZO, Elisa Maria Domenica MESSINA, Claudia AMANTE, Gaetano CAMMILLERI, Calogero ALFANO, Pietro RIOLO, Maria Drussilla BUSCEMI, Vincenzo FERRANTELLI, Andrea MACALUSO, Gianluigi Maria LO DICO

IZS Sicily, Italy

Background

Eggs are an important dietary source of animal protein, but information on PFAS contamination remains limited. Laying hens may be exposed through contaminated feed, drinking water and soil, with subsequent transfer to eggs. This study assessed PFAS occurrence in eggs produced under different environmental conditions in Sicily.

Methods

Twenty-nine egg samples were collected from commercial and rural laying-hen farms located in industrial and reference areas of Sicily (Southern Italy). Homogenised samples stored at −20 ± 3 °C were extracted using a QuEChERS procedure and analysed by liquid chromatography–tandem mass spectrometry with a triple-quadrupole analyser and an electrospray ionisation source operated in negative mode. $^{13}C_8$-PFOA and $^{13}C_8$-PFOS were used as internal standards.

Results

At least one PFAS was quantified in 19/29 egg samples (65.5%). PFOA was the most frequently quantified compound, with a mean concentration of 0.039 ± 0.014 µg kg^{-1} and a maximum of 0.062 µg kg^{-1}. PFHxS was quantified in 3/29 samples (10.3%), with a mean concentration of 0.119 ± 0.065 µg kg^{-1} and a maximum of 0.168 µg kg^{-1}. Although less frequent than PFOA, PFHxS showed the highest mean and

maximum concentrations among the target compounds. PFOS and PFNA were not quantified in any sample.

Conclusions

PFAS occurrence in hen eggs was primarily driven by PFOA, whereas PFHxS, despite its lower frequency, reached the highest concentrations. The absence of quantifiable PFOS and PFNA indicates a compound-specific contamination pattern. Eggs may represent a sensitive matrix for food-chain surveillance, supporting further investigation of exposure sources, temporal trends and potential implications for consumer health within a One Health framework.

2723 – PARTICIPATORY DEVELOPMENT OF AN ECOLOGICAL HEALTH CALENDAR: A REPORT ON EXPERIENCES WITH RIVERSIDE COMMUNITIES IN AMAZONAS. DOES THE ECOLOGICAL CALENDAR ACCURATELY REFLECT THE HEALTH REALITY OF THE COMMUNITY?

José-Joaquín CARVAJAL-CORTÉS (1), **Alessandra FERREIRA DALES NAVA** (1), Martha Cecília SUÁREZ MUTIS (2), Paulo Cesar PEITER (2), **Aneta AFELT** (3)

1: Fiocruz Amazônia Instituto Leônidas e Maria Deane Amazonas Brazil; 2: Fundação Oswaldo Cruz, Rio de Janeiro , Brazil; 3: University of Warsaw Poland, French National Research Institute for Sustainable Development France

Background: The ecological calendar is both a vital part of the cultural heritage of the indigenous communities of the Amazon and a modern tool that can be successfully applied to promote health within the public health system. We carried out three field campaigns (2024, 2025 and July 2026) in the border region shared by Brazil, Colombia and Peru, working with local communities The aim of the participatory research was to assess the suitability of using the ecological calendar method as a tool for collaboration between the health service and the local communities in limiting local epidemiological risks and participatory health surveillance.

Methods: The surveys consisted of a series of in-depth interviews and open-ended questions, tailored to gender and age groups, and conducted in the local language with the assistance of an interpreter who was a member of the local community. The results were then cross-checked and verified by scientific research findings and health care system data.Results: The results of participatory research confirmed the local community's deep, intergenerational knowledge of the relationship between epidemiological risk and climatic & growing seasons, as well as landscape structure related to specific health risks. As we interacted with the local community and listened to their accounts, we realised that they are very knowledgeable about natural cycles, the periods when diseases such as malaria and dengue fever are most prevalent, and health care practices. Much of this knowledge relates to the use of local medicinal plants, employed to alleviate symptoms, particularly in cases where treatment with conventional medicines is discontinued — which, according to health workers, happens frequently due to side effects or only partial relief of symptoms. This learning experience has shown us that traditional science and academic science need not be viewed as opposites, but rather as complementary. Local knowledge, passed down orally through the generations, contributes significantly to healthcare and should be recognised as a legitimate part of collective knowledge.

Conclusions: The ecological health calendar – as a holistic approach to health, in the understanding that it is the representation of the ecological system in which members of local communities participate – is, in fact, a reflection of the One Health philosophy, practised locally for long generations.

Acknowledgements: Results are part of the “MOSAIC” project, funded under the European Union’s Horizon Europe research and innovation programme (Horizon Europe, 2021-2027). We are deeply grateful for the MOSAIC Project research&local communities team participation.

2726 – Sentinel Sites for Nature: Ecosystem health insights from a standardized biodiversity and climate monitoring network across California

Gary BUCCIARELLI (1), Whitney ALBRIGHT (2), Collin BODE (3), Lindsey RICH (2), Steve MONFORT (3)

1: University of California, Davis, United States of America; 2: California Department of Fish and Wildlife; 3: University of California, Office of the President, United States of America

The California Sentinel Sites for Nature (CASSN) project is a state-wide biodiversity and climate monitoring network of collaboratively-managed sites administered by the California Department of Fish and Wildlife, the University of California and its network of field stations - UC Nature, the California State University system, California State Parks, UC Agricultural and Natural Resources, and non-for profits, including The Nature Conservancy and private land trust agencies. Growing from the global 30x30 conservation effort, CASSN was established as a monitoring network that could quantify the impacts of climate and land-use change to wildlife and their ecosystems. To date, we have established nearly 500 monitoring sites and deployed over 2,000 sensors spanning ~400,000 km2 in regions representing 19 of 20 major ecosystem types in the California Floristic Province. CASSN utilizes standardized monitoring protocols for capturing continuous weather data (a minimum of 10 variables), camera trap images for large and small mammals, reptiles, amphibians, and some terrestrial insects, bird and bat audio using autonomous recording units, and telemetry data via Motus antennae using three frequencies (166 Mhz, 454 Mhz, and 2.4 Ghz). Thus, CASSN provides interoperable data that can be used to track short- and long-term responses of wildlife and overall ecosystem health shifts, serving as an important utility for

providing a One Health approach to understanding the links between biodiversity, habitat quality, and human well-being. As CASSN continues to grow in size and capability, we have layered in additional monitoring approaches at sites that further enhance its practicality for a One Health approach to monitoring, including remote sensing with drones and AI-enabled technologies that can be leveraged to evaluate wildlife behavior, detect pests, or understand feedback loops between environmental conditions and human disease vectors. For example, we have incorporated seasonal sampling for microbes, fungi, and insects using environmental DNA (eDNA) and begun to explore using AI on edge systems for real-time insect monitoring. Employing standardized data processing pipelines enabled with publicly available organismal classification models and rigorous validation protocols, we are creating open occurrence and climate datasets, which we are now beginning to publish and provide to the public for query and exploration of raw data. In this presentation, I will highlight some of the initial data products from CASSN, disease surveillance and disease-vectoring animal monitoring cases, as well as planned agency uses of these datasets, AI-enabled applications and integration for wildlife monitoring and disease surveillance, opportunities within our framework, and what we hope to learn from Sentinel Sites over the coming years.

2731 – Beyond borders: The human-animal bond and canine importation

Valentina GONZALEZ RODRIGUEZ, Karine GAGNE, Jason COE, Lauren VAN PATTER, Katie CLOW
University of Guelph, Canada

Background: Canine importation into Canada increased by over 400% from 2013 to 2019, raising veterinary and public health concerns due to the introduction of infectious diseases such as rabies[1,2]. In 2022, the Canadian Food Inspection Agency banned commercial dog imports from high rabies-risk countries[3]. However, this ban does not address the motivations for canine importation or the human-dog bond, which has led to substantial opposition to this policy[4,5]. We aimed to characterize adopter demographics, motivations, and human-animal attachment, and to identify behavioural and societal determinants of adoption satisfaction, to inform evidence-based, community-oriented importation policy.

Methods: This Canada-wide mixed-methods One Health survey (n=206) collected demographic, adoption-process, motivational, and human-animal bond data using the Lexington Attachment to Pets Scale (LAPS) and the Companion Dog Owner Relationship Scale (C/DORS). Descriptive statistics, LAPS/C/DORS scoring, and univariable analyses were conducted in R.

Results: Most respondents were women (82.4%); dogs originated from 36 countries, most commonly the United States (30.1%). "Saving a life" ranked highest among 11 motivations and "Lower cost" lowest. Attachment was high: mean LAPS was 57.9/69, and on the C/DORS, adopters reported frequent Pet-Owner Interactions (52.0/60) and strong Perceived Emotional Closeness (35.0/40) alongside low Perceived Costs (22.3/50), indicating few perceived burdens of ownership (subscale α=0.74/0.85/0.82). About 20% of dogs arrived in poor or somewhat-poor health, and 15.5% of adopters did not report a pre-import rabies vaccine. Overall, 84.9% were satisfied or very satisfied with the overall adoption experience. Adopters who rated lower cost as important were less satisfied (OR 0.14, 95% CI 0.05-0.37), while those motivated by saving a life were more satisfied (OR 3.03, 1.18-7.80). Satisfaction was strongly associated with dog health at arrival (OR 4.21, 1.83-9.69), organizational support (OR 12.39, 4.68-32.82), and credible pre-adoption health information (OR 11.38, 4.48-28.94).

Conclusions: Canadian adopters were motivated primarily by altruism and the human-dog bond rather than cost. The high attachment observed here is consistent with evidence that a strong human-pet bond fosters owner responsibility and commitment and protects against relinquishment6, reinforcing the value of policy that strengthens this bond. Adoption satisfaction was influenced by behavioural and societal determinants, specifically the support and health information that adopters received from rescue organizations. This points to modifiable targets for community-based prevention and One Health education. Since healthier dogs were associated with improved adoption outcomes, knowledge translation efforts should focus on supporting rescue organizations with health screening and interventions before importation. Communication between rescue organizations and adopters should also be strengthened, so adopters are aware of the healthcare their dogs have received. Overall, our findings support an evidence-based, education-oriented importation policy that engages rescue

communities. Working with rather than against the human-dog bond will promote more sustainable uptake of policy and practices and avoid unintended consequences.

2736 – Emerging Foodborne Risks at the One Health Interface: Investigation of Moringa Leaf Powder-Associated Outbreaks

Laura GIERALTOWSKI (1), Colin SCHWENSOHN (1), Rashida HASSAN (1), Margaret KUSHNER (2), Kailey LEWIS (2), Latasha ALLEN (2), Laura KENNEDY (2), Jennifer ADAMS (1), Zachary ELLISON (1), Thai-An NGUYEN (1)

1: U.S. Centers for Disease Control and Prevention, United States of America; 2: U.S. Food and Drug Administration

Background:*Salmonella* is a leading cause of foodborne illness and is associated with a wide range of foods. Moringa leaf powder, an increasingly popular botanical ingredient, has recently emerged as a source of salmonellosis. As a minimally processed dried plant product, moringa leaf powder may be vulnerable to microbial contamination during production and processing. Between September 2025 and April 2026, four multistate outbreaks of *Salmonella* infections associated with moringa leaf products were identified in the United States, prompting coordinated epidemiologic, laboratory, and traceback investigations.

Methods: The U.S. Centers for Disease Control and Prevention (CDC), U.S. Food and Drug Administration (FDA), and state and local public health partners jointly investigated four multistate outbreaks of *Salmonella* infections linked to products made with moringa leaf powder. Cases were identified by PulseNet, CDC's national laboratory network for foodborne illnesses, through whole genome sequencing–based surveillance and patients interviewed regarding food exposures. Traceback investigations using purchase records and supplier information identified common product sources, and implicated products were collected for laboratory testing. Descriptive analyses were conducted using data from CDC's Outbreak Management System.

Results: A total of 158 outbreak-associated illnesses were identified across 38 states, with specimen collection dates ranging from September 2025 through April 2026. Forty-five patients were hospitalized; no deaths were reported. Among 105 interviewed patients, 92 (88%) reported consuming dietary supplement products containing moringa leaf powder. Outbreak strains were isolated from 10 moringa leaf products collected from patients' homes and retail locations. Traceback investigations linked implicated products to multiple suppliers with numerous food safety issues, primarily in India. Multiple U.S. firms voluntarily recalled contaminated moringa leaf products, and public health and regulatory agencies issued advisories against their sale and consumption.

Conclusions: A combination of epidemiologic, laboratory, and traceback evidence identified contaminated moringa leaf products as the source of four multistate *Salmonella* outbreaks within an eight-month period. This unusual association highlights moringa leaf powder as an emerging vehicle for foodborne illness and underscores the need for strengthened preventive controls throughout the global supply chain. Enhanced surveillance of botanical products, continued coordination among public health, regulatory, and industry partners, and collaboration including additional sectors such as academia could further reduce contamination risks.

2741 – MPOX-PROBE: Strengthening Epidemiological, Genomic, and Community Surveillance of Mpox Virus (MPXV) at the Congo River Border for DRC and RoC

Francine NTOUMI (2), Alain MOUANGA (3), Didier BOMPANGUE NKOKO (4), Antonio ALCAMI (5), Eleonora LEZZI (1), Gaia DE GABRIELE (1), **Dario SCARAMUZZI** (1), Chastel MFOUTOU-MAPANGUY (2)

1: R-Evolution Worldwide – S.r.l. Impresa Sociale, Italy; 2: FONDATION CONGOLAISE POUR LA RECHERCHE MEDICALE; 3: SOCIETE CONGOLAISE DE SANTE MENTALE SOCOSAM; 4: UNIVERSITE DE KINSHASA UNIKIN; 5: AGENCIA ESTATAL CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS CSIC

Introduction:Mpox virus (MPXV) remains a major public health concern in Central Africa, particularly in the Democratic Republic of the Congo (DRC), where the disease is endemic. Recent increases in Mpox cases, especially in Maï-Ndombe Province, highlight the need for strengthened surveillance and coordinated cross-border responses. The Republic of Congo has also experienced recurrent outbreaks,

with Brazzaville identified as the epicenter of the 2025 outbreak. MPOX-PROBE addresses these challenges through an integrated One Health surveillance approach to improve early detection, diagnostics and preparedness.

Objective:

The project aims to strengthen epidemiological surveillance, reinforce laboratory and research capacity, and support evidence-based public health interventions by integrating surveillance data with spatiotemporal risk and transmission models.

Methods:MPOX-PROBE integrates epidemiological, genomic, environmental and social science approaches. A multicentre cross-sectional Knowledge, Attitudes and Practices (KAP) survey is conducted in Mpox-affected and neighbouring districts of DRC and RoC using mixed methods. Qualitative interviews involved healthcare workers, community leaders, confirmed cases, contacts and community members. Quantitative data are collected from participants aged ≥15 years using cluster sampling and structured questionnaires assessing knowledge, attitudes, preventive practices, risk perception, stigma, exposure behaviours and healthcare-seeking behaviour. Qualitative data analysed using NVivo and quantitative data using STATA. Environmental surveillance includes hospital air sampling using CSIC-developed filtration technology implemented by UNIKIN and FCRM. In parallel, a rapid isothermal molecular assay based on Qualiphi®/Qx5 polymerase, TthPrimPol and padlock probe amplification is being developed for point-of-care Mpox DNA detection.

Results:The KAP survey conducted in the Republic of Congo by FCRM, revealed that only 5.4% of participants demonstrated comprehensive Mpox knowledge, and 26.0% reported adequate prevention and control practices. Misconceptions and stigma remained common: 24.6% considering Mpox a curse, 29.4% questioning the reality of the disease, 25.5% accepting discrimination against infected individuals and 56.3% reporting they would definitely accept Mpox vaccination if offered. qualitative findings highlighted misinformation, stigma, limited access to reliable information and vaccine safety concerns as barriers to prevention and healthcare seeking. Environmental surveillance detected orthopoxvirus DNA in 13 of 18 hospital air samples collected in DRC, including 9 positive for Mpox virus clade I, whereas all 12 hospital air samples collected in Brazzaville tested negative. The novel isothermal assay detected synthetic Mpox DNA targets, although background amplification with purified viral DNA indicates further optimisation is required to improve specificity.

Conclusions: MPOX-PROBE strengthens Mpox preparedness through integrated epidemiological, genomic, environmental and community surveillance across the DRC–RoC border. Qualitative insights underscore the need for context-adapted risk communication, targeted efforts to reduce misconceptions and stigma, enhanced community engagement and addressing structural vulnerabilities to interrupt the Mpox community transmission effectively. Preliminary findings also support the potential of hospital air surveillance and innovative molecular diagnostics to improve early detection and public health decision-making in Mpox-endemic settings.

2745 – Metagenomics Profiling of Pathogen Dynamics in Backyard Agroecosystems: A One Health Pilot Study

Leonor ELIAS (1,2), Ana ESTEVES (1,3), **Alexandra NUNES** (1,3,4), João D. SANTOS (1)

1: Genomics & Bioinformatics Unit, Dept. of Infectious Diseases, National Institute of Health Doutor Ricardo Jorge ,Portugal; 2: NOVA University - Lisbon, Portugal; 3: Animal and Veterinary Science Centre (CECAV), Faculty of Veterinary Medicine, Lusófona University, Lisbon, Portugal.; 4: I-MVET – Veterinary Medicine Research, Faculty of Veterinary Medicine, Lusófona University – Lisbon University Centre, Lisbon, Portugal

Background

Backyard Production Systems (BPS) are critical interfaces for interactions among humans, animals, and the environment, making them potential hotspots for the circulation of zoonotic pathogens within a One Health context. Despite their potential role in pathogen transmission, BPS remain poorly regulated and monitored in Portugal, limiting our understanding of their contribution to public health. Characterizing pathogen prevalence and metagenomic dynamics in these agroecosystems is challenging due to the complexity of environmental samples and the limitations of current metagenomic approaches, for which no single analytical workflow is universally suitable. As part of the BYTRACE project, this study aimed todevelopi and validate an analytical workflow (USpaceVAL), integrating the INSaFLU-TELEVIR and DME+

pipelines, to improve the accuracy and confidence of metagenomic pathogen detection from complex environmental samples.

Methods

Samples were collected from farm animals (poultry, small ruminants, pigs) and various soil locations, including areas with and without animal access and vegetable gardens.

A total of 85 samples from ten farms were analyzed using the Illumina Urinary Pathogen Identification Panel (UPIP), a semi-targeted metagenomic sequencing assay designed to detect more than 170 clinically relevant pathogens, providing greater analytical sensitivity in the detection of pathogens.

The sequencing data were processed through the DRAGEN Microbial Enrichment Plus (DME+) pipeline, implemented on the Illumina® BaseSpace Sequence Hub, which reports results exclusivity for microorganisms belonging to the panel employed. Conversely, the use of the in-house platform, TELEVIR, enables the detection of microorganisms beyond the panel's scope. USpaceVAL combines both, ensuring accuracy and reliability in the analysis.

Results

Across 85 environmental and animal-associated samples, validated microbial taxa were detected across multiple BPS ecosystems, with marked differences in taxon prevalence between sample types. Small-ruminant samples underwent the most extensive filtering during the validation workflow (Fig. 1). Integration of the DME+ and INSaFLU-TELEVIR pipelines identified ecosystem-specific taxonomic patterns and high-priority surveillance environments, and revealed significant associations between validated DME+ taxa and TELEVIR-only detections (Fig. 2). These associations highlight candidate microbial relationships that may not have been identified using either analytical approach independently.

Preliminary results demonstrate that greater comprehensive characterization of microbial communities in BPS is possible. Our approach identifies ecosystem-specific and shared microbial signatures, strengthening pathogen surveillance and supporting risk-based One Health monitoring.

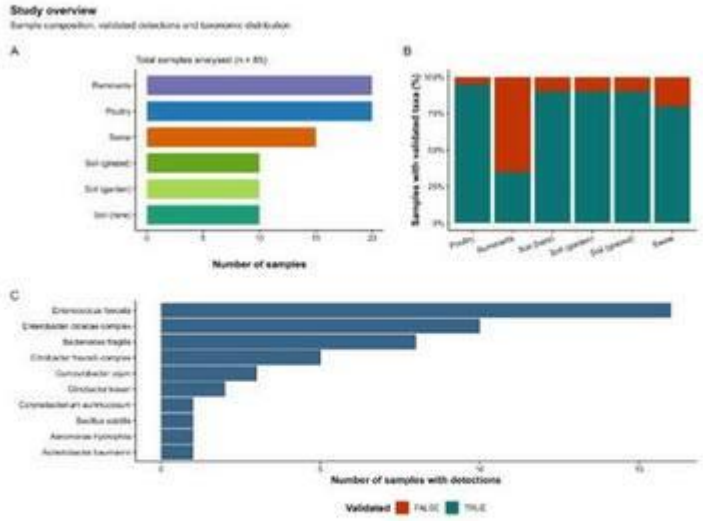


Fig 1: Overview of dataset composition and taxonomic detection structure across sample types. (A) Distribution of samples across environmental group origins, before filtering. (B) Proportion of validated versus non-validated detections across environmental group origins. (C) Top 10 most frequently detected validated taxa across all samples, ranked by number of detections.

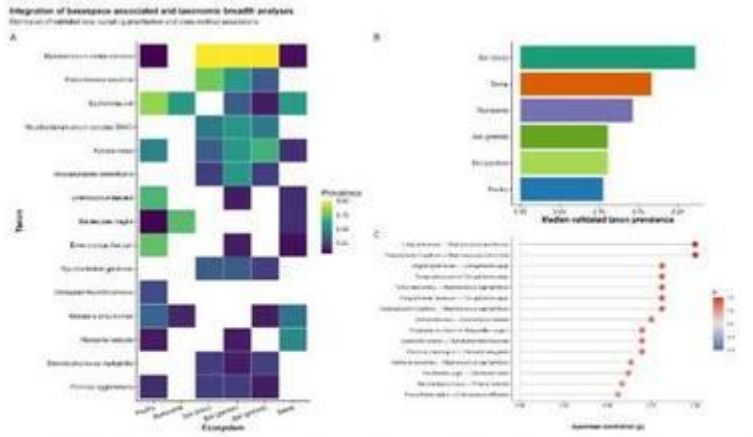


Figure 2: Integration of BaseSpace-associated and taxonomic breadth analyses. (A) Prevalence of validated taxa across ecosystems. (B) Predicted sampling priority based on median taxon prevalence within each ecosystem. (C) Associations between Televir detections and validated BaseSpace-associated taxa, based on significant Spearman correlations.

2747 – Beyond the deforestation: fractals as an early warning tool of forest fragmentation evolution for socio-ecosystem monitoring

Natalia BŁASZCZYK (1), **Aneta AFELT** (2)

1: University of Warsaw Poland; 2: University of Warsaw Poland, French National Research Institute for Sustainable Development, France

Background: How the forest is lost can be as important as how much is lost. The same reduction in forest area may produce markedly different landscape structures, ranging from a compact remnant to a highly fragmented network of corridors and gaps. These differences in spatial configuration, rather than area alone, determine habitat functionality, ecological connectivity, and the resilience of the surrounding socio-ecosystem. The consequences reach the health risks: Vector-borne disease risk is non-monotonic, e.g., malaria exposure peaking at intermediate forest cover (~50%) and under fragmentation, then receding once clearing is complete or restoration exceeds ~70% (Amazon example). Area-based proxies are blind to this signal by construction, collapsing structurally distinct landscapes into a single number. We asked whether a suite of fractal and landscape metrics can recover what those proxies discard – characterising deforestation structure reproducibly across satellite sensors, tracking its progression through time, and discriminating among disturbance types.

Methods: We proposed 5 fractal metrics to form the basis for forest fragmentation-configuration-aware monitoring as a part of a socio-ecosystem stability measure. The methodology was tested in the Área de Proteção Ambiental Triunfo do Xingu (APATX), a tropical forest protected area, under acute deforestation pressure. Annual MapBiomas binary forest masks (2016-2023) were obtained from Google Earth Engine at two resolutions (10 m Sentinel-2; 30 m Landsat). 39 spatially independent scenes across seven disturbance types were selected, each observed at eight annual time points (2016-2023). Fractal metrics were computed in a unified Python 3.11 pipeline and evaluated on three axes: cross-resolution stability, temporal sensitivity, and between-type discrimination.

Results: Metric performance proved strongly disturbance-dependent for the forest fragmentation cause. Lacunarity tracked progressive degradation more sensitively than forest cover itself, detecting gap redistribution before area accounting registers it. LCFD_std exposed structural consolidation under mining activities where forest cover held steady, a geometric reorganisation invisible to area-based monitoring by construction. FFDI gave the strongest cumulative response and the sharpest type of forest patches' spatial separation, and CoreFrac singled out open-pit clearing. Only lacunarity and LCFD_std agreed across Sentinel-2 and Landsat without calibration.

Conclusions: Fragmentation is a measurable and disturbance-sensitive property of landscape change that contains information beyond forest-cover loss. Metrics are varying across disturbance contexts; fragmentation is best interpreted through complementary metrics and their temporal evolution rather

than through any single indicator. That enables satellite-derived forest masks to function as a configuration-aware monitoring layer for socio-ecosystem long-term monitoring. Coupling fractal deforestation metrics with vector habitats is a promising avenue. The spatial configurational properties captured by these metrics, including edge density, gap structure, and corridor connectivity for the real case study forest, are directly linked to patterns of human-forest interaction and therefore provide ecologically meaningful information for One Health surveillance.

Financed by “MOSAIC” project, Horizon Europe, 2021-2027.

2749 – Genomic epidemiology of ESBL-producing Escherichia coli reveals shared high-risk lineages between children and livestock in rural Tanzania

Neyaz Ahmed KHAN (1), Joyce MBWANA (2), Dominik SCHNEIDER (4), Hagen FRICKMANN (5,6), Charity AKENTEN (3), Daniel MINJA (2), Samwel GESASE (2), Simone SCHEITHAUER (4), Denise DEKKER (1)

1: Bernhard Nocht Institute for Tropical Medicine, Germany; 2: National Institute for Medical Research, Tanga, Tanzania; 3: Kumasi Center for Collaborative Research, Kumasi, Ghana; 4: Department of Infection Control and Infectious Diseases, University Medical Center Goettingen, Germany; 5: Department of Microbiology and Hospital Hygiene, Bundeswehr Hospital Hamburg, Germany; 6: Institute for Microbiology, Virology and Hygiene, University Medicine Rostock, Germany

Background

Extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* are among the World Health Organization priority antimicrobial-resistant pathogens and pose an increasing threat to both human and animal health. However, the population structure and dissemination of ESBL-producing *E. coli* circulating at the human–animal interface in rural sub-Saharan Africa remain poorly understood. We investigated the phenotypic and genomic characteristics of ESBL-producing *E. coli* isolated from healthy children, children with diarrhoea, and livestock in Korogwe District, Tanzania.

Methods

A cross-sectional study was conducted between February 2019 and February 2020 in Korogwe District, northeastern Tanzania. Stool samples were collected from children aged ≤5 years with diarrhoea attending the outpatient department and from age-matched children without diarrhoea attending the vaccination clinic at Korogwe Town Council Hospital. Individual faecal samples were also collected from chickens raised on commercial and smallholder farms within the hospital catchment area. ESBL-producing *E. coli* were identified using standard microbiological methods and antimicrobial susceptibility testing was performed using the VITEK 2 system. Whole-genome sequencing was conducted for all isolates, of which 255 genomes passed quality control. Sequence types (STs), O-serotypes, antimicrobial resistance genes, plasmid replicons and core genome multilocus sequence typing (cgMLST) profiles were determined using established bioinformatic pipelines.

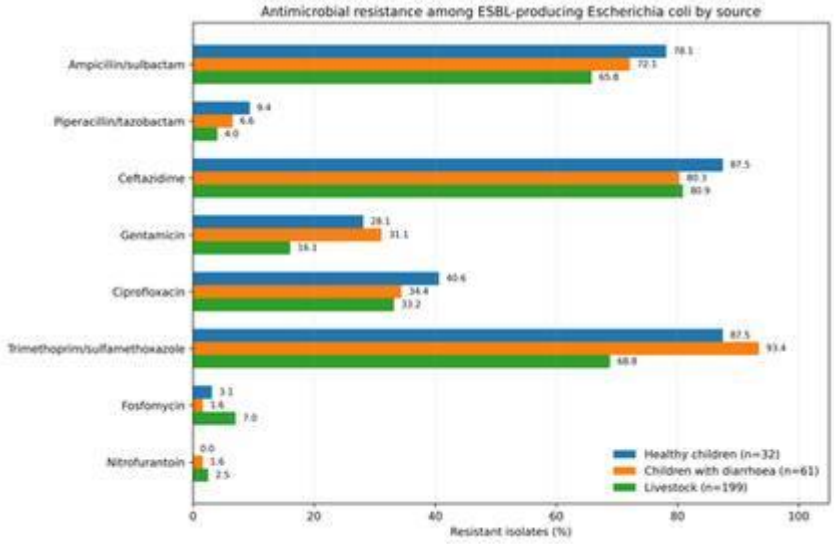
Results

Among the 292 ESBL-producing isolates, 84.2% (246/292) exhibited a multidrug-resistant phenotype, whereas susceptibility to carbapenems, fosfomycin, nitrofurantoin and tigecycline remained largely preserved. Whole-genome sequencing 255 genomes revealed a genetically diverse population comprising 60 sequence types (STs) and 36 O-serotypes. Despite this diversity, several lineages showed evidence of local clonal expansion, with ST3489 (n=17), ST38 (n=16), ST3580 (n=15), ST10 (n=15), ST361 (n=12) and ST6359 (n=11) accounting for a substantial proportion of isolates. Importantly, these dominant lineages were detected across multiple host populations, while the globally disseminated high-risk clone ST131 (n=10) was recovered from both children and livestock. The predominant ESBL determinant was *bla*CTX-M-15 (193/255; 75.7%), frequently co-occurring with *bla*TEM-1B, *bla*OXA-1, tet(A/B), sul1/sul2, dfrA, aminoglycoside-modifying enzymes and plasmid-mediated quinolone resistance determinants, consistent with the widespread multidrug-resistant phenotype. cgMLST analysis of ST3580, ST361 and ST131 demonstrated closely related isolates from different host populations, supporting dissemination of shared ESBL-producing *E. coli* lineages at the human–animal interface.

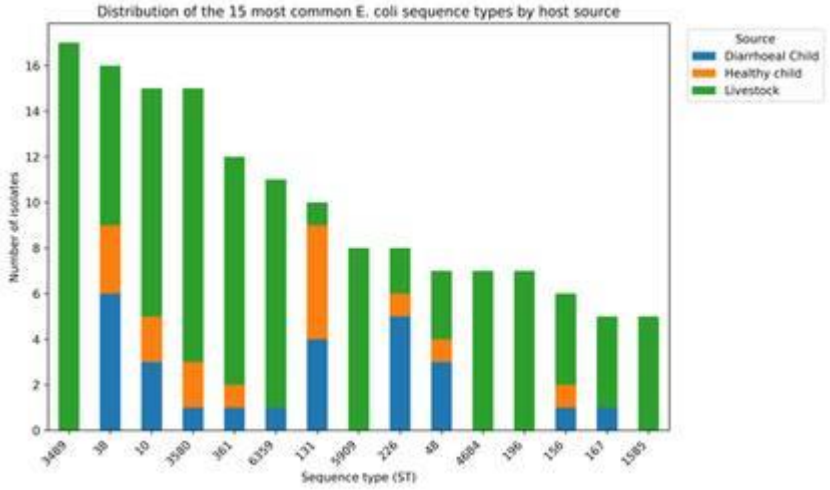
Conclusion

This study reveals a genetically diverse ESBL-producing *E. coli* population shaped by the local expansion of successful lineages and the sharing of dominant clones between children and livestock. The predominance of *bla*CTX-M-15, together with a broad repertoire of multidrug resistance determinants and

closely related isolates across host populations, highlights the human–animal interface as an important reservoir for antimicrobial resistance dissemination. These findings demonstrate the value of whole-genome sequencing for identifying locally expanding clones, tracking the movement of high-risk lineages between human and animal populations, and strengthening One Health antimicrobial resistance surveillance.



Resistance percentages are based on isolates interpreted as resistant (R); intermediate (I) isolates were not counted as resistant.



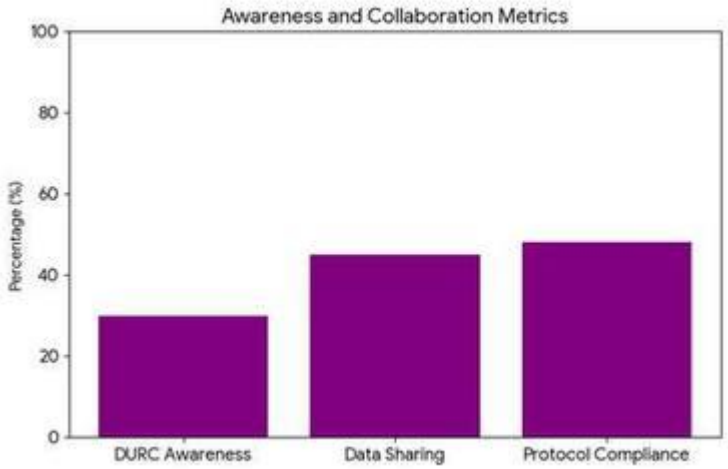
Virtual posters

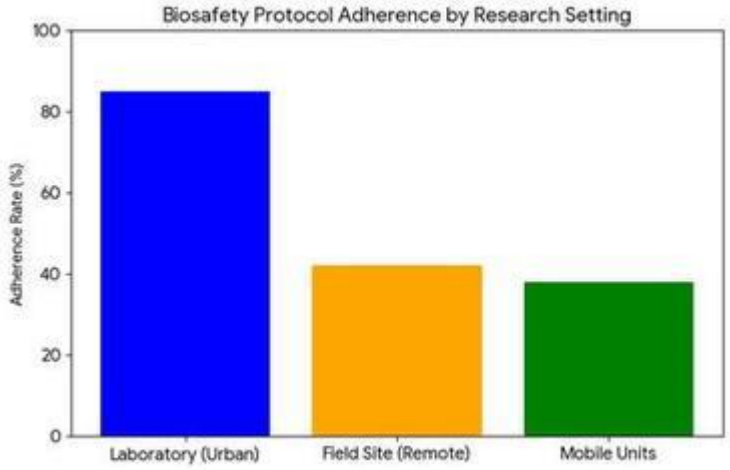
157 – Bridging the Gap: Integrating Biosafety and Biosecurity Frameworks Across Laboratory, Field, and Conflict Settings for Enhanced Global Health Security

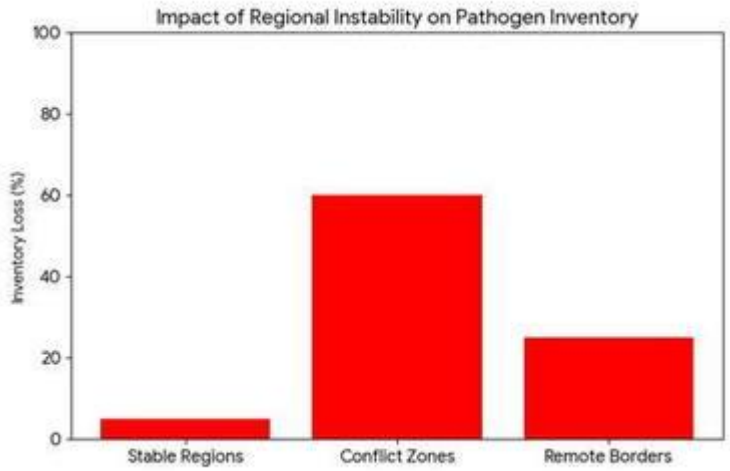
Jude EFIENOKWU (1), Mary ONWORDI (2), Emmanuel EKERETTE (3)

1: Department of Science Laboratory Technology, School of Applied Sciences, Delta State Polytechnic, Ogwashi-uku, Nigeria; 2: Department of Sociology and Criminology, Faculty of Social Sciences, University of Delta, Agbor, Nigeria; 3: Department of Genetics and Biotechnology, Faculty of Biological Sciences, University of Calabar, Calabar, Nigeria

Background: As biological research grows worldwide, the chances of accidental or intentional pathogen release increase. This study aimed to explore the weaknesses in biorisk management across various settings, including high-containment labs, ecological fieldwork, and areas affected by conflict. We assessed the idea that current biosafety frameworks are too focused on laboratories and do not address the geopolitical and dual-use risks present in fieldwork and unstable regions. The goal was to pinpoint gaps in "One Health" security and suggest a more cohesive global governance model for high-risk areas. **Methods:** This study used a mixed-methods comparative analysis conducted over 18 months from 2024 to 2025 in Nigeria. The setting included a thorough review of BSL-2 and BSL-3 facilities across six geopolitical zones, with an emphasis on major research hubs in Lagos, Abuja, and Jos. The study participants consisted of 120 Nigerian biosafety officers, lab scientists, and field researchers. Data collection included standardized surveys on Dual-Use Research of Concern (DURC) awareness, on-site safety audits of institutional labs, and qualitative interviews on how regional security issues like banditry and civil unrest affect lab and field security. We analyzed quantitative data using descriptive statistics and used thematic analysis for interviews about the impacts of conflict. **Results:** The analysis showed that compliance with biosafety protocols was highest in established Nigerian labs at 85%, but this dropped to 42% in field collection settings. Only 30% of field researchers could recognize dual-use risks related to their specific activities. In areas with ongoing conflict or high instability, the weakening of health infrastructure was linked to a 60% rise in "lost-to-follow-up" pathogen inventories, revealing a serious security hole. Additionally, 55% of respondents named geopolitical tensions and local bureaucratic issues as main obstacles to open international data sharing. Thematic findings indicated that fieldwork security often lacks standard decontamination protocols for mobile equipment, raising the risk of "zoonotic spillover" when transporting biological samples between rural and urban locations. **Conclusions:** Current biorisk management in Nigeria remains isolated. While laboratory biosafety is fairly well-regulated, biosecurity in fieldwork and conflict-prone regions is severely lacking. To achieve real Global Health Security, Nigeria must shift to a "One Biosecurity" model that combines personnel vetting and dual-use oversight with ecological and field-based research. Improving local capacity and training in high-risk areas will be more effective for sustainable biorisk management than relying on restrictive international mandates.







207 – A One Health Approach to Marburg Virus Disease Outbreak Response: Lessons from Rwanda's Multi-Sectoral Coordination

Leandre ISHEMA

Rwanda Biomedical Centre, Rwanda

Background: Marburg virus disease (MVD) is a highly pathogenic zoonotic hemorrhagic fever with case fatality rates historically ranging from 23% to 90%. On September 27, 2024, Rwanda declared its first-ever MVD outbreak, presenting unique challenges for a country with no prior experience with filovirus outbreaks. This paper describes how Rwanda's One Health coordination mechanism was operationalized during the outbreak response.

Methods: We conducted a comprehensive analysis of Rwanda's multi-sectoral response, documenting the contributions of human health, animal health, wildlife, and environmental sectors. Data were collected from outbreak investigation reports, surveillance records, and coordination meeting documentation.

Results: The outbreak resulted in 66 confirmed cases and 15 deaths (case fatality rate: 23%), the lowest ever recorded for an MVD outbreak. Healthcare workers comprised 77% of cases, with nosocomial transmission being the predominant mode of spread. Multi-sectoral investigations identified an index patient exposed to Egyptian fruit bats (*Rousettus aegyptiacus*) at a mining site. Rwanda deployed investigational therapeutics (remdesivir and MBP091 monoclonal antibody) and vaccinated 1,710 frontline workers with ChAd3-MARV vaccine within 13 days of outbreak declaration. The One Health platform

coordinated wildlife surveillance across 30 districts, established fever clinics at human-wildlife interfaces, and implemented sustainable post-outbreak monitoring systems.

Conclusions: Rwanda's successful containment of MVD within 84 days demonstrates the critical importance of pre-established One Health coordination mechanisms, strong government leadership, and rapid deployment of investigational countermeasures. The experience provides a model for integrated zoonotic disease response that can inform global health security preparedness.

208 – One Health investigation and response to a nationwide outbreak of Rift Valley fever in Rwanda – March to December 2022

Leandre ISHEMA

Rwanda Biomedical Centre, Rwanda

Rift Valley Fever (RVF) is an emerging zoonotic mosquito-borne disease caused by Rift Valley Fever Virus (RVFV), affecting both humans and animals. It is endemic to Rwanda and Tanzania and Uganda which are adjacent countries, with possible transboundary transmissions. Despite the various outbreak reports in Rwanda since 2012, information on the intensity and spread of these outbreaks and their management is scarce. We describe the 2022 outbreak that happened in Rwanda and provide insights into the One Health response implemented during the outbreak.

There were no human cases officially reported. A total of 1339 confirmed RVF animal cases were identified from 21 March until 31 December 2022. The breakdown of the cases per livestock species showed 1285 (96%) cases in cattle, 34 (3%) in goats and 20 (1%) in sheep. Of the confirmed livestock cases, 516 died and 1254 abortions were registered, in all affected species.

The outbreak response was characterized by extensive interventions such as animal spraying with pyrethroid insecticides, Vaccination, and active follow-up of animals and humans in the households with animal cases. In the first phase of the outbreak, animal movements and slaughtering were restricted in the highly affected regions. Gradually, the abbatoit slaughter activities were resumed with all animals required to test negative by RT-PCR before slaughter. Remarkably, the public services and hospital laboratories supported both capacity building of veterinary laboratory scientists and testing of animals' samples. The overall response was coordinated by district cross-sectoral teams linking national and community-level actors. Outbreak-related information was synthesized by the district teams and shared at national level while national strategies were communicated to the affected communities through the district structures.

Rwanda's response to RVF provides a proof of concept that multisectoral efforts involving community members in a One Health approach can offer efficient response to zoonotic outbreaks while still protecting the country's economy.

214 – Integrated One Health e-IDSR Joint Surveillance System: Strengthening Human, Animal, Wildlife, and Environmental Disease Monitoring in Rwanda

Leandre ISHEMA

Rwanda Biomedical Centre, Rwanda

Background: The COVID-19 pandemic exposed critical gaps in Rwanda's disease surveillance systems, particularly the absence of digital platforms for animal, wildlife, and environmental health monitoring. While the human electronic Integrated Disease Surveillance and Response (e-IDSR) system was strengthened during the pandemic, surveillance in animal and environmental sectors remained fragmented and largely manual. This limited cross-sectoral data integration, triangulation, and evidence-based decision-making essential for effective One Health action.

Objective: To establish an integrated One Health surveillance platform linking human, livestock, wildlife, and environmental disease monitoring systems across Rwanda's key institutions.

Methods: A collaborative partnership between Rwanda Biomedical Centre (RBC), Rwanda Agriculture and Animal Resources Development Board (RAB), and Rwanda Development Board (RDB) was formed to

develop a unified surveillance system built on the DHIS2 platform. Implementation followed a phased approach: system development and animal health indicator definition in 2024, followed by wildlife indicator integration, case definition development, and nationwide training of veterinarians and surveillance officers in 2025. Field users were equipped with tablets for real-time data capture, and dashboards were developed for automated reporting and data visualization. Environmental and climate-sensitive indicators are currently being developed for integration.

Results: The system now enables real-time data collection across human, animal, and wildlife sectors through a single platform, supporting SMS alerts, dashboard analytics, and cross-sectoral data triangulation. Core indicators include morbidity, mortality, case fatality, recovery rates, and intervention metrics such as vaccination, treatment, quarantine, and laboratory confirmation. Wildlife modules capture road kills, snare removals, poaching incidents, confiscations, translocations, and cases outside protected areas. The platform is fully decentralized, with steadily increasing adoption, particularly within RAB, with climate and health indicators under development for future integration.

Challenges and Lessons Learned: Key challenges included limited device availability, digital literacy gaps, persistence of parallel manual reporting, and the need for dedicated data review teams. Lessons learned highlight the importance of leadership endorsement, clear governance structures, alignment with institutional workflows, and demand-driven system adoption.

Conclusion: Rwanda's One Health e-IDSR represents a major step toward integrated human, animal, wildlife, and environmental surveillance. Planned integration of climate and health indicators, linkage with clinical data systems, predictive modeling, and AI-driven analytics will further strengthen outbreak preparedness and response. Sustained leadership commitment and full stakeholder engagement remain essential to realizing comprehensive One Health surveillance.

220 – A Single-Tube, Two-Stage Nested Isothermal Amplification for Detection of Respiratory and Tumor-Inducing Viruses

Mohamed EL-THOLOTH (1,2), Eman ANIS (3), Haim H BAU (4)

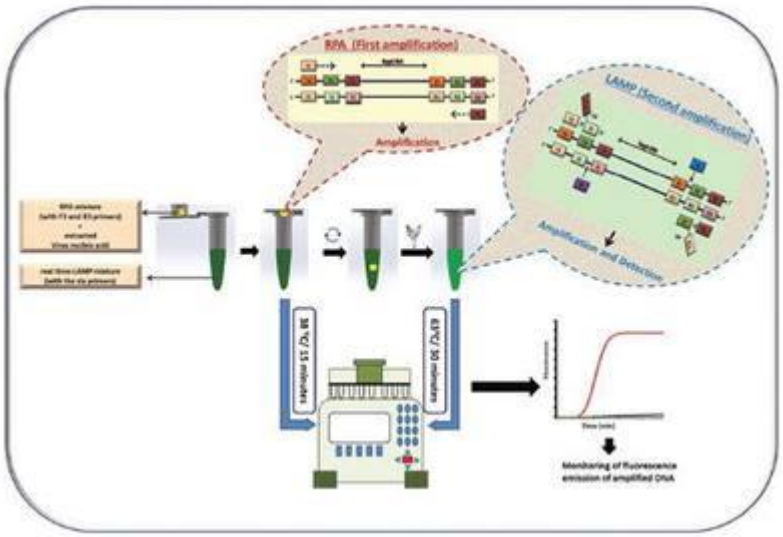
1: Health Sciences Division, Al Ain Zakhir Campus, Higher Colleges of Technology, Abu Dhabi 17155, United Arab Emirates.; 2: Department of Virology, Faculty of Veterinary Medicine, Mansoura University, Mansoura 35516, Egypt.; 3: Department of Pathobiology, New Bolton Center, School of Veterinary Medicine, University of Pennsylvania, Kennett Square, Pennsylvania 19348 United States; 4: Department of Mechanical Engineering and Applied Mechanics, University of Pennsylvania, Philadelphia, PA 19104, USA.

Background: Sensitive, specific and rapid molecular diagnosis of respiratory and tumor diseases in animals and humans is critical to facilitate appropriate control measures and treatment. Conventional polymerase chain reaction (PCR)-based molecular diagnostics requires relatively expensive equipment and trained staff, restricting its use to centralized laboratories with significant delays between sample collection and test results.

Methods: Herein, we report a highly sensitive, rapid, point-of-need, two-stage-molecular test that requires minimal instrumentation and training. Our test, dubbed Penn-RAMP, combines recombinase polymerase amplification (RPA, 38°C) and loop-mediated isothermal amplification (LAMP, 63°C) in one tube, enabling nested, two-stage isothermal amplification.

Results: We demonstrate Penn-RAMP's efficacy by testing two common viral respiratory diseases and one tumor inducing virus of chickens: infectious laryngotracheitis (ILT), infectious bronchitis (IB), and Mareks disease virus (MDV) that imposes great economic burden worldwide. Test results of clinical samples with our closed-tube Penn-RAMP assays concord with the gold standard quantitative PCR (qPCR) assay; with 10-fold better limit of detection than LAMP and qPCR.

Conclusions: Our closed-tube Penn-RAMP assays have the potential to greatly reduce false negatives while requiring minimal instrumentation and training.



264 – Community-level One Health surveillance of ESBL-producing enteric bacteria in humans, animals and the environment in Abeokuta-South LGA, Ogun State, Nigeria.

Adeyemi Olufunmilayo JOLAOSO (1), Adelekan Oluseyi OKUNLADE (2), Victor Okechuckwu AZUH (3), Yewande ALIMI (4), Robyn ALDERS (5)

1: DEPARTMENT OF VETERINARY SERVICES, MINISTRY OF AGRICULTURE AND FOOD SECURITY, OGUN STATE, NIGERIA; 2: DEPARTMENT OF VETERINARY MICROBIOLOGY, UNIVERSITY OF IBADAN, NIGERIA.; 3: BIOREPOSITORY AND CLINICAL VIROLOGY, UNIVERSITY COLLEGE HOSPITAL, IBADAN, NIGERIA.; 4: ONE-HEALTH UNIT, AFRICA CENTRE FOR DISEASE CONTROL AND PREVENTION, ETHIOPIA.; 5: DEVELOPMENT POLICY CENTRE, AUSTRALIAN NATIONAL UNIVERSITY, CANBERRA, AUSTRALIA.

Background

The rise of antimicrobial resistance, particularly from extended-spectrum β-lactamase producing enteric bacteria, continues to pose a significant global health challenge. Nigeria's One Health AMR National Action Plan (NAP 2.0) launched in 2024, provides comprehensive, integrated strategies for the human, food, animal, plant, and environmental sector; however, the absence of community-level baseline data limits effective assessment of NAP 2.0 implementation. This community-level target population pilot study establishes prevalence and carriage data for ESBL-producing entericbacteriain pregnant women, meat from food animals and environmental samples, and characterises the antibiogram and genetic relatedness of isolates to detect cross-sector reservoirs and inform future AMR surveillance and One-Health interventions.

Methods

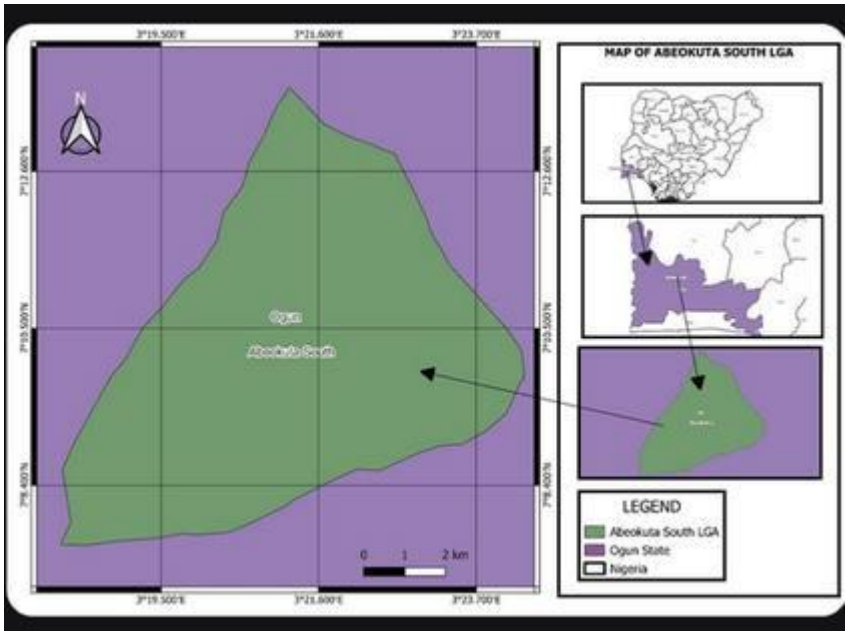
The study was conducted in Abeokuta-South Local Government Area in Ogun State, Nigeria. A total of 344 samples were collected between March and May 2025 from meat from food animals, swabs from the environment and faecal samples from pregnant women. Of these, 144 samples were identified as ESBL producers by phenotypic methods. Out of these 35 multidrug ESBL–producing enteric bacteria were subjected to molecular investigation and accession numbers were generated for the obtained sequences.

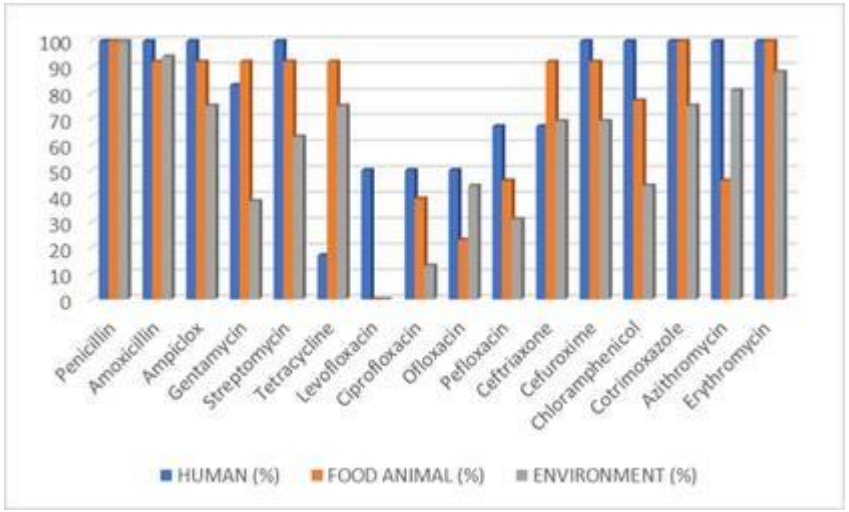
Results

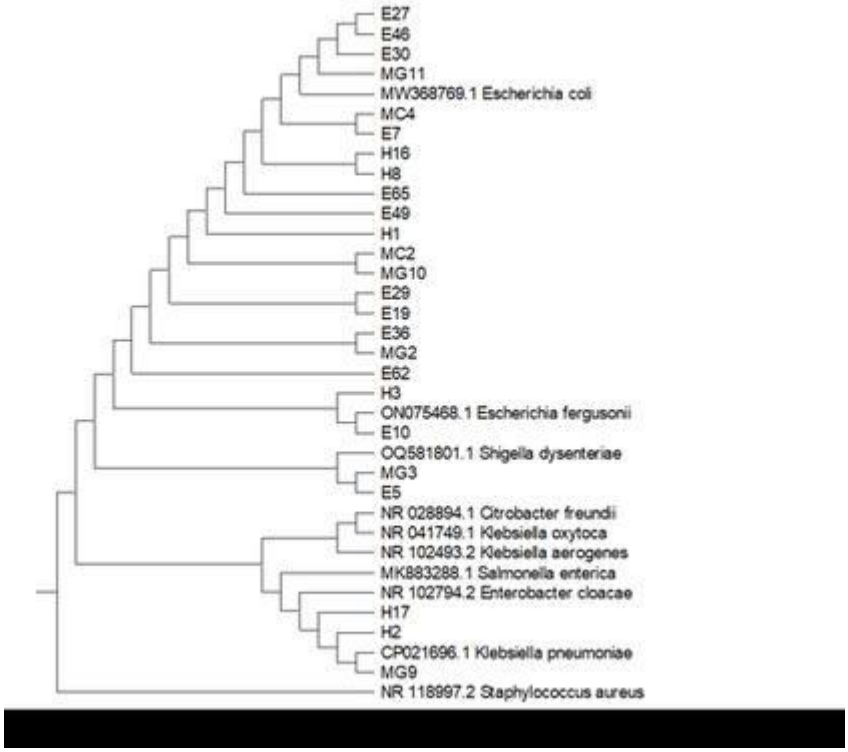
The results show that all the isolates are multidrug resistant and highest resistance was observed penicillin (100% in isolates from food animals, the environment and humans) followed by gentamicin (92%, 37% and 83% for food animals, environment and humans respectively) and streptomycin (92%, 62% and 83% for food animals, environment and humans respectively). The most frequently detected ESBL gene was blaOXA (17; 68%), while the least detected was blaSHV (3; 12%). The phylogenetic tree constructed grouped isolates into four main clusters corresponding to *Escherichia coli*, *Klebsiella pneumoniae*, *Shigella dysenteriae*, and *Escherichia fergusonii*. *E. coli* isolates clustered tightly with negligible divergence, while *K. pneumoniae* and *Shigella* formed distinct branches. The *E. fergusonii* isolate clustered closely to the *E. coli-Shigella* complex but formed a separate lineage.

Conclusion

The phylogenetic analysis showed limited genetic divergence among isolates from the three sectors, suggesting the presence of shared sources or ongoing circulation of ESBL-producing enteric bacteria across sectors. Whole genome sequencing, resistome profiling and integrating metagenomic data from environmental matrices will further elucidate the molecular mechanisms sustaining these cross-sector reservoirs. This evidence will support efforts i) to bridge the gap between policy intent and impact and contribute to strengthening the operationalisation of Nigeria's AMR NAP 2.0, and ii) provide baseline data for NAP impact evaluation.





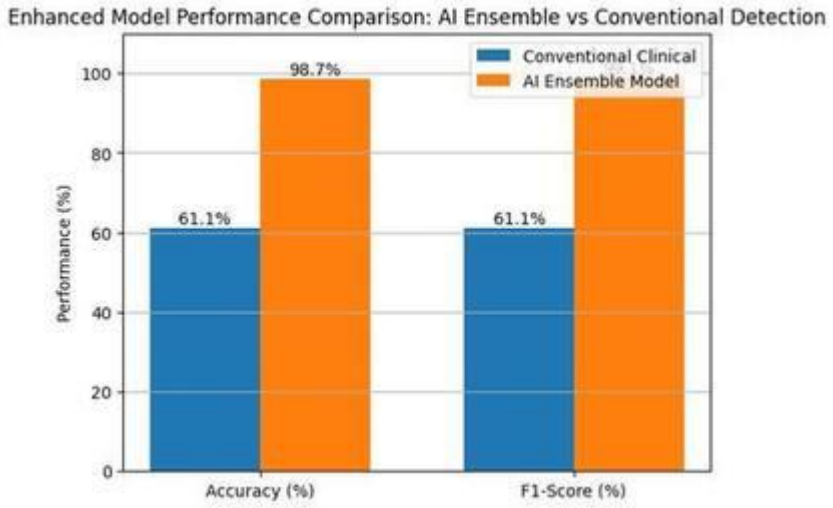


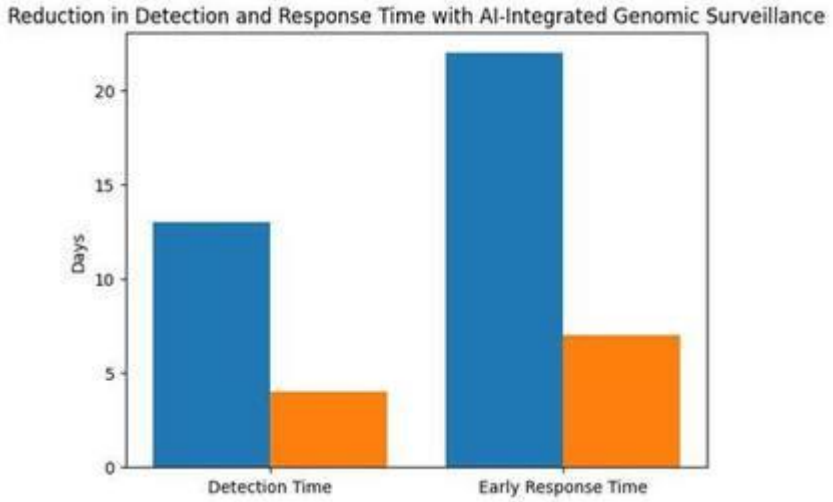
306 – Operationalizing the '7-1-7' Target through AI-Driven Genomic Surveillance at the Forest-Agroecology Interface: A Transdisciplinary Roadmap for Mitigating Lassa Fever Spillover in Ondo State, Nigeria

Oladimeji ANTHONIO (1), Opeyemi HAMMED (2), Oreoluwa AYOLEKE (3), Oluwagbemiga ODUNUKAN (4)

1: University of Ibadan, Nigeria; 2: Ladoke Akintola University, Nigeria; 3: University of Ibadan, Nigeria; 4: University of Ibadan, Nigeria

Background: Lassa fever (LF) remains a persistent public health threat in Nigeria, with Ondo State currently serving as the national epicenter, accounting for 36% of all confirmed cases in 2025. Despite national investments, recent field investigations reveal that Ondo fails to meet global 7-1-7 benchmarks, particularly in "Detection" (13 days vs. ≤7 target) and "Early Response" (22 days vs. ≤7 target). This study evaluates a transdisciplinary roadmap that integrates Artificial Intelligence (AI) and genomic surveillance to bridge these timeliness gaps at the forest-agroecology interface, where land-use changes drive rodent-to-human spillover. Methods: We conducted a cross-sectional, simulation-based study in the Owo and Ose Local Government Areas of Ondo State. Data inputs included clinical records from the Federal Medical Centre (Owo), genomic isolates from the NCBI Virus Database, and high-resolution environmental covariates (NDVI, soil moisture). We trained a Modular Stacked Ensemble Framework using XGBoost and Multi-Layer Perceptrons to differentiate LF from malaria based on clinical symptoms. Genomic analysis focused on resolving the specific circulation patterns of Lassa virus Lineage II, particularly the 2g-gamma clade prominent along the Owo-Ifon axis. Results: The AI ensemble model achieved a diagnostic accuracy of 98.7% and an F1-score of 99.1%, significantly outperforming the existing clinical detection methods which average 61.1%. Genomic profiling identified distinct eastern-to-western virus migration patterns, with seasonal spillover triggers linked to vegetation fragmentation in cocoa-based agroforestry. Implementation simulations suggest that deploying this AI-integrated genomic surveillance tool can reduce the initial detection interval from 13 days to 4 days, successfully meeting the 7-1-7 target. Conclusions: This roadmap provides a scalable model for operationalizing the Nigeria Lassa Fever Strategic Plan (2025–2029) and the One Health Joint Plan of Action. By integrating AI-driven diagnostics into SITAware frontline systems, high-burden states like Ondo can transition from reactive to proactive epidemic intelligence. This approach offers a transformative framework for mitigating emerging zoonotic threats at human-animal-environment interfaces across Sub-Saharan Africa.





402 – Temporal Asymmetry in One Health Governance: Regulating Pace as a Structural Determinant of Multispecies Health

Lina Gazu MEGO (1), Evelyne DE LEEUW (1,2,3,4)

1: Department of Social and Preventive Medicine, School of Public Health, Université de Montréal, 7101 Avenue du Parc, Montreal, QC, H3N 1X4, Canada; 2: One Urban Health, Sydney, Australia.; 3: Urban Health & Policy, UNSW Sydney, Sydney, Australia; 4: International Union for Health Promotion and Education (IUHPE), Montréal, Canada.

Background: One Health governance has expanded integration across human, animal, and environmental sectors, yet the temporal organization of governance remains underexamined. Institutional systems operate through annual reporting cycles, funding calendars, and electoral mandates that frequently misalign with ecological regeneration and microbial evolution. This structural misalignment contributes to reactive intervention, delayed detection, and uneven distribution of risk across species and generations. We introduce temporal asymmetry as a governance condition in which institutional, ecological, and biological tempos diverge, generating preventable vulnerability. We argue that effective One Health reform requires deliberate regulation of pace within governance systems.

Methods: This study develops a conceptual governance framework grounded in analysis of temporal dynamics across multispecies systems. Drawing on interdisciplinary literature in One Health, ecological resilience, political economy, and governance theory, we synthesize evidence from five illustrative domains: zoonotic spillover (Nipah virus), antimicrobial resistance in livestock systems, COVID-19 response timing, Indigenous seasonal stewardship practices, and climate-driven vector expansion. These cases are examined to identify recurring patterns of temporal misalignment between institutional cycles, ecological regeneration, and microbial evolution. We organize findings using three conceptual-analytical

categories—chronos (institutionalized linear time), kairos (context-responsive timing), and cronos (accelerative political–economic pressures).

Results: Across cases, chronos-dominant institutional cycles prioritize measurability and accountability but frequently lag behind biological change. Cronos-driven acceleration embedded in extractive production systems compresses ecological regeneration intervals while amplifying exposure and selection pressure, particularly in livestock intensification and land conversion. Kairos windows—opportune ecological or social moments for preventive intervention—are often missed when governance operates within rigid calendar structures. These interacting temporal logics generate governance lag, reactive crisis management, antimicrobial resistance amplification, accelerated spillover risk, and intergenerational inequity. Temporal asymmetry emerges not as a coordination failure but as a structural feature of institutional design.

Conclusions: One Health reform must move beyond sectoral integration to govern pace itself. Embedding temporal calibration within governance requires synchronizing surveillance with ecological rhythms, institutionalizing early-warning indicators of acceleration, and regulating production tempos that exceed regenerative capacity. Recognizing temporal asymmetry as a structural determinant reframes prevention, preparedness, and justice within One Health. Governing time—who sets the pace, who absorbs delay, and whose regenerative cycles are protected—becomes central to multispecies resilience in an era of environmental change.

---

710 – Assessment of knowledge and practical attitudes about Rift Valley fever among university students and health professionals in Southern Senegal: A pre- and post-intervention study.

Tracie YOUBONG (2), Aminata TOURE (1,2), Yacine CISSE (1,2), Amadou SECK (2), Amadou Yeri CAMARA (5), Somine DOLO (4), Simone SOSO (4), Daniel YONGA (2), Ezechiel Prosper NOALI (3), Thierry Lamare FOUAPON ASSEDI NJATOU (4), Deborah THOMSON (4), Noel Magloire MANGA (1)

1: UFR Sciences de la Santé, Université Assane Seck de Ziguinchor, Sénégal; 2: One Health Lessons®, Dakar, Sénégal; 3: One Health Lessons®, Ouagadougou, Burkina Faso; 4: One Health Lessons®, Washington DC, USA; 5: Regional Health Department, Sedhiou, Sénégal

Background: Strengthening the "One Health" approach and enhancing surveillance of priority zoonotic diseases remain significant challenges in Senegal. Rift Valley fever (RVF) is among the six priority zoonoses and currently poses major public health concerns, especially following the September 2025 epidemic. This study aimed to evaluate baseline knowledge and practical attitudes regarding RVF among students at Assane Seck University of Ziguinchor (UASZ) and professionals in the education and One Health sectors in Sédhiou. Additionally, the research sought to assess the immediate impact of a targeted educational intervention.

Methods: In our study on an innovative One Health approach to zoonotic surveillance in the Sédhiou region of Senegal, conducted from January 2025 to March 2026, a quantitative cross-sectional study was conducted from April 11 to 18, 2025. Participants attended an 8-hour training session organized by One Health Lessons® (OHL), which included a variety of materials, including slideshows and maps. Knowledge levels were assessed using a structured questionnaire administered before and after the training. The collected data included socio-demographic characteristics, awareness of One Health, and specific knowledge of RVF transmission, symptoms, and prevention.

Results: A total of 109 participants were enrolled in the study, comprising 72 students and 37 professionals. The mean age of participants was 29 years, with a male-to-female ratio of 2:0. At the outset, participants' overall knowledge of RVF was 77%. Initially, only 32.8% correctly identified the animal reservoir associated with the disease. Massive abortions in animals and increased mortality among young animals were recognized as the main clinical signs of RVF by 19% and 32% of participants, respectively. Regarding prevention strategies, vector control was recommended by 44% of participants, while 12% recommended pasteurized milk.

Additionally, 27% advocated vaccination to prevent RVF in animals. Post-intervention data indicated a significant increase in overall knowledge, rising to 90%. Specifically, 58% of participants were able to identify the reservoir, and recognition of massive abortions in animals as a primary clinical sign improved to 44%. However, the results imply that a single training session may not be sufficient to change ingrained perceptions or substantially enhance complex clinical understanding. Overall, while the data is

clear, more than one training session may be necessary to achieve a deeper clinical understanding of RVF.

Conclusion: RVF is still a poorly understood zoonotic disease in Southern Senegal, even among educated individuals. This situation reveals a significant gap in awareness of RVF, particularly in light of the recent epidemic. Therefore, it is urgent to establish ongoing, long-term educational programs and regular training courses to enhance the workers' skills and the population's knowledge in effectively combating this critical zoonosis in Senegal.

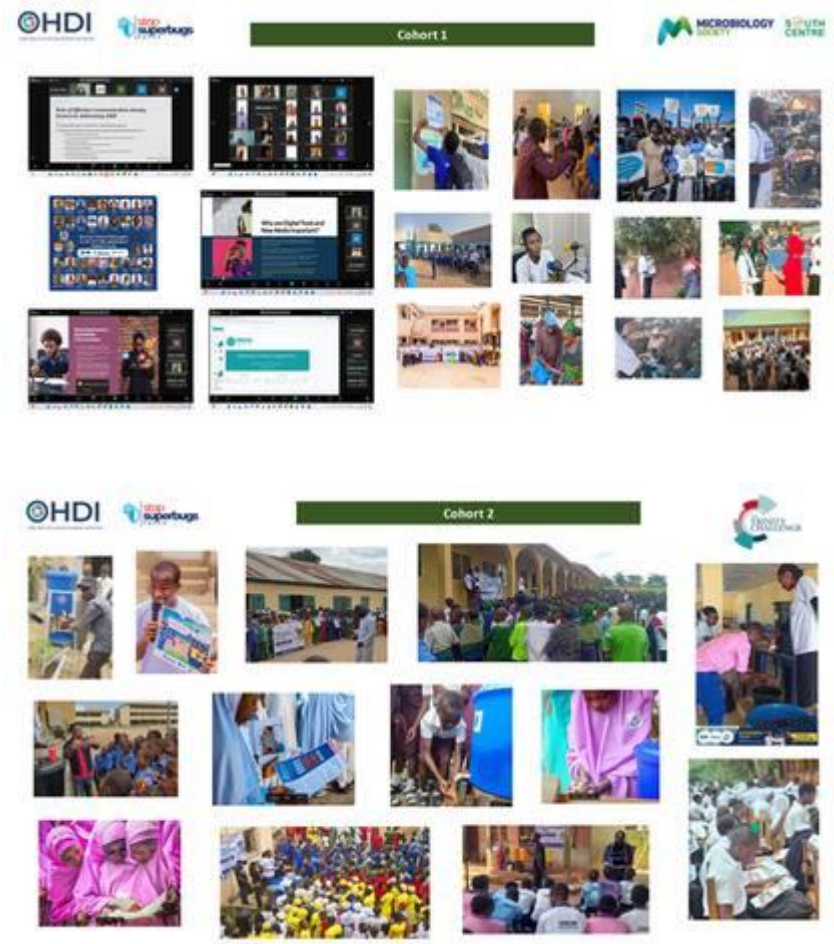
765 – Youths for AMR Communication and Action

Damilola Samuel ADESUYI (1,6), Maryam Ebunoluwa ZAKARIYA (2,6), Abdullah AL-AWAL (1,6), Maryam ABDULKARIM (3,6), Kenneth Chukwuebuka EGWU (4,6), Ibrahim ADAMU (4,6), Ahmed SAHEED (5,6), Kikiope OLUWARORE (1)

1: One Health and Development Initiative, Nigeria; 2: University of Edinburgh, Scotland; 3: University of Liverpool, England; 4: AMR Intervarsity Training Program, Nigeria; 5: Ministry of Agriculture and Food Security, Osun State, Nigeria; 6: Stop Superbugs Squad, Nigeria

Background: In Africa, limited antimicrobial resistance (AMR) education and inappropriate antimicrobial use continue to drive the emergence and spread of resistance. This project aimed to strengthen the capacity of youth AMR risk communicators and support them to lead effective AMR education and advocacy during World Antimicrobial Awareness Week (WAAW) 2024 and beyond.**Methods**: A call for youth champions received 108 applications from 65 universities across 14 African and Asian countries. A multi-disciplinary cohort of 41 youths from 28 universities in Nigeria, Cameroon, Malaysia, Rwanda, and Tanzania was selected and trained through four one-hour train-the-trainer sessions led by AMR professionals and risk communicators. Champions formed teams of four and disseminated knowledge using project-provided risk communication materials, including flyers, posters, and social media infographics, alongside small grants and endorsement letters for WAAW campaigns.The second cohort trained 38 Nigerian youths through a six-session webinar series covering AMR, WASH, campaign messaging, target audiences, social and behavioural principles, and behavioural insights in risk communication. Champions trained peers in their chapters and formed five-member teams that identified AMR and WASH knowledge gaps, myths, and misinformation in secondary schools through dialogues and informal key informant interviews guided by a co-designed scoping tool. Teams mapped schools and documented WASH infrastructure gaps. Findings informed co-designed risk communication messages and outreach plans, which were reviewed by experts, translated into local languages, and produced as social and behaviour change materials. Teams conducted school outreaches, established AMR clubs, and distributed locally made WASH aids, including soap, portable water tanks, and waste bins.**Results**: The first cohort trained 41 youths who engaged 362 youth volunteers and reached 7,634,118 individuals across English, French, Hausa, Igbo, Swahili, and Yoruba audiences. Activities included dialogues in abattoirs, markets, pharmacies, hospitals, primary healthcare centres, and universities; social media campaigns across all target countries; advocacy visits; rallies; webinars; and radio broadcasts across the six Nigerian geopolitical zones, two districts in Cameroon, and Tanzanian student populations. Among these, 28,063 individuals were reached physically, with many pledging action against AMR.For the second cohort, the trained 38 champions trained other 163 youth volunteers and reached 31,565 students in 79 schools across 18 Nigerian states. Post-session evaluations showed over 80% of students could identify at least three causes of AMR and demonstrate proper handwashing techniques. The programme established 66 WASH-on-AMR clubs with 1,762 student members. Follow-up monitoring indicated early behaviour change, including approximately 90% compliance with handwashing before meals and after breaks in one monitored school.

Conclusions: Youth-led risk communication can expand AMR awareness at scale while strengthening local prevention practices. Training young communicators and supporting community-driven outreach enables sustained, context-specific AMR education and behaviour change across diverse settings.



814 – One Health Perception and Livestock Farmers' Intention to Engage in the Prudent Use of Antimicrobials in South Korea

** Myung-Sun CHUN Eugene CHOI** Seola JOO

Research Institute for Veterinary Science, Seoul National University, Korea, Republic of (South Korea)

Background: Antimicrobials used as growth promoters in livestock were banned in South Korea in 2011. Nevertheless, reducing antimicrobial use in livestock production remains a challenge, despite Korea's continuous monitoring of antimicrobial use at the national level. Korean consumers strongly support the Prudent Use of Antimicrobials (PUA) from the perspectives of food safety and animal welfare. However, they report relatively low trust in the control of antimicrobial overuse on livestock farms (Joo, Park, and Chun, 2024). In this context, livestock farmers are key stakeholders in the successful implementation of PUA. This study examined livestock farmers' perceptions of antimicrobial use and assessed the role of One Health perception in shaping their intention to engage in PUA.

Methods: A survey was conducted between June and September 2025 with 345 livestock farmers working in swine, poultry, and cattle farms, including dairy operations, across four regions of South Korea: Gyeonggi, Jeolla, Chungcheong, and Gangwon. The questionnaire included items on demographics, antimicrobial use, perceived AM risks, One Health value perception, perceived effectiveness of PUA programs, and intention to engage in future PUA practices. Surveys were administered during mandatory group training sessions for livestock farmers and through on-farm visits. Data were analyzed using SPSS version 29. Hierarchical regression was used to identify factors associated with intention to engage in PUA.

Results: One-third of respondents perceived antimicrobial use on livestock farms to be greater than appropriate, with the highest proportion among swine farmers (40.0%). Frequent disease outbreaks and pressure to secure economic benefits were most cited drivers of overuse. Compliance with PUA principles

varied across livestock species, with poultry farms showing the highest compliance and cattle and pig farms showing weaker compliance, particularly in disposing of leftover antimicrobials, following veterinary diagnoses and prescriptions, and maintaining antimicrobial use records. Hierarchical regression showed that the explained variance in intention to engage in PUA increased from 27.3% to 64.5% after adding variables related to antimicrobial use and risk perception. One Health perception added 10.6 percentage points, and the expected effects of PUA programs added a further 6.4 percentage points. The final model explained 81.5% of the variance ($R^2 = .815$, $p < .001$), and One Health perception ($\beta = .290$, $p < .001$) emerged as the strongest positive predictor.

Conclusions: Livestock farmers' intention to engage in PUA was associated with perceived antimicrobial risks, One Health perception, and confidence in the expected effectiveness of stewardship programs. These findings suggest that effective PUA strategies should incorporate One Health values and practical guidelines that strengthen farmers' confidence in the benefits of PUA programs.

Reference: Joo, S., Park, H., & Chun, M. S. (2024). Attitudes of South Korean consumers toward the prudent use of antimicrobials in livestock animals. One Health, 18, 100754.

834 – Wastewater Surveillance for Early Warning and Outbreak Preparedness: A Systematic Review within the One Health Framework

Rachita PRADHAN, Sucharita PANIGRAHI, Matrujyoti PATTNAIK, Debaprasad PARAI, Debdutta BHATTACHARYA, **Sanghamitra PATI**

ICMR Regional Medical Research Centre, Bhubaneswar, India

Background: Early detection of infectious disease threats is essential for effective outbreak preparedness and resilient public health systems. Wastewater surveillance (WWS) has emerged as a population-level environmental monitoring approach capable of detecting pathogens shed by both symptomatic and asymptomatic individuals, providing a non-invasive indicator of community transmission. However, evidence on the effectiveness of WWS for early outbreak detection within a One Health framework remains fragmented. Therefore, this systematic review aims to assess the effectiveness of wastewater surveillance in providing early warning signals and supporting the prevention of infectious disease outbreaks using a One Health approach.

Methods:A systematic literature search was conducted in Medline, EMBASE, ProQuest, and CINAHL for studies published up to 28 October 2024. Two reviewers independently screened titles, abstracts, and full texts, with disagreements resolved by a third reviewer. Studies conducting longitudinal wastewater monitoring and triangulating environmental data with clinical or animal surveillance were included. Data were extracted using a standardised template, and methodological quality was assessed using the Joanna Briggs Institute (JBI) critical appraisal tools. Owing to heterogeneity in study designs and outcome measures, a qualitative evidence synthesis was performed. The review protocol was registered in PROSPERO (CRD42024605101).

Results:

From 539 records identified, 16 studies met the inclusion criteria. Most studies were conducted in high-income countries, with limited representation from low- and middle-income settings. The predominant pathogens detected included SARS-CoV-2, enteroviruses, hepatitis E virus, influenza A virus, and antimicrobial resistance genes. Several studies demonstrated significant correlations between pathogen concentrations in wastewater and clinically reported cases, with some reporting wastewater signals preceding increases in clinical infections, highlighting its potential as an early warning indicator. Evidence from selected studies also demonstrated the integration of environmental, human, and animal health data, reflecting a One Health surveillance approach. For example, genomic similarities between human, swine, and wastewater hepatitis E virus strains suggested shared transmission pathways. Seasonal patterns in viral circulation were also observed, and targeted wastewater sampling in high-density and socially vulnerable communities enabled early identification of transmission hotspots. However, some studies reported inconsistencies in the temporal relationship between wastewater signals and clinical case detection.

Conclusions: Wastewater surveillance offers a scalable and non-invasive approach for monitoring pathogen circulation and strengthening early warning systems. Integrating WWS within a One Health

framework can enhance outbreak preparedness by linking environmental surveillance with human and animal health systems. Expanding surveillance infrastructure, improving methodological standardisation, and strengthening intersectoral coordination will be critical to fully harness the potential of wastewater surveillance for global health security.

889 – The contribution of the One Health approach to emerging infectious disease prevention in the Democratic Republic of Congo: A system-based approach

Marc YAMBAYAMBA (1), Marlène METENE (2), Rolly PAKU (2), Chris LUNTONDA (2), Florence NGOLOLE (2), Stéphanie MALTAIS (3), Sheila MAKIALA (2), Justin MASUMU (2), Simon RÜEGG (1)

1: Section of Epidemiology, Vetsuisse Faculty, University of Zurich, Switzerland; Department of Epidemiology and Biostatistics, University of Kinshasa School of Public Health, Kinshasa, DR Congo; 2: Projet DOPERAUS, Institut National des Recherches Biomédicales, Kinshasa, DR Congo; 3: Department of Health Management, Evaluation and Policy, School of Public Health, Université de Montréal, Canada

Background

Emerging infectious diseases (EIDs) such as Ebola and Mpox continue to pose major public health, social, and economic challenges in the Democratic Republic of the Congo (DRC). These diseases arise from complex interactions among human, animal, and environmental systems, meaning that effective prevention requires approaches that go beyond sector-specific and outbreak-driven responses. However, despite widespread endorsement of the One Health approach, the extent to which it contributes to the prevention of EIDs in practice—and the socio-ecological conditions that shape its effectiveness in the DRC—remain insufficiently understood. This study examines how the One Health approach contributes to EID prevention in the DRC by analysing the socio-ecological system within which prevention efforts are embedded.

Methods

We conducted three interlinked studies. The first analysed the institutionalisation of the One Health approach in the DRC using qualitative methods. The second evaluated One Health implementation at national and subnational levels, focusing on knowledge integration across sectors using the Network for Evaluation of One Health (NEOH) tool. The third adopted a systems thinking perspective to map the socio-ecological system of EID prevention through participatory causal loop diagrams developed with stakeholders across governance levels.

Results

The findings show that the DRC has been an early adopter of the One Health approach, establishing a national One Health platform and achieving progress in coordination, training, and policy development. Nevertheless, these achievements remain fragile. Limited domestic financing, dependence on external partners, and leadership and coordination challenges constrain the sustainability and preventive orientation of One Health governance. The results further demonstrate that knowledge integration capacity remains limited and is undermined by short-term implementation cycles, crisis-driven decision-making, and weak sector-specific operational capacity. Systems mapping reveals that while increases in the number of infected individuals trigger responses across governance levels, the underlying drivers differ substantially. National and provincial dynamics are shaped primarily by political commitment, public investment, and governance capacity, whereas community-level dynamics are dominated by socio-economic conditions, livelihood practices, and local awareness. Across levels, prevention remains weakly prioritised and governance responses largely reactive.

Conclusion

Overall, the findings indicate that the contribution of the One Health approach to EID prevention in the DRC is constrained by insufficient resource allocation, limited operational and knowledge integration capacity, and weak integration of community perspectives. Meaningful contribution of the One Health approach requires shifting from a reactive outbreak response approach to a proactive investment in prevention. To address these challenges, the study proposes a five-step implementation framework that emphasises the sequential strengthening of sectoral operational capacity as a prerequisite for effective multisectoral knowledge integration.

943 – SmartChip Biosecurity Platform for One Health AMR surveillance

Windi MUZIASARI, William NURMI, **Denise PEZZUTTO**
Resistomap, Finland

Background

Antimicrobial resistance (AMR) is a One Health challenge: genes and resistant organisms circulate between humans, animals and the environment, and water and wastewater in particular concentrate signals that are essential for early detection and intervention.

Private-sector leadership can close critical operational gaps by investing in standardised operations, scalable laboratory systems, validated assays, quality frameworks and advanced analytics that convert raw results into decision-ready intelligence. Resistomap's mission to make environmental AMR monitoring practical, comparable and actionable led to an industry-ready solution, combining Takara Bio's SmartChip ND high-throughput qPCR system with Resistomap's validated assays and workflows and cloud analytics to support routine One Health surveillance across sectors.

Methods

The SmartChip Biosecurity Platform is an end-to-end product offered as a laboratory service or on-premise deployment model, combined with advanced analytics. Technically, the Takara Bio SmartChip ND runs thousands of nanolitre-scale qPCR reactions in parallel, enabling high-throughput quantification of hundreds of AMR targets per run. Resistomap provides validated assays, standard operating procedures for environmental matrices, and an optimised quality assurance framework. Laboratory outputs are uploaded to the Resistomap Platform, which produces actionable metrics (for example the Antibiotic Resistance Gene Index, Gene Reduction, and Comparative Health Risk Score), benchmarking, and visualisations suitable for operational decision-making.

Results

Offered to researchers, water utilities, governmental agencies, hospitals, agri-food industry and pharmaceutical manufacturers, the SmartChip Biosecurity Platform converts high-throughput measurement into comparable, auditable surveillance. Since 2020, Resistomap has supported 470+ projects and analysed over 32,000 environmental samples from 58 countries, showing the feasibility of scaling standardised environmental AMR measurement using the SmartChip qPCR system globally. The technical approach delivers substantially greater throughput per run at lower per-sample cost than classical qPCR workflows, and Resistomap Platform translates results into insights and recommendations, making routine monitoring financially and operationally feasible for diverse users. Recent public procurements further validate the model: Resistomap secured several public sector contracts for environmental AMR surveillance, including a £240,000 Bangor University contract in 2025 and a contract to provide AMR analysis services under CIRAD's SEMSOP project, indicating growing institutional demand for scalable private-sector AMR surveillance capacity.

Conclusions

Private-sector investment and industry partnerships are critical to translate laboratory innovation into routine surveillance of AMR within the One Health framework. The SmartChip Biosecurity Platform demonstrates how private partnerships can produce standardised, cost-efficient AMR intelligence that supports hotspot detection, treatment performance assessment and benchmarking. Public-private partnerships and competitive procurement models can accelerate deployment, reduce unit costs and enable the actionable, comparable environmental surveillance required for timely One Health action.

958 – No-Carriage Policies and the Donkey Skin Trade: A One Health Partnership Model for NGOs and Corporations

Esme WHEELER
The Donkey Sanctuary, United Kingdom

This session explores how voluntary corporate policies adopted by global transport and logistics companies- specifically “no-carriage” commitments for donkey skins- can evolve into impactful, industry-driven interventions that support livelihoods and advance One Health outcomes.

The Donkey Sanctuary (TDS) calls on the transport sector to adopt no-carriage policy for donkey skins, establishing a model now taken up by leading carriers such as Emirates, Air Canada, and Swire Shipping.

Corporate sustainability policies can respond directly to urgent One Health challenges. These include zoonotic spillover risk, biodiversity loss, and insecure supply chains. They also address the widespread theft, trafficking, and slaughter of animals- including wildlife and working donkeys- which destabilise livelihoods and community health in vulnerable regions and threaten both human and animal health. In 2020, TDS tested 108 donkey skins from a Kenyan slaughterhouse, with 2 testing positive for African Horse Sickness virus and 88 for Staph aureus (of which 44 proved positive or methacillin resistance and 3 for PVL-encoding gene), respectively demonstrating equine infectious disease, antibiotic-resistance and virulent zoonotic potential.

As demand for donkey skins to produce ejiao (traditional medicine made from donkey skin gelatin) continues to drive unregulated cross-border movement, transport companies increasingly recognise that strengthened due diligence and ethical carriage standards are essential for protecting public health, animal welfare, and environmental integrity. These policies function as de facto biosecurity mechanisms: reducing exposure to unregulated animal products, reducing the potential risk of pathogen-transmission, and improving traceability within complex global supply chains. They also reinforce community resilience by protecting working equids, critical assets for rural populations- thereby supporting socioeconomic stability and the broader social determinants of global health.

The session aims to unite animal, human, and environmental health perspectives around policy ambition. TDS’ panel provides cross-cutting expertise across public affairs, environmental and veterinary science, alongside leading transport industry professionals. Together, this multidisciplinary configuration ensures that One Health issues are addressed holistically, with policy, science, and operational realities considered interconnected rather than siloed domains.

Diversity and inclusion underpin the panel’s construction. It includes representation from the NGO, veterinary, policy, and private-sector spheres; reflects gender balance; and expertise.

The session has four objectives:

Show how corporate policies can drive meaningful change from a One Health perspective.

Provide evidence-based guidance for wider adoption across the transport sector.

Highlight opportunities for integration into multilateral policy instruments.

Offer practical insights into designing, implementing, and verifying effective corporate standards.

Amid increasing scrutiny of practices and behaviours that convert hazards into risks at the human–animal-environmental interface, the session showcases how the corporate sector can align policy and practice-implementing no-skins carriage policies that function as One Health measures to fortify ethical leadership and pave the way for sustainable, safer systems that safeguard biodiversity, animal welfare and human health for generations to come.

1082 – Strengthening Food System Resilience Through One Health Surveillance in Emerging Livestock Communities : A Comprehensive Review

Sherifat BALOGUN-RAJI (1), Vivian IWAR (2), Bolanle AKANBI-HAKEEM (3), Latifah LAWAL (4), Zikrullah GIWA (5), Latifah ABDULKARIM (6)

1: FCTA Agriculture and Rural Development Secretariat (ARDS), Nigeria; 2: Center for Animal Research and Development (CARD); 3: University of Global Health Equity; 4: NIRSAL Plc; 5: Center for Holistic Livestock Development Initiative (CHOLD); 6: Sahel Consulting

Background

Livestock-based food systems are vital for food security, nutrition, and livelihoods. in many communities, particularly in Africa. Rapid population growth and rising demand for animal protein are transforming livestock production and supply chains. While these changes support economic growth and improved

nutrition, they also increase risks of zoonotic diseases, foodborne infections, and antimicrobial resistance (AMR). In many low- and middle-income countries, livestock value chain activities, including production, transportation, distribution, and marketing often occur in informal or weakly regulated settings where animals, humans, and the environment interact closely. Weak biosecurity practices, low sanitation standards, and poor waste management in livestock markets and slaughter facilities further heighten disease risks. Fragmented surveillance systems and weak coordination among One Health sectors also limit early detection and response to emerging threats, highlighting the need for integrated surveillance and stronger cross-sector collaboration.

Method

This is a comprehensive review of existing literature, policy frameworks, and institutional reports addressing One Health surveillance and food system resilience in livestock-dependent communities. Relevant peer-reviewed publications, global health reports, and international policy documents were examined to identify surveillance gaps and opportunities for cross-sectoral collaboration. We assessed surveillance practices across key points in the livestock value chain, including livestock farms, animal transport and distribution systems, livestock markets, abattoirs, and food distribution networks. Particular attention was given to structural and institutional barriers that limit effective disease monitoring and outbreak response in low- and middle-income countries. Evidence from the literature was synthesized using a One Health system to explore how integrated surveillance approaches can strengthen early detection and response to zoonotic and foodborne disease threats.

Results

Our review shows that livestock value chains in emerging economies operate within complex systems where close interactions between animals, humans, and the environment increase pathogen transmission risks. Common vulnerabilities identified in the literature include poor sanitation in livestock markets and slaughter facilities, weak biosecurity enforcement, inadequate waste management, and limited animal health monitoring during transport and slaughter. Informal livestock trade networks, where animals from multiple sources are aggregated, further increase disease spread risks. Institutional fragmentation among animal health, (public) human health, and environmental sectors, also limits collaboration among experts, coordinated surveillance and data sharing. Limited laboratory diagnostic capacity, delayed disease reporting, and shortages of trained personnel constrain early detection of emerging threats. Additionally, unregulated antimicrobial use in livestock production contributes to the growing burden of AMR within food systems.

Conclusions

Strengthening food system resilience in livestock communities requires integrated surveillance grounded in the One Health framework. Coordinated monitoring across animal, human, and environmental health sectors improves early detection of zoonotic and foodborne threats. Strategic investments in diagnostics, digital surveillance, workforce capacity, and cross-sector collaboration are critical for safer livestock systems and stronger protection of public health.

1111 – Power and participation in One Health governance: gender and geographic inequities in global leadership

Neil VEZEAU (1), Kim Laura WEISZHAR (2), Verónica ORMEA (3), Christina PETTAN-BREWER (4), Angela OPONDOH (5), Easrat Jahan ESHA (6), Lillian OMUTOKO (7), **Phaedra HENLEY** (8), Heidi AUERSWALD (9), Grace VEZEAU (10), Lilian Wangechi WAIBOCI (11), Robyn ALDERS (12), Andrea Sylvia WINKLER (2,13)

1: Lincoln Memorial University - College of Veterinary Medicine at Orange Park, Orange Park, United States; 2: Department of Neurology, TUM University Hospital and Center for Global Health, TUM School of Medicine and Health, Technical University of Munich (TUM), Munich, Germany; 3: Facultad Ciencias de la Salud, Universidad Peruana de Ciencias Aplicadas, Lima, Peru; 4: Department of Comparative Medicine, School of Medicine, University of Washington, Seattle, United States; 5: Department of Geography & Environmental Studies, University of the Witwatersrand, Johannesburg, South Africa; 6: Fleming Fund Country Grant Bangladesh, DAI Global, Dhaka, Bangladesh; 7: Department of Educational Management, Policy and Curriculum Studies, University of Nairobi, Nairobi, Kenya; 8: Center for One Health, University of Global Health Equity, Butaro, Rwanda; 9: Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise Giuseppe Caporale, Teramo, Italy; 10: Personal Capacity; 11: Department of Biochemistry, University of Nairobi, Nairobi, Kenya; 12: Development Policy Centre, Crawford School of Public Policy, Australian National University, Canberra, Australia; 13: Department of Community Medicine and Global Health, Institute of Health and Society, Faculty of Medicine, University of Oslo, Oslo, Norway

One Health (OH) has emerged as a prominent framework for addressing complex health challenges at the human–animal–environment interface. The approach emphasises interdisciplinarity and international collaboration. Leadership composition within OH networks may influence whose perspectives shape agendas, priorities, and resource allocation. While gender disparities in leadership have been documented across science and global health institutions, representation within the expanding OH movement has not been systematically examined. This study assessed gender and geographic representation among leaders of global OH networks.

A cross-sectional analysis was conducted using a pre-existing compilation of global OH initiatives. Publicly available information from organisational websites and related materials was reviewed to identify individuals holding leadership roles. For each leader, inferred gender, leadership position within the network, and country of residence were recorded. Positions were further classified to identify top executive roles. Countries were categorised by World Bank income group to assess geographic representation. Descriptive statistics were used to examine gender distribution overall, within executive leadership, and across country income categories.

Data were extracted for 173 OH networks, yielding 1,177 identifiable leaders. Overall, 496 leaders (42.1%) were inferred to be women, while no gender minorities were identifiable from available information. Among 266 top executive roles, 97 (36.5%) were inferred to be women. Geographic distribution of leadership was also uneven. Leaders based in low- and middle-income countries were underrepresented compared with those residing in high-income countries. These patterns suggest a concentration of leadership authority within a relatively limited demographic and geographic group.

This study provides the first systematic baseline assessment of gender and geographic representation in leadership across global OH networks. The findings indicate persistent inequities that may influence agenda-setting, governance, and allocation of resources within the OH movement. Leadership diversity is relevant to the legitimacy and effectiveness of OH initiatives, particularly when addressing health challenges that disproportionately affect low- and middle-income settings. Strengthening representation across gender and geographic contexts may support more inclusive governance and enhance the capacity of OH networks to respond to complex global health challenges. Future research should examine additional dimensions of diversity and explore how leadership composition shapes decision-making and implementation within the OH ecosystem.

1119 – Addressing Snake Venom Variation in India through the establishment of envisaged Regional Venom Centres (RVCs) across the Country

Ajit SHEWALE, Gajendra SINGH, Jitesh KUWATADA, Simmi TIWARI
National Centre for Disease Control, Ministry of Health and Family Welfare, Govt. of India, India

Background

India bears a disproportionately high burden of snakebite envenoming, accounting for more than half of global snakebite-related deaths in 2019. Although antivenoms remain the only specific therapy for snakebite envenoming and are effective when appropriately matched to the biting species, several challenges limit their effectiveness across the country. The geographically restricted sourcing of snake venoms for antivenom production fails to account for regional and intraspecific variation in venom composition, leading to variable neutralization efficacy and inconsistent clinical outcomes. Additionally, suboptimal compliance with WHO standards and the lack of captive venom collection systems is another challenge. However, important challenges hamper the availability of potent and clinically effective antivenom within Indian health system. At present, Indian polyspecific antivenom is manufactured using venom from the Big Four species, sourced from limited geographical areas in southern India. This geographically restricted venom sourcing fails to account for intraspecific variation in venom immunology across regions, resulting in significant geographic differences in the neutralization efficacy and clinical effectiveness of available antivenoms. Snakebite envenoming can cause a wide range of clinical manifestations, including neuroparalysis, haemorrhage, severe local tissue damage, and acute kidney injury, resulting in significant morbidity and mortality

Methods

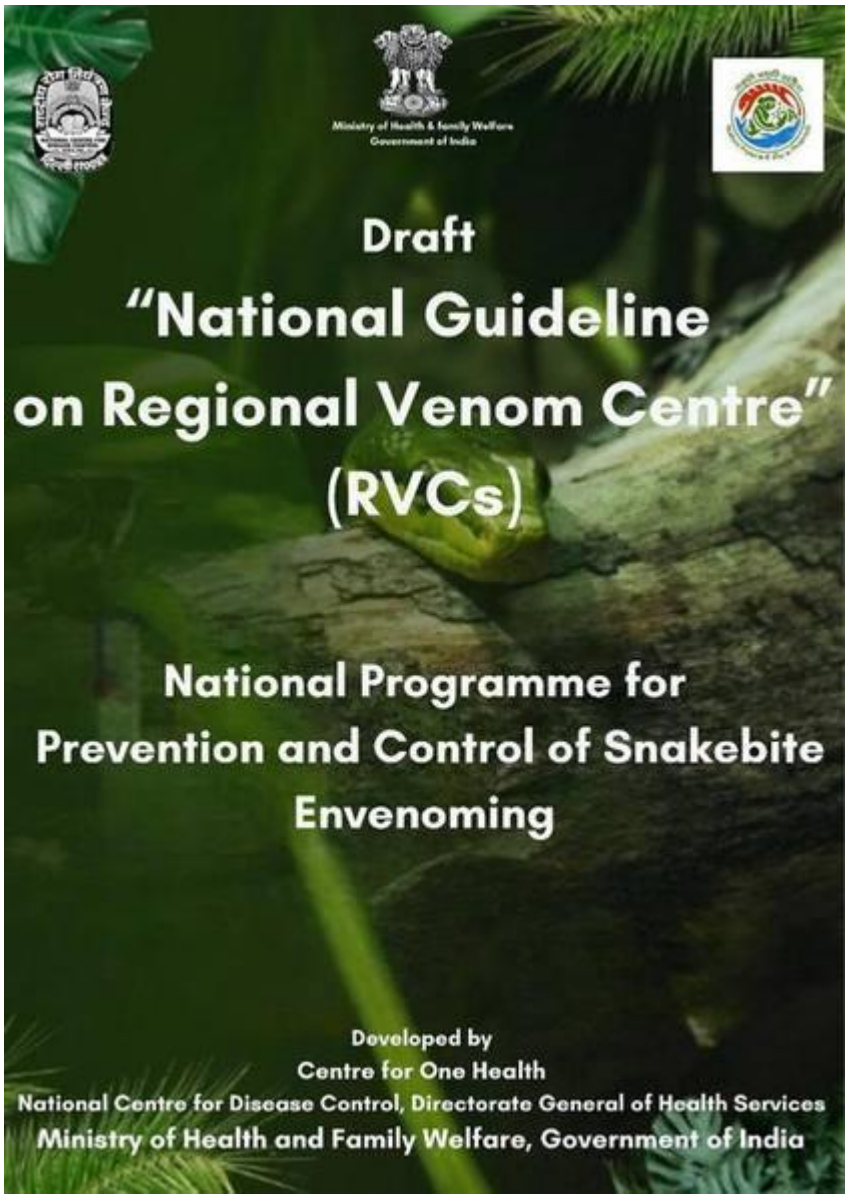
Recognizing these challenges, the National Centre for Disease Control (NCDC), under the Ministry of Health and Family Welfare, launched the National Action Plan for Prevention and Control of Snakebite Envenoming (NAPSE) in March 2024 with One Health approach. The establishment of Regional Venom Centres (RVCs) across different geographical regions of the country to facilitate the collection of region-specific snake venoms for antivenom production is envisaged. To support this initiative, NCDC convened multiple stakeholder consultations and constituted a Technical Expert Group comprising experts from Central Ministries, government institutions, universities, research organizations and NGOs, including clinicians, herpetologists, venom scientists, wildlife experts and international experts. Based on the recommendations, NCDC developed the National Guidelines on Regional Venom Centres (RVCs).

Results

The guidelines provide a standardized framework for the establishment and operation of RVCs, aligning with modern international practices for snake venom extraction and WHO standards. The establishment of RVCs will enable venom collection from medically important snake species across the country which improve the quality and diversity of venom used in antivenom production, and enhance the neutralization efficacy of antivenoms across different regions of India.

Conclusions

The establishment of RVCs represents a strategic approach to address venom variation and improve the efficacy of antivenom. By establishment of venom centres and aligning practices with WHO standards, the RVC framework will contribute to improved antivenom quality, better clinical outcomes, and reduced mortality and morbidity due to snakebite envenoming. This initiative is expected to significantly support commitment to reducing snakebite-related death by 50% by the year 2030.



1122 – An Integrated Public Health Approach to Snakebite Prevention and Control in India: Strengthening Health Systems, Community Engagement and Surveillance

Ajit SHEWALE, Nidhi KHANDELWAL, Jitesh KUWATADA, Simmi TIWARI
National Centre for Disease Control, Ministry of Health and Family Welfare, Govt. of India, India

Background

Snakebite envenoming remains a major public health concern in India, particularly in rural and agrarian communities where human–snake interactions are common. Delays in treatment, inadequate awareness regarding appropriate first aid and gaps in surveillance contribute to preventable morbidity and mortality. In response, the Government of India through National Centre for Disease Control (NCDC) under its National Programme for Prevention and Control of Snakebite Envenoming launched the National Action Plan for Prevention and Control of Snakebite Envenoming (NAPSE), aiming to halve the snakebite-related deaths by 2030 through a comprehensive public health strategy focusing on capacity building of healthcare professionals, strengthening community awareness and improving national surveillance mechanisms. This study highlights key programmatic interventions and evaluates improvements in healthcare professionals' knowledge following structured training programme.

Methods

A national cascade training model was implemented to build the capacity of healthcare professionals across different levels of public health system. Training sessions were conducted for medical officers and other healthcare providers on standardized clinical management of snakebite envenoming, including early recognition of symptoms, evidence-based first aid, timely administration of anti-snake venom and appropriate referral practices. A structured pre- and post-training assessment consisting was used to evaluate knowledge improvement among participants. Community engagement initiatives were simultaneously implemented through Information, Education and Communication (IEC) materials developed by the Government of India in multiple regional languages, including print, audio, and video formats. Efforts are also underway to establish a dedicated national surveillance mechanism to systematically report snakebite cases and deaths.

Results

Cascade trainings have been conducted in 22 States/Union Territories out of 36 States/UTs in India, covering approximately 1,200 medical professionals. Analysis of pre- and post-training assessments demonstrated a significant improvement in participants' knowledge and understanding, with overall test performance improving by approximately 30% after training. The assessments, based on multiple-choice questions addressing key aspects of snakebite prevention and clinical management, indicated enhanced understanding of early recognition of envenoming, appropriate first aid practices, anti-snake venom administration, and referral protocols. Community awareness initiatives using multilingual IEC materials facilitated dissemination of accurate information on snakebite prevention and early care-seeking behaviour. In parallel, several states have already notified snakebite as a reportable condition, while others are in the process of implementing notification systems to strengthen national surveillance and reporting.

Conclusions

The integrated approach adopted under NAPSE, combining health system strengthening, community engagement, and improved surveillance, represents a comprehensive strategy for addressing snakebite envenoming in India. Cascade training programmes significantly improved healthcare professionals' knowledge on snakebite management, while community awareness initiatives and strengthened surveillance systems are expected to enhance early reporting and timely treatment. Continued implementation of these integrated strategies will be critical for reducing snakebite-related morbidity and mortality in India.

1124 – Evaluating Community Conversations as a One Health Education Intervention in the Horn of Africa Using a Newly Validated OH-KAP Instrument

Farah I. MUMIN (1,2,3), Siobhan M. MOR (1,2)

1: University of Liverpool; 2: international Livestock Research Institute; 3: Red Sea University

Background: Pastoral and agro-pastoral communities in the Horn of Africa face high exposure to interconnected health risks, including zoonotic diseases, antimicrobial resistance, and food and water safety that require an integrated One Health response. Yet these communities remain underserved by conventional top-down health interventions. This study evaluates Community Conversations (CC) as a participatory health education intervention in the Horn of Africa and reports the development and psychometric validation of the OH-KAP instrument designed to measure community knowledge, attitudes, and practices in low-literacy agro-pastoral settings.

Methods: An initial item pool of 155 items was refined through expert content validation, with 126 items field-tested in a sample of 300 adults in Somalia. Exploratory factor analysis, bifactor item response theory models, and exploratory graph analysis were used to produce a validated instrument. The instrument was then applied in a pre-post evaluation of the CC intervention in which four facilitated sessions were delivered over two to three months across 19 communities in Ethiopia, Kenya, and Somalia (n=358). Within-person changes were assessed using paired Wilcoxon and McNemar tests; predictors of change were examined using mixed-effects regression models.

Results: The final OH-KAP instrument comprised 27 knowledge, 19 attitude, and 29 practice items. Knowledge loaded onto a general One Health factor with four domain-specific subfactors (α=0.94;

CFI=0.96; RMSEA=0.08); attitudes onto five subfactors (α=0.93; CFI=0.99; RMSEA=0.05); and practices clustered into four stable domains (bootstrap stability >65%). CCs produced significant improvements across all three domains (knowledge mean theta: 0.04→1.39; attitudes: 0.07→1.07; practices mean network-weighted composite: 1.06→1.66; all p0.001). Positive gains were observed across all three countries and most participant subgroups, with shifts in knowledge and attitudes emerging as significant predictors of improved practices.

Conclusions: The developed instrument is a concise, field ready tool for measuring integrated OH-KAP. It supports baseline assessments and monitoring associated with awareness-creation and behaviour-change programming. Future work should assess invariance across settings and languages. The findings support CCs as a scalable, community engagement model with potential to strengthen health knowledge beliefs and behaviours in resource-limited contexts. Together these tools provide a replicable foundation for community-level One Health measurement and health education programming across the Horn of Africa and comparable settings.

1130 – Community-led zoonoses prioritization in Somalia: development and field application of a participatory One Health decision-making tool

Farah Isse MUMIN (1,2,3), Siobhan M. MOR (1,2)

1: University of Liverpool; 2: International Livestock Research Institute; 3: Red Sea University

Background: Zoonotic diseases impose a major burden on low- and middle-income countries, requiring contextually appropriate approaches to prioritising limited resources. However, commonly used prioritisation tools are difficult to adapt to local contexts and rely heavily on expert knowledge. To address this gap, we developed the Community Zoonoses Prioritization (CZP) tool, combining the inclusivity of Participatory Epidemiology (PE) with the analytical structure of Multicriteria Decision Analysis (MCDA), and applied it at scale in Somalia to identify community-prioritised zoonoses.

Methods: The CZP tool guides community groups through a standardized six-step procedure: health problem mapping, zoonoses listing, criteria selection and weighting using proportional piling, consensus disease scoring, action planning, and contextual reflection. Sessions use visual aids and a standardized scoring matrix to ensure accessibility and analytical rigour. Following a successful pilot in one village that confirmed the tool's feasibility, it was applied in 40 gender-segregated sessions across four regions of Somalia (Bari, Sool, Middle Shabelle, and Gedo), engaging 480 pastoral and agro-pastoral participants (240 men, 240 women). Agreement in disease rankings was assessed using Kendall's W for within-group concordance and Kendall's τ for correlations between genders and regions.

Results: Communities identified 26 zoonoses with anthrax, bovine tuberculosis, brucellosis, child diarrhoea associated with raw milk, toxoplasmosis, and sarcoptic mange identified as the highest priorities. Agreement in priorities was strong within male (W=0.659, p0.001) and female groups (W=0.614, p0.001), with high correlation between genders (τ=0.882, p0.001) and moderate to high correlation across regions (τ=0.600 to 0.854, p0.001). Gender differences emerged in criteria weighting, actions, and responsibility attribution. When contextualised alongside broader health concerns, zoonoses ranked lower than other human and animal health problems. Community priorities also diverged from those identified in the national prioritization exercise.

Conclusions: The CZP is a feasible and reproducible tool for generating policy relevant evidence on community perceptions on zoonotic priorities in low literacy settings. By introducing a bottom-up mechanism, it complements expert driven frameworks and reveals livelihood-based concerns that national processes often overlook. Integrating community level prioritization into One Health planning can strengthen the relevance, legitimacy, and sustainability of interventions in Somalia and similar settings.

1193 – Prevalence, Temporal Trends, and Predictors of H9 Avian Influenza Virus in Kenyan Live Bird Markets, 2021-2024.

Annah MUDAMBA (1), Maurice OWINY (2), Jack OMOLLO (3), Bonface MWANGI (2), Jane GITHUKU (2), Caren NDETA (2)

1: Ministry of Agriculture and Livestock Development, Kenya; 2: Africa Field Epidemiology Network, Nairobi, Kenya; 3: Department of Agriculture, Livestock Development and Blue Economy, County Government of Kilifi, Kenya

Background: Avian influenza (AI) is a viral zoonotic disease that poses a serious threat to both animal and human health, with highly pathogenic strains such as H5N1 causing severe poultry outbreaks and sporadic human infections. Kenya remains at risk due to porous borders, shared ecosystems with countries reporting AI outbreaks, and its location along migratory flyways for wild waterfowl, natural reservoirs of AI viruses. To monitor this risk, the Directorate of Veterinary Services (DVS), in collaboration with stakeholders, established an active surveillance system in live bird markets (LBMs) in Nairobi, Nakuru, Kisumu, Kiambu, and Busia, as well as in wild bird habitats around Lake Victoria and the Rift Valley lakes. Despite these efforts, recent epidemiological patterns in Kenyan LBMs remain unclear. This study aimed to characterize the prevalence, temporal trends, and predictors of H9 avian influenza virus (AIV) in Kenyan LBMs from 2021 to 2024.

Methods: Surveillance data from LBMs (2021–2024) were obtained from the repository in Excel and analyzed using R. The primary outcome was AIV positivity, with year, market, and month of collection as independent variables. The Shapiro–Wilk test assessed data distribution. Descriptive statistics summarized median positivity across years, markets, and months. Differences in median positivity were assessed using the Kruskal–Wallis test. The effects of year, market, and month on AIV positivity were evaluated using generalized linear models.

Results: Between 2018 and 2020, surveillance detected influenza A viruses in poultry and wild birds, with 3.9% positivity in LBMs. From 2021 to 2024, the overall H9 positivity rate was 15.7% (1,718/10,958). Median positivity was highest in 2022 (12.6%; IQR: 3.7–39.8) and lowest in 2024 (4.2%; IQR: 0–25.1). Positivity was highest in May (10.5%; IQR: 2.6–34.5) and lowest in February (0%; IQR: 0–26.4). Nakuru recorded the highest median positivity (25.5%; IQR: 0–54.7), while Makueni had the lowest (0%; IQR: 0–3.9). Positivity varied significantly across markets ($\chi^2 = 57.55$, p 0.001) and years ($\chi^2 = 9.41$, $p = 0.024$), with Nakuru, Burma, and Kawangware showing higher median rates, and 2022 demonstrating higher positivity. There was no significant seasonal variation ($\chi^2 = 6.52$, $p = 0.8363$).

In multivariable analysis, year and market were significant predictors of AIV positivity. Samples collected in 2022 had higher odds of positivity (OR = 2.10; 95% CI: 1.18–3.85; p = 0.014), and Nakuru had higher odds of positivity compared to other markets (OR = 1.96; 95% CI: 1.19–3.23; p = 0.009).

Conclusion: This study confirms continued circulation of AIV Kenyan in LBMs, with the highest positivity in Nakuru. Findings highlight the need for sustained surveillance and strict implementation of national AIV guidelines. Future studies should explore drivers of high positivity in Nakuru, including trade patterns, market density, and climatic factors that may favor virus persistence.

1248 – Strengthening the One Health Workforce: The Role of Kenya Field Epidemiology and Laboratory Training Program

Maurice OMONDI OWINY (1), Caren Ndeta WAMBUA (2), Bonface WAWERU (2), Athman MWATONDO (1)

1: African Field Epidemiology Network, Kenya; 2: Kenya Field Epidemiology and laboratory Training Program

Background: A wide range of emerging and re-emerging infectious diseases have become a major threat to global health. Approximately 75% of these diseases are zoonoses. Kenya has had frequent zoonotic disease outbreaks that often require effective prevention, detection, and response by a fit-for-purpose multidisciplinary workforce capable of operating within a One Health framework. The Field Epidemiology and Laboratory Training Program (FELTP) was established to strengthen public health capacity through competency-based training in applied epidemiology and laboratory systems. The program enrolls various professionals and trains them as cohorts using the same curriculum. We highlight the value of FELTP in enhancing the One Health workforce.**Methods**: We conducted a descriptive review of Kenya FELTP training activities, workforce outputs, and contributions to multisectoral public health responses from 2004 through 2025. Information was obtained from program reports, trainee field projects, outbreak investigation reports, and surveillance evaluations conducted by FELTP residents. Key indicators included participation of multidisciplinary professionals, involvement in zoonotic disease surveillance and outbreak response, and collaboration across human, animal, and environmental health sectors.**Results**:

The Kenya FELTP trained and graduated 20 cohorts made of 328 trainees into the advanced level program from 2004 through 2025 with 212 (64.6%) of them being male, 123 (37.5%) were human health doctors, 47 (17.4%) were medical laboratory scientists, 41 (12.5%) were animal health doctors and 25 (7.6%) were from the environment and public health cadres. The competencies acquired during the two years of training include public health disease surveillance, outbreak investigation and response, scientific communication, and the conduct of planned epidemiologic studies. All cadres are involved in responding to public health events, thus creating synergy. Using field-based training, the residents jointly investigated disease outbreaks using the One Health approach, including cholera (40), COVID-19 (20), malaria (15), anthrax (11), and Rift Valley Fever (10). Residents have contributed to improved surveillance and use of data for decision-making through surveillance system evaluations. Among the systems evaluated are the Integrated Disease Surveillance and Response, Kenya Animal Bio-surveillance System, and Kenya Health Information System. The enrolment of various cadres trained together has strengthened collaboration among ministries responsible for human health, animal health, and environmental management. FELTP graduates have played critical roles in responses to zoonotic outbreaks, implementation of integrated disease surveillance systems, and development of evidence-based policies that support the One Health approach.**Conclusion**: FELTP is a critical platform for building a competent One Health workforce capable of addressing complex public health threats at the human–animal–environment interface. By promoting multidisciplinary training, field-based learning, and cross-sectoral collaboration, FELTP strengthens national and regional capacity for disease surveillance, preparedness, and response. Continued investment in FELTP and integration of One Health principles within training programs will further enhance global health security.

1285 – Unifying the Urban Front: A Strategic Framework for Private Sector Engagement through Metropolitan Surveillance Units in India

Shubhangi KULSANGE, Himanshu CHAUHAN, Satyam SIL, Ranjan DAS
National Centre for Disease Control, India

Background: Effective disease surveillance requires timely detection, reporting, and response to health events. In India, a significant proportion of patients first seek care in the private health sector. However, despite its significant contribution to service provision, the private sector remains underutilized in formal surveillance systems. Disease surveillance in India is primarily coordinated under the Integrated Disease Surveillance Programme (IDSP). Strengthening private sector engagement is therefore essential for improving early detection, reporting, and response to disease outbreaks. Major concentration of private sector is in metros. Metropolitan Surveillance Unit (MSUs) are established as a dedicated surveillance infrastructure to address the urban disease surveillance needs, with one of the key objectives of enhanced engagement of private sector in disease surveillance. Integrated Health Information Platform (IHIP) is a web based near real time reporting platform used by IDSP for capturing the case-based information of 50 plus epidemic prone disease conditions. Objective was to assess the status of private sector engagement and possible mechanisms involved in improving the private health facilities engagement and reporting.

Method: Under the PM-ABHIM program 20 MSUs are established in India since 2024. Currently, 10 MSUs are operational, in Mumbai, Ahmedabad, Bhubaneswar, Nagpur, Chennai, Bengaluru, Pune, Thane, Hyderabad and Patna. The total health facilities reporting across these MSUs comprise of Public and private facilities. Private sector engagement is critically reviewed by the program and necessary steps for increasing private sector engagement were undertaken as a program strategy. The data reported on IHIP through two mandated forms P & L (presumptive and Laboratory case form respectively), is analyzed for this purpose.

Result: The total P form health facilities reporting on IDSP-IHIP across these 10 MSUs are 3353, of which 55.71% (1868) are private facilities. Whereas, L form reporting facilities are 3400 of which 61.06% (2076) are private facilities. The average reporting on P from is 60.94% whereas L form is 58.98% by these private facilities. The key strategy followed at these MSUs was sensitizations and trainings. The total of 60 training/sensitization workshops were held and more than 400 private health facilities and more than 15,000 health care professionals were trained. Other strategies for increase private sector engagement were stakeholders' meetings (6 meetings), compulsory enrollment of private facilities on IHIP through clinical establishment act at Chennai and Hyderabad MSUs.

Conclusion: This study highlights the enablers to improve the reporting from the private sector and the policy level interventions which helped the Hyderabad and Chennai corporations to onboard private health facilities on IHIP. The MSUs plays a major role in sensitization of these health facilities and maintaining quality reporting on IDSP-IHIP. This helps in higher proportion of notifiable and epidemic-prone disease cases being captured on the IHIP and reducing the public health response time.

1364 – Seabirds as ecological sentinels of carbapenem resistance: blaKPC detection at a coastal South Atlantic interface

Letícia MOURA DIONÍSIO (1), Marta Jussara CREMER (3), Luiz Felipe FERREIRA DE SOUZA (1), Barbara SCHMINSKY DE FRANÇA (1), Amanda FERMINO (1), Jorge DE SOUZA FRANCISCO JUNIOR (1), Cinthia Graziela CANDIOTO DE OLIVEIRA (2,3), Giulia GAGLIANONE LEMOS (2,3), Lia YUKI GENDA (2,3), Jenyffer VIERHELLER VIEIRA (2,3), Mariane BATISTI (1), Roseneide CAMPOS DEGLEMANN (1), **Paulo Henrique FRANÇA CONDEIXA** (1)

1: Centro Integrado de Análises Moleculares e Microbiológicas em Saúde Única da Universidade da Região de Joinville (Univille), Joinville, SC, Brasil; 2: Universidade da Região de Joinville (Univille), Centro de Reabilitação de Fauna Marinha, São Francisco do Sul, Brasil; 3: Laboratório de Ecologia e Conservação de Tetrápodes Marinhos e Costeiros, Universidade da Região de Joinville (Univille), São Francisco do Sul, SC, Brasil

Background: Antimicrobial resistance (AMR) is a complex ecological process shaped by anthropogenic selective pressures and the circulation of resistance genes across interconnected environmental compartments. Coastal ecosystems represent critical interfaces linking urban effluents, port activities, and marine biodiversity. Seabirds function as ecological sentinels and potential vectors of resistant bacteria along coastal gradients and migratory routes. This study investigated the occurrence of Gram-negative bacteria (GNB) with phenotypic resistance to carbapenems and the presence of the blaKPC gene in seabirds on the northern coast of Santa Catarina, southern Brazil. Methods: Between September 2025 and January 2026, cloacal and tracheal samples were collected from debilitated seabirds in southern Brazil through the Santos Basin Beach Monitoring Project (PMP), conducted under the federal environmental licensing of Petrobras oil and gas activities by IBAMA (ABIO 640/2015). Samples were stored in Cary-Blair medium, refrigerated, and processed within 48 h. Following isolation and cryopreservation, bacteria were cultured in BHI broth and plated onto carbapenem-selective medium for phenotypic screening, KPC ChromoSelect. Isolates showing growth were identified by MALDI-TOF MS (scores ≥ 2.0). Genomic DNA was extracted by thermal shock, and DNA integrity was confirmed by amplification of the 16S rRNA gene. Detection of blaKPC was performed by PCR using specific primers. Differences in the distribution of resistant isolates between anatomical sites were assessed using the Chi-square test, while blaKPC occurrence between ecological groups was evaluated using Fisher's exact test. Results: Birds from two ecological groups were sampled: coastal (*Sula leucogaster, Fregata magnificens* and *Larus dominicanus*) and migratory (*Spheniscus magellanicus* and *Stercorarius antarcticus*). Ten individuals were analyzed, distributed among the five species as follows: 1, 2, 3, 3, and 1 individuals, respectively. A total of 217 GNB was isolated, of which 50 (23 %) exhibited growth on carbapenem-selective. Differences were not detected in the phenotypic resistance between the trachea (29.1 %) and cloaca (19.8 %), (Chi-square, p = 0.16). The most prevalent bacterial species were *Escherichia coli* (40 %), *Pseudomonas aeruginosa* (14 %), and *Enterobacter bugandensis* (10 %). The blaKPC gene was detected in 10 isolates, predominantly from cloacal samples (32 % *vs* 8 %; p=0.073). All blaKPC-positive isolates were obtained from *S. magellanicus* and included multiple bacterial taxa (*P. aeruginosa, E. coli, Raoultella ornithinolytica,* and *Enterobacter kobei*). Conclusions/implications: The detection of carbapenem-resistant GNB in seabirds supports the hypothesis of widespread environmental dissemination of resistance determinants in anthropized coastal systems. The presence of blaKPC across different bacterial species suggests horizontal gene transfer within environmental reservoirs. The concentration of blaKPC-positive isolates in a migratory seabird species highlights the potential role of wildlife in long-distance dissemination of AMR. Integrating seabirds into ecological surveillance frameworks is essential to understand connectivity between coastal environments, wildlife mobility, and the global spread of AMR genes.

1375 – Operationalizing One Health for Rabies Elimination in Nigeria's Underserved Communities Using Digital Innovation: A Mini Review

Omotola ISHOLA-BADAMASI (1), Sherifat BALOGUN-RAJI (2), Abdullateef AJADI (3), Evans OSABUOHIEN (4)

1: AwaVet Ltd, Nigeria; 2: FCTA Agriculture and Rural Development Secretariat (ARDS); 3: Department of Pathology, College of Veterinary Medicine, Tuskegee University, Alabama, United States; 4: Professor, Covenant University, UNEP GEO-7 Global Author

Background

Rabies remains one of the most preventable yet persistently neglected zoonotic diseases, responsible for approximately 59,000 human deaths annually, predominantly across Africa and Asia. Nigeria bears a disproportionate burden in rural and peri-urban communities where weak surveillance infrastructure, inadequate dog vaccination coverage, fragmented reporting, and limited access to post-exposure prophylaxis (PEP) perpetuate endemic transmission cycles. Poor coordination across veterinary, public health, and environmental sectors undermines scalable control efforts. Digital health technologies including mobile reporting systems, geospatial tools, AI-supported analytics, and community-based platforms offer opportunities to strengthen surveillance, enhance cross-sectoral coordination, and accelerate elimination within a One Health framework.

Methods

This mini-review synthesizes evidence from peer-reviewed literature, global health reports, and policy documents published between 2005 and 2025, addressing rabies control, One Health implementation, and digital health innovations in zoonotic disease surveillance. Sources were retrieved from PubMed, Web of Science, Scopus, Google Scholar, and repositories of WHO, FAO, WOAH, UNICEF, and the NCDC. Screening followed a PRISMA-guided approach, with quality independently appraised using the CASP checklist. Studies were eligible if they directly addressed digital surveillance tools, One Health frameworks, or rabies control strategies applicable to low and middle-income country contexts. Sixty-seven publications met inclusion criteria, with findings contextualised against Nigeria-specific epidemiological data to ensure local relevance.

Results

Digital innovations substantially enhance One Health strategies for rabies control. Mobile-based surveillance systems have reduced outbreak detection delays by up to 40% in comparable Sub-Saharan African settings, accelerating real-time reporting of animal bites and suspected cases. Geospatial mapping tools enable precise identification of transmission hotspots, with evidence indicating up to 30% improvements in vaccination campaign targeting efficiency, optimising resource allocation in constrained environments. Digital vaccination registries strengthen monitoring of dog immunization coverage, supporting evidence-based planning for mass vaccination programmes. Community-based mobile reporting platforms empower frontline actors including community health workers, animal health assistants, and local residents to participate in early warning systems and decentralised surveillance networks. Integration of veterinary and human health data through interoperable platforms improves cross-sectoral information sharing, enhancing risk stratification, coordinated outbreak response, and post-exposure case management.

Conclusions

Digital innovation represents a transformative pathway for operationalizing One Health approaches to rabies elimination in Nigeria's underserved communities. Aligned with the WHO/FAO/WOAH *"Zero by 30"* target of eliminating dog-mediated human rabies deaths by 2030, this review recommends phased integration of interoperable digital surveillance platforms within Nigeria's One Health coordination structures, prioritising highest-burden states. National policy must institutionalize community-based reporting mechanisms, standardize digital vaccination registries across veterinary and public health systems, and establish cross-ministerial data-sharing protocols. However, realizing this potential demands critical implementation barriers including digital infrastructure deficits, limited health worker digital literacy, data governance concerns, and sustained multi-sectoral funding to ensure equitable, and scalable translation of digital innovation into measurable rabies elimination.

1462 – Cross-national analysis of National Bridging Workshop Roadmaps assessing country needs for strengthening multisectoral collaboration at the human-animal-environment interface, with a focus on variations in capacity levels and priority-setting patterns.

Barbara ALESSANDRINI (1), Carmen ALFONSO-DILLEY (2), Mario Ignacio ALGÜERNO (1), Guillaume BELOT (2), Stéphane DE LA ROCQUE (2), Ravi DISSANAYAKE (3), Jennifer LASLEY (1), Julio PINTO (3)

1: World Organisation for Animal Health; 2: World Health Organization; 3: Food and Agriculture Organization of the United Nations

Background: The devastating effects of global health threats at the human-animal-environment interface have highlighted the continued need to improve intersectoral collaboration. The National Bridging Workshop (NBW) Programme contributes to this effort, by facilitating health sectors to assess their collaborative capacities and develop joint Roadmaps to strengthen them. A first study entitled *'Analysing countries' needs to improve multisectoral collaboration against health threats at the human-animal-environment interface: a study of 51 National Bridging Workshop Roadmaps'*identified the 60 most frequent priority actions; however, these "common" activities are not always present. A second study entitled *'Variation in NBW Roadmap Content: Insights into Capacity Levels and Priority Setting'* is intended to answer the question of why certain high-frequency actions are not included in every Roadmap.

Methods: A document analysis of 51 Roadmaps was conducted using a hybrid inductive-deductive coding approach. Activities were coded, categorized, and quantified for descriptive analysis. Hierarchical

clustering (HCA) and principal component analysis (PCA) were applied to examine co-occurrence and variability across countries and activities. Jaccard index was used to assess inter-country alignment and regional trends were evaluated. To investigate why certain high-frequency activities are absent from some countries' Roadmaps, a qualitative analysis is being conducted to determine whether these omissions reflect existing national capacity, differences in priorities, contextual relevance, or other factors linked to varying stages of capacity development.

Results: The analysis identified 60 distinct activity types, grouped into six key themes, describing 2028 activities, providing unique and meaningful insight into how countries plan to improve their One Health capacity. Of these 60 activity types, 37 were present in a third of Roadmaps or more. The HCAs revealed an absence of clustering between activities or countries and the PCA confirmed a high degree of variability. The highest Jaccard similarity score between two countries was 0.64, and intra-regional (0.34) and inter-regional (0.32) average similarity scores were almost identical. The second analysis' expected outcomes are: a dataset linking roadmap omissions to their underlying reasons; a comparative analysis across regions and technical areas; a new ranking of the 60 activities; and a potential "reference roadmap" combining the most impactful and widely relevant activities.

Conclusions: Activity needs, and their frequency, can help streamline international efforts to support countries in building their multisectoral collaborative capacities. With no dominant patterns of activity inclusion identified across countries or regions, our results offer concrete evidence for the need to tailor the One Health approach to countries' national contexts. Understanding the reasons for high-frequency activities omissions is also essential; absence may reflect differences in national priorities, capacities or contextual factors. By clarifying these reasons, we can better interpret roadmap content, distinguish between true needs and deliberate exclusions, and gain insights into how countries shape their One Health priorities.

1477 – Adapting a global programme for intersectoral collaboration assessment and planning at the Human–Animal–Environment interface.

Barbara ALESSANDRINI (1), Mario Ignacio ALGÜERNO (1), Guillaume BELOT (2), Jesse BONWITT (2), Stéphane DE LA ROCQUE (2), Ravi DISSANAYAKE (3), Sithar DORJEE (2), Kinzang DUKPA (1), André FURCO (1), Gyanendra GONGAL (2), Jessica KAYAMORI LOPES (2), Jennifer LASLEY (1), Gerald MUCHERU (3), Nadja MUENSTERMANN (4), Julio PINTO (3), Pablo SAGREDO MARTIN (4), Asma SAIDOUNI (2), Marie-yon STRUECKER (4), Zelalem TADESSE (3), Tieble TRAORE (2), Lillian WAMBUA (1), Chadia WANNOUS (1)

1: World Organisation for Animal Health; 2: World Health Organization; 3: Food and Agriculture Organization of the United Nations; 4: United Nations Environment Programme

Background:

The health of humans, animals and ecosystems are closely interconnected, as many diseases affecting humans originate from animals and can be driven by the degradation of ecosystems and spread through direct contact, food, or the environment. International organizations such as the FAO, UNEP, WHO and WOAH provide guidance and technical support for managing health risks at the human–animal–environment interface. For almost a decade, the National Bridging Workshop (NBW) Programme has proved to be a useful tool to strengthen collaboration, identify strengths and gaps and develop joint roadmaps to better prevent, detect, and control health threats through a One Health approach.

However, factors such as biodiversity loss, pollution, climate and land-use change, unsustainable agriculture, globalization, and wildlife trade have increased health risks, prompting a revision of the One Health definition to emphasise sustainable balance between people, animals, and ecosystems. Lessons learned from more than 60 NBWs worldwide, and alignment with the Quadripartite One Health Joint Plan of Action (OH JPA) have highlighted the need to adapt the NBW methodology.

Methods:

The NBW methodology review process responds to a qualitative analysis of feedback from NBW facilitators and participants, field experience, and country requests to integrate the environment into the process. Additionally, the inclusion of UNEP in the Quadripartite alliance and its involvement in NBWs is contributing progressively to this objective.

Results:

Updates to the programme include initial efforts to integrate the environment sector, especially in the workshop preparation engaging and guiding participants in the One Health concept; refinement and modernization of content and materials, incorporating innovative designs to better leverage knowledge, innovation and improve deliverable efficiency.

Key changes: aligning the One Health concept with the OHHLEP definition and the inclusion of the "Quadripartite vision"; addition of scenarios reflecting risks linked to ecosystem degradation that drive negative health outcomes at the human–animal–environment interface (e.g., river ecosystem collapse and harmful algal blooms) and relevant environmental frameworks/agreements and tools; upstreaming 'prevention' as an important One Health component, through the introduction of a dedicated technical area covering biodiversity conservation and community participation; and stronger linkages with the OH JPA and other mandated national and international strategies/plans to support effective and coordinated roadmap implementation.

Conclusions:

The evolution of the NBW Programme responds to emerging health threats and the changing global context by introducing methodological refinements and innovations. These improvements and adaptations reflect a flexible approach that promotes inclusion of the environment sector and supports context-specific One Health assessment and planning aligned with national priorities and global frameworks. Flexibility incorporating feedback and iteratively adapting the methodology is essential to sustain the long-term impact and relevance of the programme at country level. The full integration of the environmental dimension into the methodology remains an objective for future adaptations.

1506 – Advanced Data, Technology and One Health capacity within the PVS Pathway

Barbara ALESSANDRINI, Valentyna SHARANDAK, Rahul SRIVASTAVA, Jennifer LASLEY, Mario Ignacio ALGÜERNO
World Organisation for Animal Health

Background:

The digitalisation of the PVS Pathway – the WOAH flagship capacity building programme - and the structured data available provide an important opportunity to perform analyses on national surveillance capacities, multisectoral coordination mechanisms, and the application of the One Health approach. These digital datasets also offer valuable insights into the costing elements related to the public health interface, enabling a clearer understanding of the roles and responsibilities of Veterinary Services within broader national health systems. By leveraging this consolidated information, WOAH Members can better assess gaps, identify priority investments, and strengthen evidence-based planning to enhance their surveillance architecture and One Health collaboration.

Methods:

The analysis was conducted within the context of national Veterinary Services assessed through the PVS Pathway. The setting includes institutional, operational, and field-level structures responsible for surveillance, coordination, public health interface, and One Health implementation.

Data were extracted from PVS reports, targeting analyses on capacities related to surveillance systems, One Health coordination mechanisms, analytical capacities, and public health interface elements (including costing and resource needs).

A qualitative content analysis was conducted to identify common themes and patterns across countries, structured around PVS Critical Competencies.

Results:

The analysis of digitalised PVS Pathway reports yielded several consolidated findings across surveillance, coordination, and One Health capacities. Overall, Members demonstrated diverse levels of advancement, with common strengths. Integrated One Health (OH) practices were present in many institutional frameworks, but their operationalisation remained uneven.

Members (62%) underwent the PVS Pathway, demonstrating fully functional cross-sectoral surveillance, particularly in terms of real-time data exchange with public health, food safety, or environmental authorities.

In terms of coordination mechanisms, most PVS reports referenced formal structures—such as inter-ministerial committees or One Health platforms—yet their actual functionality was inconsistent. Evidence from the reports showed that while coordination existed on paper, regular joint planning, simulation exercises, and harmonised monitoring were still limited. Environmental sector engagement was the least developed, with collaboration typically focused on human-animal health interfaces.

Costing elements (by analysing Gap Analysis reports) related to the public health interface were identifiable but fragmented. While several countries had estimated resources for surveillance operations and laboratory networks, very few had dedicated budgets for joint OH activities, shared information systems, or cross-sector workforce development.

Conclusions:

Overall, the consolidated results show that countries possess foundational surveillance structures and recognise the importance of OH coordination, but many lack the digital infrastructure, technical capacity, and structured budgeting required for fully integrated OH surveillance and data driven decision making. The digitalisation of the PVS Pathway proved valuable in systematically identifying these patterns and highlighting opportunities for targeted capacity strengthening within the PVS Pathway.

1514 – One Health in Action: How Public–Private Partnerships Contribute to Reducing Antimicrobial Resistance in Animal Health

Barbara ALESSANDRINI, Rahul SRIVASTAVA, Myriam CARPENTIER, Camille LOI, Valentyna SHARANDAK, Hana ABDELSATTAR, Jennifer LASLEY, Mario Ignacio ALGÜERNO, Miftahul Islam BARBARUAH, Xyomara CHAVEZ PACHECO

World Organisation for Animal Health

BackgroundAntimicrobial resistance (AMR) is a major One Health challenge affecting human, animal, and environmental health. In the animal health sector, limited investment, estimated at only about 0.4% of global human health spending, often constrains the capacity of Veterinary Services to effectively prevent diseases, conduct surveillance, and promote responsible antimicrobial use. Public–private partnerships (PPPs) have emerged as a strategic approach to address these limitations by mobilising resources, sharing expertise, and aligning incentives between governments and industry stakeholders. The World Organisation for Animal Health (WOAH) has developed guidelines and a global PPP database that document collaborative initiatives in animal health systems. This study analyses PPP initiatives aimed at reducing AMR in animal health and explores how capacity-building efforts can strengthen their impact. The objective was to review existing PPP initiatives and identify key models that contribute to improved antimicrobial stewardship and One Health outcomes.

MethodsThe study reviewed the WOAH PPP database to identify initiatives on antimicrobial stewardship, surveillance, vaccination, and veterinary service strengthening. It analysed examples to categorise PPP models and assess their contributions to mitigating AMR. Insights from WOAH capacity-building workshops, including stakeholder consultations, were also examined to understand implementation approaches and challenges. The analysis aimed to identify effective partnership structures and interventions that contributed to reducing AMR.

ResultsThree major categories of PPP initiatives were identified. First, national consultation and coordination platforms facilitate dialogue and joint planning between veterinary authorities, producers, industry groups, and researchers. Examples include national animal health platforms in Australia, Canada, and Ireland, which support collective decision-making on disease prevention, antimicrobial stewardship, and risk monitoring.

Second, integrated AMR intervention programmes combine policy measures, surveillance systems, and behavioural change strategies. National strategies such as France's EcoAntibio programme and Denmark's integrated surveillance initiatives demonstrate significant reductions in antibiotic use through coordinated monitoring systems, training programmes, and farmer engagement.

Third, PPPs support preventive measures that reduce reliance on antimicrobials, particularly through vaccine development and disease control initiatives. Examples include collaborative vaccine development programmes, livestock disease control initiatives, and data-driven surveillance systems that

enable early detection and targeted responses. These initiatives also strengthen veterinary extension services and promote best practices among farmers.

Across all models, veterinarians, veterinary paraprofessionals, and community animal health workers play a critical role in ensuring responsible antimicrobial use. Capacity-building initiatives, such as training programmes, professional guidelines, and knowledge-sharing platforms, help improve stewardship practices and reinforce AMR prevention strategies.

ConclusionsPPPs are vital for applying One Health approaches to AMR in animal health. They enhance shared responsibility and coordinated planning, strengthen Veterinary Services, and promote sustainable antimicrobial stewardship. Evidence shows that collaboration improves surveillance and reduces antimicrobial use. Continued investment in frameworks, training, and collaboration is essential to scale these efforts and combat AMR effectively.

1587 – Understanding and Addressing the Climate Change and Antimicrobial Resistance Nexus with an Equity Lens

Sunday OCHONU OCHAI

International Centre for Antimicrobial Resistance Solutions (ICARS), Denmark, Denmark

Introduction: Health and food systems in low- and middle-income countries (LMICs) face converging pressures from climate shocks, rising disease burdens, and demands for sustainable productivity, and these pressures are not felt equally. Climate change, antimicrobial resistance (AMR), and food security rank among the most pressing global challenges, yet spatial evidence on where climatic stress overlaps with AMR or antimicrobial use (AMU) burdens remains limited, particularly in LMICs, where roughly 600 million small-scale farmers depend on food animals for their livelihoods and often have the least access to quality animal and human health services. Identifying this overlap is critical for prioritising surveillance, research investment, and climate-sensitive, equitable disease mitigation.

Methods: We developed 10 × 10 km² maps of "hotspots", defined as the spatial co-occurrence of climatic stress and normalised estimates of AMR and AMU in terrestrial and aquatic food animals. Climatic stress was characterised through a composite index integrating long-term changes in minimum land surface temperature, frequency of extreme humid-heat days, and extreme rainfall events. Hotspot distributions were modelled using Bayesian Spatial Beta Regression within the Integrated Nested Laplace Approximation framework.

Results: An estimated 16.4% of cattle, 35.8% of chickens and 23.2% of pigs in LMICs fell within high-risk hotspots. Distribution was strongly associated with food animal density, human population density and gross domestic product, with clustering in Latin America, the Middle East, India, and Eastern and South-Eastern Asia. For aquatic food animals (analyses restricted to Asia), southern India and several South-Eastern Asian countries showed the highest density of high-risk AMR hotspots, primarily driven by human population density.

Conclusions and Implications: The convergence of climatic stress with high AMR and AMU burdens concentrates in regions where marginalised, subsistence-dependent communities are least equipped to absorb additional shocks, reinforcing that climate-AMR risks track existing inequities. Although these maps do not establish causal relationships, they provide a scalable, policy-relevant framework to guide targeted surveillance, strategic research prioritisation, and climate-informed AMR mitigation across One Health sectors, and a foundation for embedding gender- and equity-focused lenses in AMR agendas so that women, youth, and marginalised groups benefit equitably from resulting interventions.

1608 – Mussels as Natural Biofilters: Experimental and Shotgun Metagenomic Analysis of Extracellular DNA-Mediated Accumulation of Antimicrobial Resistance from the Marine Environment

Stefano DALLE PALLE (1), Arianna PERUZZO (1,4), Pietro ANTONELLI (1,4), Giorgia FABBRI (1,4), Aurora DALL'OCCO (1), Periyasamy SIVALINGAM (3), Giuseppe ARCANGELI (2), Raffaella SABATINO (3), Andrea DI CESARE (3), Carmen LOSASSO (1)

1: Laboratorio di Ecologia Microbica e Genomica dei Microrganismi, Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università 10, 35020 Legnaro, Italia; 2: Centro Specialistico Ittico, Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università 10, 35020 Legnaro, Italia; 3: Consiglio Nazionale delle Ricerche (CNR) – Istituto di Ricerca sulle Acque (IRSA), Largo Tonolli 50, 28922 Verbania, Italia; 4: PhD National Programme in One Health Approaches to Infectious Diseases and Life Science Research, Departiment of Public Health, Experimental and Forensice Medicine, University of Pavia, Pavia 27100, Italy

Background:

Marine ecosystems are increasingly recognized as reservoirs of antibiotic resistance genes (ARGs), yet the role of filter-feeding organisms such as mussels (*Mytilus galloprovincialis*) in linking aquatic environments to human exposure remains insufficiently understood, particularly regarding the contribution of extracellular DNA (eDNA). This study aimed to: (i) characterize the resistome of mussels, seawater, and sediments by distinguishing intracellular (iDNA) and extracellular DNA (eDNA) fractions; (ii) investigate ARGs exchange dynamics among environmental matrices and mussels; and (iii) estimate potential human exposure to selected ARGs through mussel consumption.

Method:

Shotgun metagenomics was applied to DNA from mussels and to both iDNA and eDNA fractions from seawater and sediments. ARGs were identified using a read-based approach. Alpha- and beta-diversity analyses, differential abundance testing, and Spearman correlation analyses were performed on reads counts. An in vivo experiment using a plasmid carrying the streptomycin resistance gene aadA was performed to evaluate the uptake and accumulation of eDNA in mussel tissues. An Estimated Weekly Intake (EWI) model was developed to assess potential ARGs exposure through consumption.

Results:

The mussel resistome showed significantly lower diversity compared to environmental matrices, but appeared selectively enriched of clinically relevant ARGs. In fact, acrB a multidrug efflux gene, and AAC(6')-Ib-cr6 (aminoglycosides and fluoroquinolones resistance), were significantly more abundant in mussels than in both seawater DNA fractions. Although less abundant, kdpE (aminoglycosides resistance) also displayed higher abundance in mussels.

Beta-diversity analyses demonstrated a clear separation of resistome among matrices. Overall resistome correlations between matrices were moderate (rho 0.5), but the highest similarity was observed between mussels and seawater. At single-gene level, significant correlations were detected between ARGs in mussels and those found in the eDNA fractions of both matrices, with a higher number of associations detected with seawater eDNA fractions.

Exposure modelling identified acrB as the ARG with the highest EWI, followed by AAC(6')-Ib-cr6, highlighting the potential relevance of multidrug resistance genes for consumers.

The in vivo experiment confirmed that ARGs as plasmid free eDNA can accumulate in mussel tissues, with the highest levels detected in gills.

Conclusions/implications:

Wild mussels act as selective accumulators of specific ARGs rather than passive mirrors of the environmental resistome. Seawater, and especially its extracellular DNA fraction, emerges as the main driver shaping ARG composition in mussels. The enrichment and exposure of genes such as acrB underscore the need to integrate marine ecosystems and extracellular resistomes into AMR surveillance and food safety risk assessment frameworks.

1730 – Understanding behavioural drivers of zoonotic disease transmission amongst high-risk populations in Sawai-Madhopur, Rajasthan, July- August 2025

Sowntappan BALASUBRAMANIAN (1), Pradeep GODARA (1), Simmi TIWARI (2), Sushma CHOUDHARY (3), Ajit SHEWALE (2), Anurag DHOUNDIYAL (3), Jitesh KUWATADA (2), Ramesh CHANDRA (1), Praveen ASWAL (4), Ruchi SINGH (4), Ankoor TYAGI (4)

1: Division of Epidemiology, National Centre for Disease Control, Delhi, India; 2: Centre for One Health, National Centre for Disease Control, Delhi, India; 3: South Asia Field Epidemiology and Technology Network(SAFETYNET), India; 4: State Health Department, Rajasthan, India

Background:

Zoonotic diseases cause over 2.5 billion cases worldwide annually. Between 2018 and 2023, it accounted for 8% of reported outbreaks in India. People in Sawai Madhopur, Rajasthan, India, predominantly rural, depend on livestock and forest resources and frequently interact with wildlife that poses zoonotic risks. This study assessed community knowledge of zoonotic diseases, behaviours, and barriers affecting the adoption of safer practices in high-risk populations.

Methods: We conducted a convergent mixed-methods study from March to November 2025 in 20 randomly selected villages from the 125 villages within a 10 km range of Ranthambore National Park, Rajasthan. In each village, we randomly selected 11 households and interviewed one adult per household. We collected data using a structured questionnaire in EpiCollect5 on socio-demographic factors, zoonoses knowledge, risk and preventive practices. We also conducted in-depth interviews with 12 key informants and six focus group discussions(FGDs). Quantitative analyses were performed in SPSS 23.0. Qualitative data were manually coded using deductive and inductive approaches within a socioecological framework, and a Joint Display table was used to integrate both datasets.

Results: We interviewed 220 participants for a quantitative survey with a median age of 45 (IQR 35–55), 151 (69%) were male. Among them, 76 (35%) received no formal education, 157 (71%) were engaged in farming, and 83 (38%) in animal husbandry. Participants were aware of animal-to-human transmission (137,62%), and 154 (70%) believed zoonoses are preventable. Residents reported hand hygiene after animal contact (154,78%), and 18(8%) used personal protective equipment (PPE). Households kept livestock (189,86%), vaccinated animals (150,68%) and isolated sick animals (88,40%). Cultural practices included animal sacrifices (33,15%) and 158 (72%) attributed illness to environmental factors. Community recognises education's impact on behaviour (142,64%), and 156 (71%) are willing to adopt preventive changes. Barriers to adopting safe practice include cost (51%), lack of knowledge (37%), and cultural beliefs (16%). Enablers are training (73%), awareness campaigns (63%), veterinary services (60%), and PPE access (37%). Thematic analysis identified key themes: knowledge gaps, high occupational risks, varied risk perceptions, unsafe animal handling, vaccination and traditional food practices, barriers and enablers of safer practices, health-seeking behaviour, human–wildlife interface threats, and fragmented intersectoral coordination efforts. Low awareness and misconceptions (Individual level) lead to the normalisation of risky behaviours (household level), weak community messaging (community level), a fragmented health system (system level), and policy gaps (structural level), resulting in ongoing high-risk practices.

Conclusion: Despite moderate awareness of zoonotic diseases, safer practices remain limited, constrained by behavioural factors embedded in their livelihood practices. We recommended subsidised PPE and behaviour change training with One Health Interventions, involving frontline workers, ANMs, and Paravets could bridge awareness-to-action gaps in high-risk settings.

1753 – A One Health Gender-Responsive Approach to Improving Milk Hygiene and AMR Stewardship in Colombia's Dairy Value Chain: Mixed-Methods Evidence from Caquetá

Diana Cristina SANCHEZ AREVALO (1), Natalia Margarita CEDIEL BECERRA (2)
1: UNIVERSIDAD DE LA AMAZONIA, Colombia; 2: UNIVERSIDAD DE LA SALLE, Colombia

Background Colombia faces growing antimicrobial resistance (AMR) pressures in food-animal systems, threatening public health and market access. Addressing AMR requires integrated, community-engaged strategies that align milk hygiene, prudent antibiotic use, and women's participation within the dairy cattle value chain. We assessed whether a gender-responsive capacity-strengthening intervention improved milk safety, AMR stewardship, and empowerment in Caquetá.

Methods

We conducted a mixed-methods study on 37 farms across 11 municipalities, concentrating measurements in two dairy clusters—North and South. The intervention comprised: (1) a "Milking School" module on hygienic routines and microbiological risk; (2) on-farm protocol strengthening and follow-up; (3) AMR-stewardship messaging (diagnosis-led therapy, withdrawal periods); and (4) gender-transformative facilitation (GALS) with women-centered learning. Milk safety was evaluated with pooled-can somatic cell counts (SCC) pre/post; changes were tested using paired Wilcoxon tests (non-normal data). Udder bacteriology with antibiograms profiled pathogens and resistance. Knowledge was measured pre/post with a modified, conversation-based box test. Women's empowerment was assessed with WELI and

qualitative inquiry; inferential tests (independent-samples t-tests) compared Step-1 (pre) vs. Step-2 (post) indicators

Results

Pre-intervention SCC averaged 589,000 cells/µL (North) and 733,000 cells/µL (South). Post-intervention SCC decreased to 263,000 cells/µL (North) and 278,000 cells/µL (South); both reductions were statistically significant (Wilcoxon p 0.05). Cultures showed staphylococci predominance with elevated resistance to penicillin, amoxicillin, and cephalexin. AMR perceptions shifted toward stewardship: more participants linked mastitis control and adherence to withdrawal periods with reduced antibiotic use; reports of non-prescription/prophylactic use declined, though pockets persisted. Women's technical learning consolidated: 100% correct answers in the post-test among women. Training coverage reached 100% in both clusters and was statistically significant (North p = 0.004; South p = 0.0002). Affiliation to groups increased in the North (p = 0.037). Other empowerment dimensions (self-efficacy, autonomy, life satisfaction, mobility) trended upward descriptively but were not statistically significant, consistent with small samples and dispersion. Qualitatively, gender-segregated sessions and GALS fostered safe learning, greater household co-responsibility, and collective action (e.g., a rural-tourism/water-conservation initiative in the South). Time burdens contributed to a 17% decline in women's participation, underscoring structural constraints.

Within a One Health framing, these changes reflect coupled human–animal–environment gains: safer milk for consumers, fewer udder infections requiring antibiotics, and strengthened community norms around diagnosis-led treatment and withdrawal compliance.Environmental co-benefits emerged via water-conservation actions linked to milking routines. Together, evidence indicates an integrated pathway to resilience applicable to Colombian departments and regional dairy systems.

Conclusions The intervention worked: SCC dropped significantly, women's technical knowledge of milk safety consolidated, AMR stewardship norms strengthened, and specific empowerment and organizational indicators improved. Remaining gaps—pockets of non-prescription antibiotic use, time poverty, and uneven group cohesion—underscore the need for sustained, policy-backed One Health efforts that couple hygienic practices, antimicrobial stewardship, and gender equity in Caquetá.

1768 – Leveraging global and regional partnerships to strengthen One Health governance and implementation in Africa

Lillian Wayua WAMBUA

WOAH

Background: Africa remains significantly affected by zoonotic outbreaks and vector borne diseases, food safety hazards, antimicrobial resistance (AMR), and climate-driven health risks, which pose urgent challenges to the continent, underscoring the interconnectedness of human, animal, and environmental health. Addressing these complex risks requires strong governance mechanisms and coordinated action across sectors and institutions. The One Health approach therefore remains crucial for strengthening prevention, preparedness, and response to health threats.

Relevance: This session will explore the evolving governance and implementation of the One Health approach at continental, regional and country levels, leveraging partnerships within the Quadripartite (FAO, UNEP, WHO, WOAH) and its scientific advisory group the One Health High-Level Expert Panel (OHHLEP), the Africa Union (Africa CDC and AU IBAR), Regional Economic Communities and Regional organizations.

Educational outcome: This session will showcase Africa's experiences in strengthening One Health governance at continental, regional, and national levels. It will highlight how the Quadripartite is working with the Africa Union and other partners, to establish and/or strengthen One Health governance and coordination mechanisms at regional and national levels, aligned with the OH Joint Plan of Action and Implementation Guide as global frameworks. Implementation through capacity-building initiatives and high-level political commitment will be discussed. Quadripartite collaboration with African members of OHHLEP to further strengthen the scientific basis for implementing One Health tools and frameworks at regional and national levels, will be demonstrated. Finally, efforts on One Health Governance Community

of Practice (CoP) in the region, fostering multisectoral collaboration, knowledge exchange, and co-development of governance solutions will be shared.

The session will demonstrate accomplishments of these partnerships including the continental adoption and institutionalizing of One Health principles aligned to the global Frameworks contextual to the African Continent. The session will spotlight success on Africa Union-Quadripartite joint advocacy on AMR, and domestication of strategies such as the African Union One Health Zoonotic Disease Prevention and Control Strategy (2025-2029), aligned to the JPA. Regional efforts to advance One Health governance through the Regional Economic Communities (ECOWAS, EAC, SADC), and regional institutions have also been made, with key achievements including regional declarations and development of action plans to institutionalize and operationalise One Health in Member States (Table 1).

At national level, the session will highlight experiences of Member States, which have established national coordination platforms/committees, adopting various formats of governance that bring together ministries responsible for health, agriculture, environment, wildlife, and other sectors to work towards shared OH goals of strengthening multisectoral collaboration and coordinated responses to health threats (Table 2).

Format: A 90-minute session outline is proposed (Table 3). The session format will comprise two moderated panel discussions with interaction of the audience showcasing regional adoption and institutionalization, case studies and partnership perspectives.

Table 1: Selected frameworks adopted for One Health governance and implementation in Africa

Name	Source	Scope	URL
One Health Joint Plan of Action (JPA)	Quadripartite (FAO, UNEP, WHO, WOAH)	Global	Link
JPA Implementation Guide	Quadripartite (FAO, UNEP, WHO, WOAH)	Global	Link
Prevention and Control Strategy (2025 - 2029)	Africa Union	Africa	Link
Development Strategy and Action Plan (2022-2032)	Africa Union	Africa	Link
ECOWAS Regional One Health Strategic Plan (2025–2029)	ECOWAS	West Africa	
SADC Roadmap for One Health 2026-2035	SADC	Southern Africa	
East African Community One Health Strategy	EAC	Eastern Africa	

1775 – Socioecological Interconnections in One Health across human, animal and environmental health: a Scoping Review about food safety in Brazil

Leonor SANTOS (1), Verônica GINANI (1), Maria Carolina MESQUITA (1), Soniellson FERREIRA (2), Sindy SILVA (3), Mayara COSTA (1), **Jessica MEDEIROS** (1)

1: Universidade de Brasília, Brasil; 2: Universidade Federal da Paraíba, Brasil; 3: Global Health and Tropical Medicine, Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, Portugal

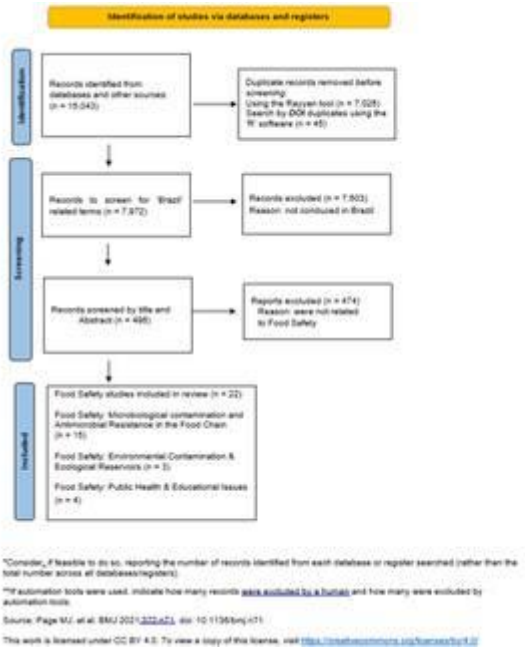
Background: One Health is a unified, cooperative, transdisciplinary approach to human, animal, and environmental health, aiming to address the challenges posed by emerging and re-emerging diseases, pandemics, zoonoses, antimicrobial resistance, food safety, climate change and other public health threats. This scoping review focus on the key aspect of Food Safety in Brazil, involving the physical, chemical, and biological risks throughout the food production chain: breeding, slaughtering, processing, transportation, marketing.

Methods: The review protocol was already published, following the methodology of the Joanna Briggs Institute's and the Preferred Reporting Items for Systematic Reviews and Meta-Analyses, extension for Scoping Reviews (PRISMA-ScR) checklist. The review included original articles, formally established references and gray literature (dissertations and theses, policy documents), that discuss strategies actions and experiences about the socioecological interconnections of One Health, published between 2004 and 2025. As evidence sources, we employed the following scientific literature databases: MEDLINE via PubMed, LILACS via BVS, Health Systems Evidence Social Systems Evidence, SciVerse Scopus, Web of Science and Google academics for gray literature.

Results: The initial search identified 15,043 records. After removing duplicates using the Rayyan software, and also by DOI matching in the R software 7,972 records remained. An automated filter in R was then applied to retain only studies conducted in Brazil, resulting in 496 records. These records were screened for eligibility based on title and abstract, which reduced the sample to 248 studies related to the following One Health topics: food safety, antimicrobial resistance, zoonoses, environmental health and One Health policies. After full-text assessment, 22 publications addressing the topic of food safety were included in the final sample. These studies were related to three main themes. The first was microbiological food safety and antimicrobial resistance in the food chain (n=15), involving studies with raw milk, dairy products, meats, eggs, and fresh vegetables. The second theme addresses environmental contamination and ecological reservoirs of pathogens (n=3), including analyses of water, soil, sediments, industrial environments, and natural resources associated with food production. The third theme encompasses epidemiological, educational, and behavioral issues related to public health (n=4). These include reviews on Chagas disease transmitted orally, assessments of knowledge about toxoplasmosis, and discussions about the role of the consumer in the production of safe food.

Conclusions: The studies analyzed emphasize the interactions of the One Health and highlight the role of the food chain and the environment in the spread of pathogens and antimicrobial resistance genes. The analysis indicates that strategies to contain foodborne illnesses must combine these elements. Otherwise, greater losses will occur, such as food contamination with emerging and re-emerging

pathogens that are increasingly adapted to adverse environments. However not all studies did in fact employ unified, cooperative and transdisciplinary methodologies, necessary to One Health approaches.



1908 – High Pathogenicity Avian Influenza (H5N1) Spillover into Indian Flying Fox Bats (Pteropus medius) at Shared Bird–Bat Roost Interfaces

Ariful ISLAM (1), Claude Kwe YINDA (2), Mohammad Enayet HOSSAIN (3), Pronesh DUTTA (4), Emama AMIN (4), Md. Arif KHAN (4), Mohammed Abdus SAMAD (5), Mohammed Ziaur RAHMAN (3), Tahmina SHIRIN (4), Marcel KLAASSEN (6), Jade K FORWOOD (8), Vincent J MUNSTER (2), Jonathan H EPSTEIN (7)

1: Charles Sturt University and Institute of Epidemiology, Disease Control and Research (IEDCR), Bangladesh, People's Republic of; 2: Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT 59840, USA; 3: One Health Laboratory, International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Bangladesh; 4: Zoonotic Disease Research Program, Institute of Epidemiology, Disease Control and Research (IEDCR), Mohakhali, Dhaka, 1212, Bangladesh; 5: National Reference Laboratory for Avian Influenza, Bangladesh Livestock Research Institute, Savar, Bangladesh; 6: Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, Geelong, Victoria, Australia; 7: One Health Science, Mt Kisco, New York, USA; 8: Gulbali Institute, Charles Sturt University, Wagga Wagga, NSW 2678, Australia

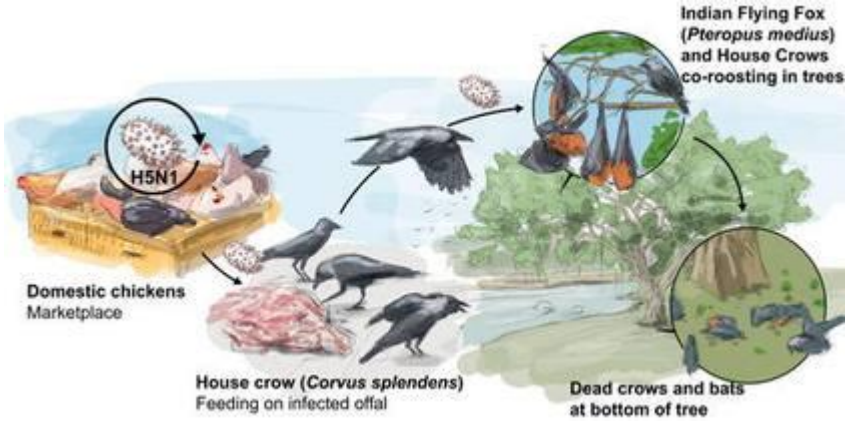
Background: High pathogenicity avian influenza (HPAI) outbreaks are of concern because of their pandemic potential, socioeconomic impact, and risks to wildlife conservation. Here, we report unusual mortality of Indian flying fox (Pteropus medius) bats and the potential spillover of H5N1 viruses into bat populations. Additionally, this study examines the phylodynamic of H5N1 within Bangladesh, elucidating evolutionary patterns and transmission dynamics in bat populations sharing roost sites with infected wild birds.

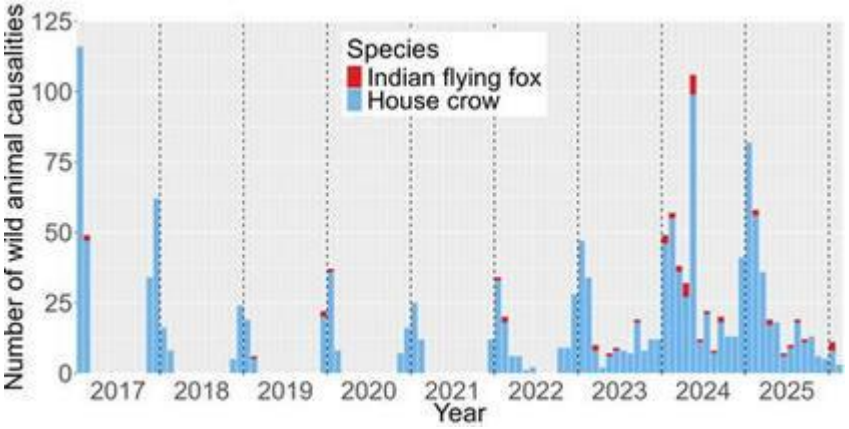
Methods: We conducted surveillance of house crow (Corvus splendens) mortality events in Dhaka city between 2017 and 2025. During wild bird mortality events investigation, we observed crow-bat cohabitation in shared roosts and occasionally observed dead bats in the affected roosts. We collected swab and tissue samples from dead crows and bats. We tested the swabs and tissue samples for the presence of AIV matrix gene, followed by the H5, H7, and H9 subtyping using rRT-PCR.

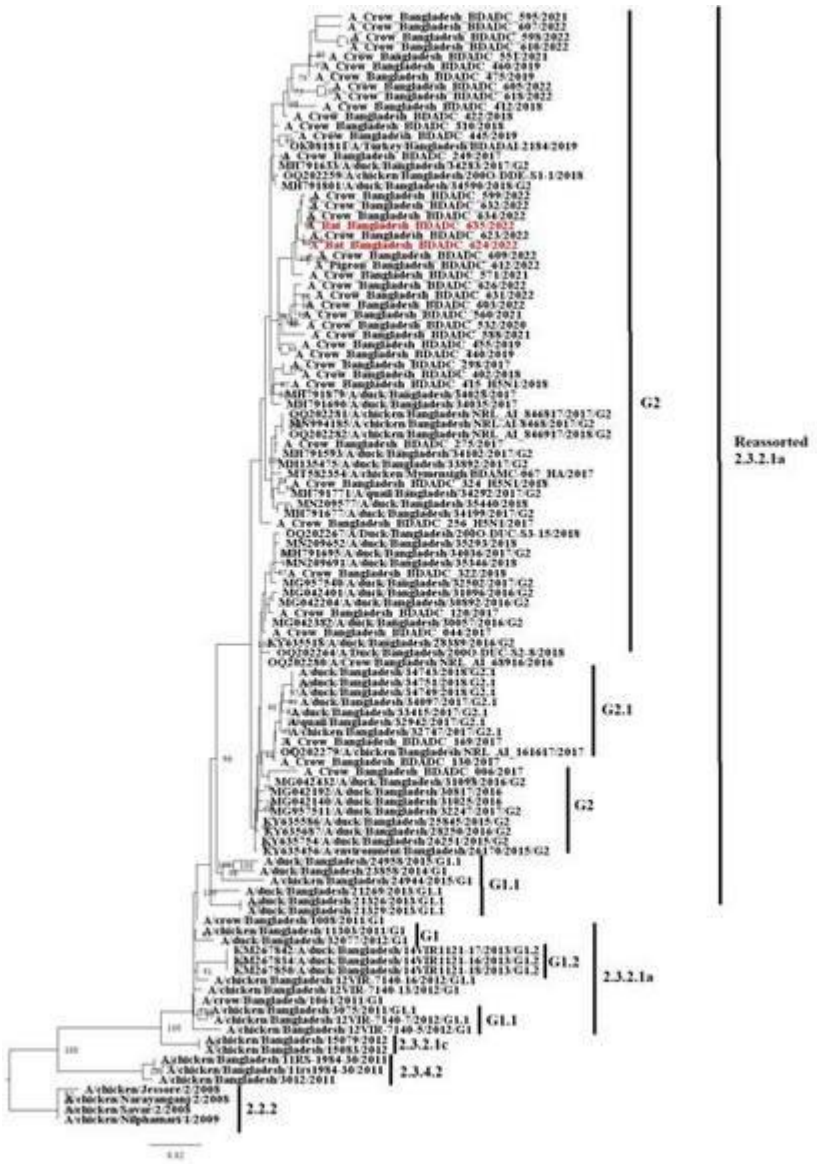
Results: Beyond house crows, we identified 18 Indian flying foxes infected with HPAI H5N1. We detected the H5N1 virus in all investigated tissue samples (trachea, kidney, liver, lungs, and brains) of these bats, indicate the systemic infection with H5N1 and could be the reason for the bats' mortality, and potential risk of HPAI viruses to mammalian hosts. We compared the complete sequence of the HPAI H5N1 virus found in the bats with other HPAI H5N1 virus sequences circulating in Bangladesh including the virus found in the house crows. Phylogenetic analysis revealed that the bat sequences belonged to the 2.3.2.1a clade and a close relationship between bat sequences and those from house crows and ducks in

Bangladesh. The 2.3.2.1a clade has been divided in two major lineage: G1 and G2. Phylogenetic analysis further indicated that the G2 lineage in Bangladesh is undergoing continuous evolution, resulting in the formation of multiple subclusters within this lineage. Notably, our two bat sequences were assigned to distinct clusters within the G2 lineage. We found bat H5N1 sequences contain several amino acid mutations and genetic markers of mammal adaptation,

Conclusion:We report the first detection of the H5N1 virus in bats in Bangladesh, concurrent with H5N1 in sympatric wild birds. Our findings suggest acute disease caused by the virus as the likely cause of mortality events in bats cohabiting with infected crows. This demonstrates HPAI virus potential to cross host barriers and infect mammals, highlighting significant public health concerns, as incidental spillover events may represent early stages of mammalian adaptation.







2327 – Doing More with Less: Cost–Benefit Analysis of Bat Viral Surveillance Using Global Data and a Cambodia Case Study

Morgane LABADIE (1,2), David R. J. PLEYDELL (1,2,3), Cherie YU (1,2,3), Thavry HOEM (4), Tey Putita OU (4), Julia GUILLEBAUD (1,2,5), Vibol HUL (4), Veasna DUONG (4), Erik A. KARLSSON (4), **Julien CAPPELLE** (1,2)

1: CIRAD, UMR ASTRE, F-34398 Montpellier, France; 2: ASTRE, Univ de Montpellier, CIRAD, INRAE, Montpellier, France; 3: INRAE, UMR ASTRE, F-34398 Montpellier, France; 4: Virology Unit, Institut Pasteur du Cambodge, Pasteur Network, Phnom Penh, Cambodia; 5: Virology Unit, Institut Pasteur de Madagascar, Pasteur Network, Antananarivo, Madagascar

Background : Viral surveillance in the field among bats, including the detection of coronaviruses, is essential for monitoring zoonotic risks and limiting the spread of future epidemics. In particular, surveillance of *Sarbecoviruses*, a group of bat-associated coronaviruses including SARS-CoV and SARS-CoV-2, is key for the early detection of zoonotic threats. These activities are often limited by logistical complexity and financial resources. These constraints are particularly pronounced in low- and middle-income countries, where surveillance programs often lack the human and financial resources to ensure effective surveillance. However, regardless of the country, all actors involved in surveillance face similar questions: how to optimize surveillance strategies while taking budgetary constraints into account, how to identify the most favorable sampling periods to maximize viral detection, and how to determine the optimal sample size to achieve surveillance objectives based on the sampling method used. This study

addresses these challenges by proposing a framework for optimizing viral surveillance in bats, tailored to specific surveillance objectives.

Methods : We developed a comparative framework to compare surveillance strategies in bats, based on three objectives: (i) detecting the presence or absence of coronavirus and sarbecovirus; (ii) estimating viral prevalence; and (iii) assessing viral diversity. The study was conducted in two main steps. First, the model was calibrated using longitudinal datasets of coronavirus surveillance in bats reported in the scientific literature, allowing us to parameterise temporal patterns of viral circulation and sampling performance across different contexts. Second, the calibrated framework was applied to empirical surveillance data from Cambodia to test the method for comparing surveillance strategies. Specifically, we used viral detection data from Sarbecovirus surveillance in *Rhinolophus shameli* in two Cambodian provinces to evaluate the performance of different sampling strategies under realistic budget and logistical constraints.

Results : The optimal surveillance strategy varied considerably depending on the objective. For detecting the presence or absence of the virus, guano sampling consistently outperformed rectal sampling due to its lower cost and the ability to collect a large number of samples per mission. Estimating prevalence required more balanced strategies, as rectal sampling offered better resolution at the individual level but at a higher financial cost. Temporal analyses identified specific sampling windows that significantly increased the probability of detection, thereby reducing the number of samples needed to achieve surveillance objectives.

Conclusion : This study shows that the effectiveness of viral surveillance hinges on clearly defined objectives, timely implementation, and explicit consideration of resource limitations. By showing that no single strategy is optimal in all situations, our framework provides practical guidance for designing surveillance programmes that are tailored to specific goals and resource constraints. The Shiny application promotes transparent, data-driven decision-making and facilitates the broader application of this approach in various ecological and epidemiological contexts.

2338 – Socio-cultural drivers of wildlife trade and zoonotic risk perceptions in two rural provinces of northern Cambodia: A knowledge, attitudes, and practices study during the COVID-19 pandemic

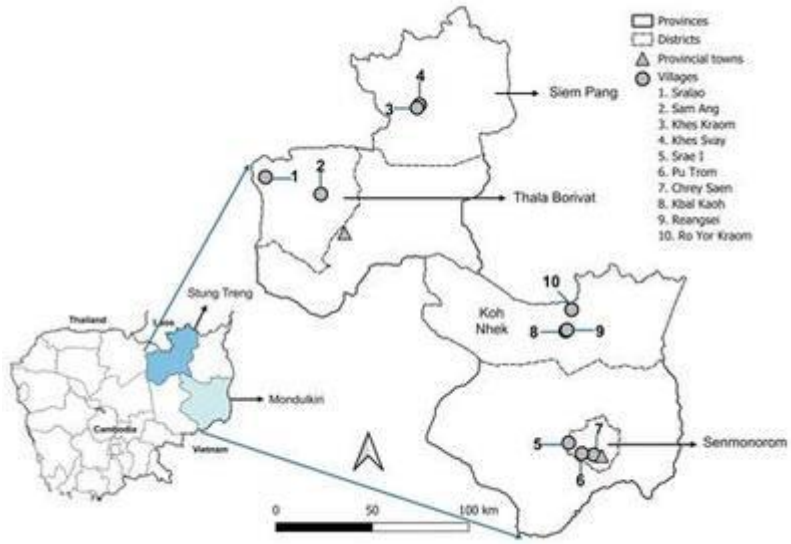
Thavry HOEM (1,2,3), Julia GUILLEBAUD (1,4,5), Samorn SRENG (6), Veasna DUONG (1,7), Julien CAPPELLE (3), Navin CHHIN (8), Srean CHHIM (9), Veronique CHEVALIER (3,4,5,6), Sopheab HENG (9), Helene GUIS (3,4,6)

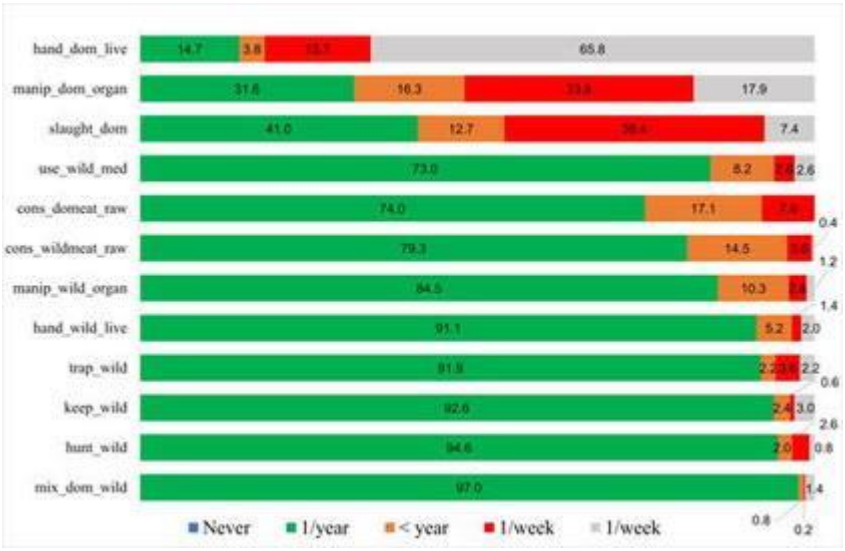
1: Virology Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia; 2: Montpellier University, Doctoral School, Biology of Interactions, France; 3: ASTRE, University of Montpellier, CIRAD, INRAE, F-34398 Montpellier, France; 4: CIRAD, UMR ASTRE, Phnom Penh, Cambodia; 5: CIRAD, UMR ASTRE, 101 Antananarivo, Madagascar; 6: Epidemiology and Public Health Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia; 7: Pandemic and Emergency Readiness Lab, McGill University, Montreal, Quebec, Canada; 8: Forestry Administration, Ministry of Agriculture, Forestry and Fisheries, Phnom Penh, Cambodia; 9: School of Public Health, National Institute of Public Health, Phnom Penh, Cambodia

Methodology: A cross-sectional community survey was conducted in 2021 among adults in Stung Treng and Mondulkiri provinces, using a cluster sampling design. A standardized questionnaire captured wildlife consumption, wildlife-related activities, and zoonotic risk knowledge and perceptions. KAP scores were attributed by assigning points to participants' responses. Multivariate logistic regression identified factors associated with KAP scores.

Results: Of 503 participants, 62.0% were female, mean age was 39 ± 14 years, and 74.6% were farmers. Knowledge of zoonotic diseases was suboptimal, with only 58.0% able to cite at least one zoonosis; recognition of wildlife zoonoses was weaker than domestic animal zoonoses. Participants were frequently in contact with domestic animals (65.8% weekly) and wildlife (74.2%), but wild meat consumption was rare, typically once per year. Higher knowledge was strongly associated with education (adjusted odds ratio [AOR] 2.19, 95% CI: 1.35-3.56 for primary/secondary school; 9.38, 95% CI: 4.15-21.22 for higher education) and Khmer ethnicity (AOR 1.64, 95% CI: 1.02-2.65). Positive attitudes toward zoonotic disease prevention were less frequent among 25-49 years (AOR 0.52, 95% CI: 0.30-0.90), but more common with higher income (AOR 1.61, 95% CI: 1.05-2.46), higher knowledge (AOR 2.23, 95% CI: 1.52-3.26), and Khmer ethnicity (AOR 2.16, 95% CI: 1.35-3.44). Safe practices were associated with female gender (AOR 1.79, 95% CI: 1.21-2.65), Khmer ethnicity (AOR 1.92, 95% CI: 1.23-2.99), and positive attitudes (AOR 2.27, 95% CI: 1.56-3.32).

Conclusion: Suboptimal KAP, particularly among non-Khmer participants, highlights the need for culturally sensitive, community-based education. Interventions should target wildlife-related zoonoses, safe animal handling, and wild meat consumption, particularly among minorities and rural populations with limited access to health information. Further research should assess inequalities in health information access and the impact of behaviour change programs on KAP.





2352 – Impact of global health funding disruptions on One Health programs in selected sub-Saharan African countries

Chidozie IWU, Amanda DEBUO DER, Steve GLOYD, **Julianne MEISNER**
University of Washington, United States of America

Introduction

Foreign health assistance has contributed greatly to global health progress, especially in HIV, tuberculosis, malaria and integrated One Health programs across low- and middle-income countries. Recent funding freezes and aid reductions are disrupting health systems, including zoonotic surveillance, veterinary services, environmental monitoring, and multisectoral collaboration. This study explored the impact of recent global health funding disruptions on One Health programs in selected sub-Saharan African countries to identify strategies that promote resilience and sustainability.

MethodsWe conducted a Rapid Qualitative Analysis in five sub-Saharan African countries between October–December 2025, to generate rigorous yet timely evidence to inform ongoing policy and programmatic decisions. Semi-structured online interviews were conducted with program leaders, researchers, and institutional representatives from international non-governmental organizations (INGOs), academic or research institutions, and government agencies that had received external global health funding for One Health activities. Interviews explored funding related impacts, institutional responses, and future strategies. Transcripts were analyzed thematically using a matrix-based approach to identify recurring patterns across participants.

ResultsA total of 11 participants were interviewed across five countries: Kenya (n=5), Rwanda (n=2), Mozambique (n=2), Tanzania (n=1), and Ethiopia (n=1). Participants were from INGOs (n=6), academic/research institutions (n=4), and county level government (n=1); 10 were male and 1 female, and all (n=11) reported being affected by funding cuts. Interviews identified five central themes: (1) Disruptions to research activities, public health programs, and service delivery, including interrupted surveillance, data collection, community engagement, and ongoing projects across agriculture and disease control; (2) Workforce and institutional vulnerability, resulting to job losses and weakened institutional capacity; (3) Community level consequences, health risks, and widening inequities, including reduced vaccination and prevention activities, service gaps affecting food security, and increased risk of under detected and re-emerging diseases; (4) Training and research impacts, with academic and training pipelines directly affected, threatening future workforce development; and (5) Adaptation and new partnerships, with institutions diversifying funding sources and calling for greater domestic investment despite continued uncertainty.

ConclusionForeign funding disruptions affects surveillance, veterinary and public health prevention activities, and workforce capacity needed for zoonotic disease detection and response, increasing risks to both human and animal health. Sustained progress will require stronger collaboration, diversified funding sources, and increased domestic investment to strengthen One Health resilience.

2370 – The Impact of Community One Health Volunteers in Quarterly Household Surveillance and Reporting Disease occurrences in Remote Areas of Uganda

Phiona KATUSHABE (1), Teddy NAMAGGA (1), Ssali R. OGWAL (2), Gladys K. NAKANJAKO (1,3), Joseph MUTYABA (1), Babi NACKSON (1), Mercy HAUMBA (1), Micheal RABWONI (1), Wilber SSEMBAJJWE (4), Lisa T. NAKUYA (1), Rehemah NAKIMBUGWE (1), Collins AGABA (4), Eric M. ENYEL (5), Deo B. NDUMU (3), Gladys K. ZIKUSOKA (2), Musa SEKAMATTE (6), Dennison KIZITO (1), Janet SEELEY (7), Julius J. LUTWAMA (1)

1: Uganda Virus Research Institute, Uganda; 2: Conservation Through Public Health (CTPH), Entebbe, Uganda; 3: National Animal Disease Diagnostics and Epidemiology Centre (NADDEC), Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Uganda; 4: Medical Research Council, Uganda Virus Research Institute & London School of Tropical Medicine and Hygiene, Entebbe-Uganda; 5: Uganda Wildlife Authority (UWA), Kampala Uganda; 6: National One Health Platform (NOHP), One Health Coordination Office (OHCO), Ministry of Health, Kampala, Uganda; 7: London School of Hygiene & Tropical Medicine (LSHTM), University in London, United Kingdom

Background:

Communities at human-livestock-wildlife interfaces are at high-risk for infection, making One Health community-based surveillance essential for mitigating outbreaks.Community One Health Volunteers (COHVs); a tripartite team comprising Village Health Teams, Animal Husbandry Officers, and wildlife scouts, bridge surveillance gaps at Uganda's human-livestock-wildlife interfaces. COHVs conduct grassroot surveillance for early disease detection and lead community education by sharing knowledge on One Health and zoonotic diseases. This study evaluated the impact of COHV-led surveillance on community knowledge transfer, disease detection and response capacity.

Methods: This was a prospective longitudinal community-based surveillance carried out from July, 2023 to May, 2026 in Bwindi-Mgahinga (BMCA), Queen Elizabeth (QECA), Lake Mburo (LMCA), and Murchison Falls Conservation Areas (MFCA). A total of 127 COHVs conducted quarterly surveillance across assigned 50-household (HH) clusters per COHV. Using Kobo Collect application on tablets, they submitted near real-time data on demographics, WASH indicators, zoonotic disease knowledge, and seasonal livestock disease patterns. Data was analyzed using Statistical package for Social Sciences (SPSS) to give the descriptive statistics, trend analysis, and evaluate changes in community health indicators and reporting

frequency over time. Reports were centralized at the Uganda Virus Research Institute (UVRI) server, and shared with the National One Health Platform and other stakeholders for action.

Results: Quarterly surveillance data showed significant HH improvements: latrine usage rose from 79.8% to 91%, handwashing facilities from 38.7% to 52.1%, and mosquito net usage from 71.1% to 87.8%. Community knowledge of zoonotic disease transmission increased (75.6% to 87.6%), leading to increased safer carcass disposal by burying (64.4% to 80.9%), reduced wild meat consumption (37.2% to 11.5%), and decreased shared human-animal shelters (61.6% to 51.8%). Livestock health improved through tick control with a decrease in the number of those who don't spray or dip or hand pick (10.3% to 7.6%), increased veterinary service access and utilization (41.2% to 55.2%), resulting in a decline abnormal livestock deaths (41.9% to 19.8%).

Seasonal patterns revealed livestock illnesses and abortions peaked during the dry season in BMCA (7.2%), LMCA (15.4%) and QECA (24.1%), whereas MFCA reported higher incidences during the wet season (27.5%). Risk analysis by household responsibility for animal care revealed that husbands were at a higher risk of infections from cattle and goats (55.8% and 41.8% respectively), wives were at a higher risk of infection from pigs (58.9%), and children were at a higher risk of rabies and dog bites (35.5%). Syndromically, COHVs detected and reported Monkeypox, Red Eye, Foot and Mouth Disease, and Anthrax within their communities.

Conclusion:COHVs proved to be a robust, cost-effective early warning system that significantly improved community-level practices, zoonotic disease prevention, and detection. Integrating these volunteers into national frameworks is essential for strengthening surveillance in remote areas and mitigating future pandemic threats.

2389 – Mapping Reported Modes of Transmission of Highly Pathogenic Avian Influenza A (H5N1) to Humans

Nicole BILLIAS (1,2,3), Victoria D'ALESSANDRO (1,2), Dimitra POULIOPOULOU (1,2), Jessica WONG (1,2,8), Erin MILLER (1), Jessica HOPKINS (4,5,6), Eleni BOUTSIKARI (7), Lauren CIPRIANO (8), Tiago DA VEIGA PEREIRA (9), Jennie JOHNSTONE (10), Saverio STRANGES (11,12,13), J. Scott WEESE (14), Joy MACDERMID (1,2,3), Kieran QUINN (4), David FISMAN (4), Pavlos BOBOS (1,2,11)

1: School of Physical Therapy, Western University, London, ON, Canada; 2: Western's Bone and Joint Institute, Western University, Canada; 3: Lawson Research Institute, St. Joseph's Health Care London, London, ON, Canada; 4: Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada; 5: Public Health Ontario, ON, Canada; 6: Department of Health Research Methods, Evidence, and Impact, McMaster University, Hamilton, ON, Canada; 7: Faculty of Medicine, University of Athens, Athens, Greece; 8: Richard Ivey School of Business, Western University, London, ON, Canada; 9: Nuffield Department of Population Health, University of Oxford, Oxford, England; 10: Department of Medicine, University of Toronto, Toronto, ON, Canada; 11: Department of Epidemiology and Biostatistics, Schulich School of Medicine & Dentistry, Western University, London, ON, Canada; 12: Department of Family Medicine, Schulich School of Medicine & Dentistry, Western University, London, ON, Canada; 13: Department of Clinical Medicine and Surgery, Federico II University, Naples, Italy; 14: Ontario Veterinary College, University of Guelph, Guelph, ON, Canada

Background:

Highly Pathogenic Avian Influenza A (subtype H5N1) poses a threat to human health, and its pandemic potential emphasizes the need to better understand detailed reported transmission pathways to humans. Existing literature is outdated or lacks detailed, comprehensive analysis of the range of transmission routes and how the virus may enter the human body.

Methods:

A scoping review methodology was used to comprehensively map all reported H5N1 transmission pathways to humans, as well as viral entry routes. CINAHL, Embase, MEDLINE, Scopus, PubMed, grey literature, and reference lists (of included studies) were searched up to October 29th, 2025, with no language restrictions. Observational studies and grey literature reporting H5N1 transmission evidence to humans were included. Two reviewers conducted duplicate screening independently. One reviewer completed data extraction, which was cross-verified for accuracy by a second. Findings were summarized narratively.

Results:

120 sources met inclusion criteria (70 studies, 50 grey literature). Reported H5N1 transmission pathways were classified into animal-to-human (111 of 120 sources, 92.5%; including poultry-to-human in 102 sources [85.0%] and cattle-to-human in nine sources [7.5%]), environment-to-human (37 of 120 sources, 30.8%), and human-to-human (14 of 120 sources, 11.7%). Reported transmission pathways were further classified as direct or indirect contact, synthesized, and linked to suspected routes of human entry, including mucosal entry (eyes, nose, mouth), inhalation of aerosols or droplets, ingestion, and percutaneous exposure. Entry routes are biologically plausible and do not imply relative likelihood or causal attribution.

Conclusions:

There are multiple reported pathways of H5N1 exposure, and a single pathway may involve multiple ways to infect humans. Further research is needed to determine causal mechanisms, identify specific risk factors and measures of association, and strengthen evidence-based prevention strategies.

2411 – Gaps in One Health and Planetary Health Education Across Health Disciplines: A 2026 Global Survey

Fabien MURHULA BAKENGA (1,4,14), **Deborah THOMSON** (2,3,14), Emmanuel J. AWOSANYA (1,4,14), Doris MA (2,14), Osman ABDUL-FATAWU IDDRISU (5,16,17), Danielly MAGALHAES (6), Balkiss ABDELMOULA (7,15), Jelena MALOGAJSKI (8), Asger LUNDORFF JENSEN (2), Charles MULEKE (2), Zoi DOROTHEA PANA (9), Paul VAN DER MERWE (2), Kasey BELLEGARDE (10), Christina PETTAN-BREWER (2,11), William BOGRAKOS (12), Marta MASSERDOTTI (13), Ekaa DESAI (13), Noel MAGLOIRE MANGA (17), Priscilla ROBINSON (18)

1: Pan African University Life and Earth Sciences (including Health and Agriculture)_PAULESI, University of Ibadan, Nigeria; 2: World Veterinary Association One Health Education Subgroup (WVA-WOHES); 3: World Veterinary Association One Health Working Group (WVA-OHWG); 4: University of Ibadan (UI); 5: World Veterinary Association (WVA); 6: Global Consortium on Climate and Health Education (GCCHE); 7: Junior Doctors Network (JDN); 8: Planetary Health Alliance (PHA); 9: International Network for Health Workforce Education (INHWE); 10: International Council of Nurses (ICN); 11: One Health Latinoamérica, Ibero y el Caribe (OHLAIC); 12: World Association of Disaster and Emergency Medicine (WADEM); 13: International Veterinary Students' Association (IVSA); 14: One Health Lessons® (OHL); 15: World Medical Association (WMA); 16: School of Public Health, Kwame Nkrumah University of Science and Technology; 17: Université de Ziguinchor; 18: World Federation of Public Health Associations (WFPHA)

Background:

The fields of "One Health" and "Planetary Health" have evolved to meet the needs of a changing planet with more complicated health challenges.

However, health professional education remains fragmented, with minimal baseline data on how well health professionals across disciplines are being prepared to work collaboratively across human, animal, environmental, and planetary health systems.

This global initiative aims to evaluate the past and present exposure of health professionals and students to One Health and Planetary Health in formal training programs, explore how they view their own role in advancing the two concepts in their careers, and determine key implementation gaps, the urgent needs, and short-/long-terms strategies to address them.

Methods:

This is a global online survey-based research initiative. Using convenience sampling, a minimum of 10,000 professionals and students across multiple health disciplines (including Medicine, Nursing, Veterinary Medicine, Dentistry, Global Health, Public Health, One Health, and corresponding paraprofessionals) are targeted.

Data on demography, past and recent educational experience in Planetary Health and One Health, and individuals' career on health will be obtained. Data will be collected from six continents, using the REDCap® survey platform, from June to September 2026, in multiple languages (English, Spanish, French, Italian, Portuguese, Hindi, Arabic, Chinese, and Hausa).

Descriptive, summary statistics will be applied to categorical data and data on a Likert scale. Chi-square goodness of fit test will be applied to test the Null hypothesis of equal proportions of the various options.

Results:

Preliminary results will be available by the end of August 2026. The authors expect to identify educational deficiencies across multiple health disciplines in regards to One Health and Planetary Health.

The study's survey evaluates the time of (or lack of) learning of the multiple topics including environmental determinants of health, impacts of climate on infectious diseases, environmental history, biodiversity loss, ecosystem services, health system resilience strategies, environmental justice, inclusion of Indigenous knowledge, and more.

The survey will provide a synchronized global "snapshot in time" of current and past educational and professional preparedness for interdisciplinary collaboration in addressing emerging diseases, environmental change, ecosystem disruption, and other complex global health challenges.

Conclusions:

Identified gaps and opportunities will represent a strategic roadmap that will help to generate clear, actionable recommendations aligned with the United Nations Sustainable Development Goals, UN Quadripartite, UNESCO Goals for Tertiary Education, and Global Health Security and Workforce Preparedness to strengthen interdisciplinary education, support climate and ecosystem resilience, improve health workforce preparedness, and advance global health security.

2417 – Strengthening Veterinary Services at the Front Line of Global Biothreat Prevention: A One Health Approach

Beatrice RODRIGUES MOUILLE, Frederic POUDEVIGNE, **Gisela GIOIA**
FAO

Background

Biological threats emerging at the human–animal–environment interface increasingly challenge global health security. The deliberate misuse, accidental release, or natural emergence of animal pathogens can generate cascading impacts on public health, food systems, ecosystems, and national economies. Livestock systems are particularly vulnerable due to dense animal populations, high pathogen diversity, and globalized supply chains. However, biosafety, biosecurity, and surveillance capacities remain uneven across regions. Strengthening veterinary services as a front-line component of the One Health architecture is therefore essential to prevent, detect, and respond to biological threats before they escalate into wider crises. This study describes the approach and initial outcomes of the FAO BIOSHIELD initiative, which aims to institutionalize biological threat reduction within veterinary services through an integrated One Health framework.

Methods

The BIOSHIELD initiative applies a multi-component capacity-development approach linking laboratory systems, surveillance networks, and operational preparedness. The programme supports national veterinary authorities through three complementary pillars. First, veterinary laboratory biosafety and biosecurity capacities are strengthened through risk-based assessments, improved pathogen inventory management, and enhanced cybersecurity practices. Second, national animal health surveillance systems are evaluated and reinforced to improve early detection of unusual or suspicious events that may signal emerging diseases or deliberate biological incidents. Third, multisectoral preparedness is promoted through joint training and simulation exercises involving veterinary services, public health authorities, environmental actors, and law-enforcement agencies, with emphasis on joint investigation procedures and chain-of-custody management of biological evidence.

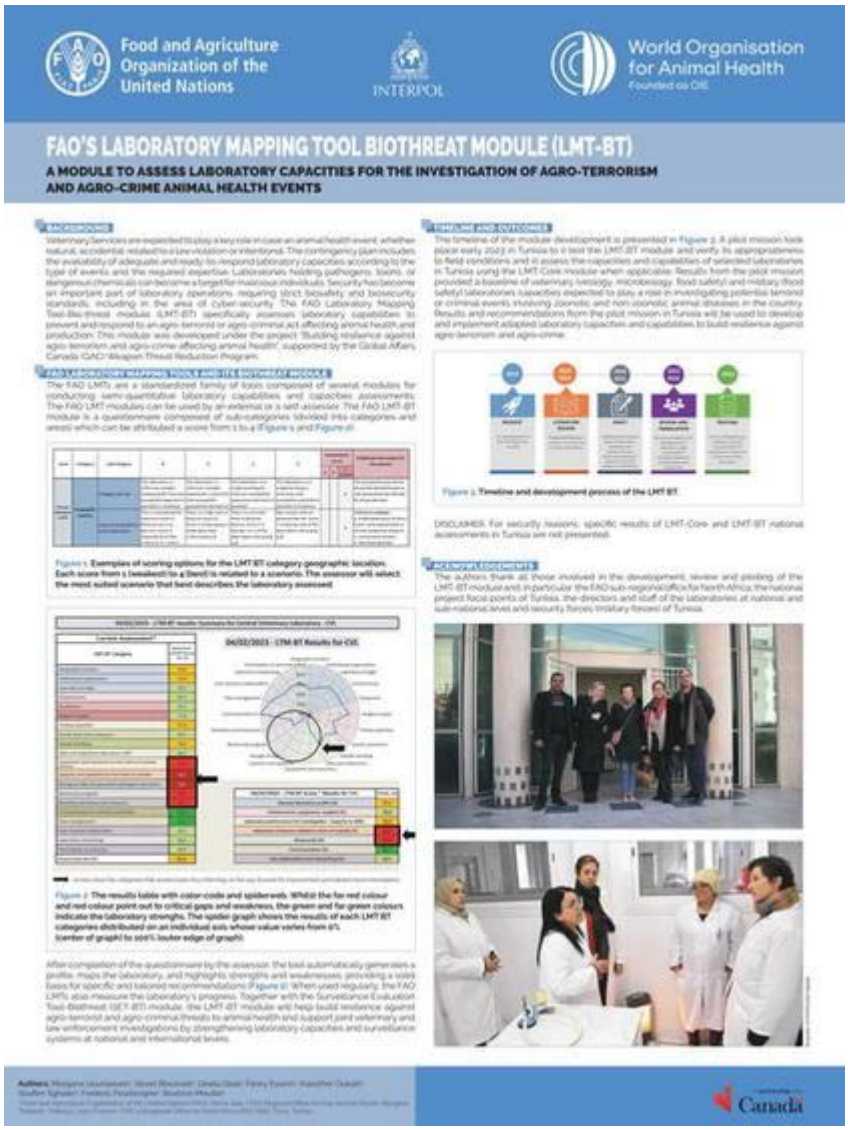
Results

Implementation builds on FAO-developed assessment and preparedness tools, including the Laboratory Mapping Tool Biothreat module (LMT-BT), the Surveillance Evaluation Tool Biothreat module (SET-BT), and the Good Emergency Management System Biothreat module (GEMP-BT). These tools enable countries to identify systemic vulnerabilities across laboratory, surveillance, and emergency response systems and to develop evidence-based national action plans for biological threat mitigation. Early applications have demonstrated improved cross-sectoral dialogue, stronger integration between veterinary surveillance

and national biosecurity frameworks, and enhanced operational readiness for investigating and responding to suspected biological incidents affecting animal populations.

Conclusions

Strengthening veterinary services within a One Health framework provides a critical entry point for reducing biological risks at their source. The BIOSHIELD initiative demonstrates that integrated governance, improved laboratory biosecurity, and coordinated multisectoral preparedness can substantially enhance national resilience against biological threats. Institutionalizing these capacities contributes not only to animal health protection but also to broader global health security by preventing animal-origin biological risks from escalating into major public health or economic crises.



Food and Agriculture Organization of the United Nations

INTERPOL

World Organisation for Animal Health
Founded as OIE

FAO'S LABORATORY MAPPING TOOL BIOTHREAT MODULE (LMT-BT)

A MODULE TO ASSESS LABORATORY CAPACITIES FOR THE INVESTIGATION OF AGRO-TERRORISM AND AGRO-CRIME ANIMAL HEALTH EVENTS

BACKGROUND

Veterinary Services are expected to play a key role in case an animal health event, whether natural, accidental, related to a bio-incursion or intentional. The contingency plan includes the availability of adequate and ready-to-respond laboratory capacities according to the type of events and the required expertise. Laboratories holding pathogens, toxins, or dangerous chemicals can become a target for malicious individuals. Security has become an important part of laboratory operations requiring strict biosafety and biosecurity standards, including in the area of cyber-security. The FAO Laboratory Mapping Tool-Bio threat module (LMT-BT) specifically assesses laboratory capabilities to prevent and respond to an agro-terrorist or agro-criminal act affecting animal health and production. This module was developed under the project "Building resilience against agro-terrorism and agro-crime affecting animal health", supported by the Global Affairs Canada (GAC) Weapon Threat Reduction Program.

FAO LABORATORY MAPPING TOOLS AND ITS BIOTHREAT MODULE

The FAO LMTs are a standardized family of tools composed of several modules for conducting semi-quantitative laboratory capabilities and capacities assessments. The FAO LMT modules can be used by an external or a self-assessor. The FAO LMT-BT module is a questionnaire composed of sub-categories (divided into categories and areas) which can be attributed a score from 1 to 4 (Figure 1 and Figure 2).

Figure 1. **Examples of scoring options for the LMT BT category geographic location. Each score from 1 (weakest) to 4 (best) is related to a scenario. The assessor will select the most suited scenario that best describes the laboratory assessed.**

Figure 2. **The results table with color code and spiderweb. Whilst the far red colour and red colour point out to critical gaps and weakness, the green and far green colours indicate the laboratory strengths. The spider graph shows the results of each LMT BT categories distributed on an individual axis whose value varies from 0% (center of graph) to 100% (outer edge of graph).**

After completion of the questionnaire by the assessor, the tool automatically generates a profile, maps the laboratory, and highlights strengths and weaknesses, providing a solid basis for specific and tailored recommendations (Figure 3). When used regularly, the FAO LMTs also measure the laboratory's progress. Together with the Surveillance Evaluation Tool-Biothreat (SET-BT) module, the LMT-BT module will help build resilience against agro-terrorist and agro-criminal threats to animal health and support joint veterinary and law enforcement investigations by strengthening laboratory capacities and surveillance systems at national and international levels.

TIMELINE AND OUTCOMES

The timeline of the module development is presented in Figure 3. A pilot mission took place early 2023 in Tunisia to i) test the LMT-BT module and verify its appropriateness to field conditions and ii) assess the capacities and capabilities of selected laboratories in Tunisia using the LMT-Core module when applicable. Results from the pilot mission provided a baseline of veterinary (virology, microbiology, food safety) and military (food safety) laboratories capacities expected to play a role in investigating potentials terrorist or criminal events involving zoonotic and non-zoonotic animal diseases in the country. Results and recommendations from the pilot mission in Tunisia will be used to develop and implement adapted laboratory capacities and capabilities to build resilience against agro-terrorism and agro-crime.

Figure 3. **Timeline and development process of the LMT BT.**

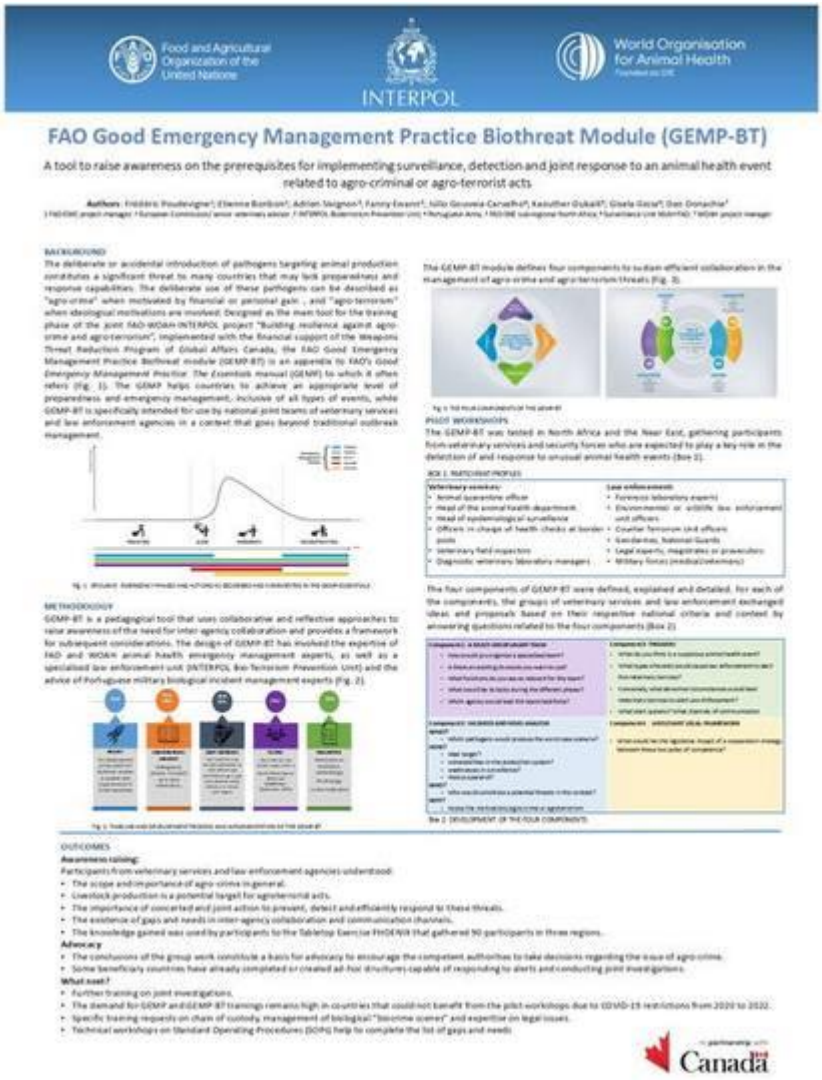
DISCLAIMER: For security reasons, specific results of LMT-Core and LMT-BT national assessments in Tunisia are not presented.

ACKNOWLEDGEMENTS

The authors thank all those involved in the development, review and piloting of the LMT-BT module and, in particular the FAO sub-regional office for North Africa, the national project focal points of Tunisia, the directors and staff of the laboratories at national and sub-national level and security forces (military forces) of Tunisia.

Authors: Morgane Loukiadis*, Sibel Bozkurt*, Cevdet Ozel, Fanny Evanin, Kaouther Dukali, Steffen Eghaim, Frederic Paraboeuf, Beatrice Meuller

Canada



2421 – Field-Deployable Nanopore Metagenomics for Pathogen Surveillance at the Human-Livestock-Wildlife Interface in Uganda

Margaret TUSIIME (1), **Paula SCHWEIZER** (2), Behrouz ALIZADEH (2), Ravi KANT (3), Ilja WEINSTEIN (3), Luke NYAKARAHUKA (1), Sylvia A. BALUKA (4), Mathias AFAYOA (5), Wilfred ENEKU (5), Lonzy OJOK (5,7), Judah SSEKITOLEKO (5,8), Patrick OROMA (5), Steven ODONGO (6), Arianna CERUTI (2), Wisal A. ELMAGZOUB (2), Uwe TRUYEN (2), Ahmed ABD EL WAHED (2), Julius B. OKUNI (5)

1: Department of Biosecurity, Ecosystems and Veterinary Public Health, College of Veterinary Medicine, Animal Resource and Biosecurity, Makerere University, Kampala, Uganda; 2: Institute of Animal Hygiene and Veterinary Public Health, Faculty of Veterinary Medicine, University of Leipzig, Leipzig, Germany; 3: Department of Veterinary Biosciences, Faculty of Veterinary Medicine, University of Helsinki, Helsinki, Finland; 4: Department of Livestock Industrial Resources, College of Veterinary Medicine, Animal Resource and Biosecurity, Makerere University, Kampala, Uganda; 5: Department of Veterinary Pathobiology, College of Veterinary Medicine, Animal Resource and Biosecurity, Makerere University, Kampala, Uganda; 6: Department of Biomedical Laboratory Technology and Molecular Biology, College of Veterinary Medicine, Animal Resource and Biosecurity, Makerere University, Kampala, Uganda; 7: Department of Pathology, Gulu University, Gulu, Uganda; 8: Department of Livestock Health Research, Rwebitaba Zonal Agricultural Research and Development Institute, National Agricultural Research Organisation, Entebbe, Uganda

Background: In many low- and middle-income countries, infectious disease surveillance at high-risk ecological interfaces remains constrained by a reliance on centralized laboratories and pathogen-specific diagnostics. These conventional approaches risk missing novel or co-circulating agents, thereby delaying critical public health responses. Consequently, field-deployable, culture-independent genomic

technologies are urgently required to facilitate integrated One Health surveillance in these vulnerable environments.

Methods: We deployed a portable, suitcase-based Oxford Nanopore Technologies platform to conduct integrated metagenomic surveillance at Katwe Kabatooro, a recognized human-livestock-wildlife interface near Queen Elizabeth National Park, Uganda. A total of 260 diverse samples were collected, comprising feces from cattle (n=85) and wildlife (Uganda kob and African buffalo; n=51), ticks (n=51), wastewater from various municipal and agricultural sources (n=71), and pooled mosquitoes (n=2). Utilizing portable workflows, on-site nucleic acid extraction and rapid library preparation were performed, with samples processed across seven sequencing runs in parallel field and laboratory settings. Reads were taxonomically classified using reference-based alignment, enabling subsequent microbial composition profiling and diversity analyses.

Results: Sequencing generated an average of 368,650 reads per run. Bacterial taxa predominated across all sample matrices, with ubiquitous detection of *Escherichiacoli*, *Klebsiella* spp., *Enterococcus* spp., *Salmonellaenterica*, and *Acinetobacterbaumannii*. Wildlife fecal metagenomes exhibited multi-kingdom complexity, revealing the co-occurrence of bacterial, protozoan, and viral agents, including *Helicobacter pylori*, *Clostridium botulinum*, *Toxoplasmagondii*, and wildlife-associated herpesviruses. Tick microbiomes contained *Babesia* spp., indicative of transmission risk to vertebrate hosts at this wildlife–human ecological interface. Wastewater samples displayed the highest compositional heterogeneity, reflecting convergent inputs from human, agricultural, and environmental sources. Furthermore, comparative analyses between field- and laboratory-based sequencing workflows demonstrated robust reproducibility, evidenced by Bray-Curtis similarity scores ranging from 0.615 to 0.704 and an absence of statistically significant differences in alpha diversity metrics across most sample comparisons.

Conclusions: This study demonstrates the efficacy of portable nanopore sequencing for real-time, robust metagenomic surveillance across diverse ecological compartments within a One Health framework. The platform exhibited consistent field performance and capacity to simultaneously detect various microbial agents, underscoring its viability as a scalable, decentralized diagnostic tool for resource-limited settings. Although no novel emerging infectious disease has been identified, continuous genomic surveillance remains essential for the early detection of zoonotic spillover events. Ultimately, integrating these deployable technologies into routine monitoring will significantly strengthen early warning systems in hotspot regions.

2461 – From Protocol to Practice: Early Implementation of the Caraga One Health Initiative for Universal Health Coverage in the Philippines

Jesson BUTCON (1), Michelle JAPITANA (1), Geminn Louis APOSTOL (2)
1: Caraga State University, Philippines; 2: Ateneo de Manila University, Philippines

BackgroundThe Caraga region in Mindanao, Philippines faces converging human, animal, and environmental health threats driven by climate variability, agrochemical use, mining, and endemic zoonoses, historically addressed through siloed sectoral responses. The Philippine Universal Health Care (UHC) Act (RA 11223) creates policy space for multisectoral One Health (OH) platforms embedded in routine governance and service delivery. Building on a previously developed Caraga One Health protocol, we report post-protocol implementation data from a regional OH initiative that leverages strategic research and structured coalition-building to institutionalize OH governance, integrated surveillance, and capacity development as core strategies for advancing UHC in a resource-constrained setting.

MethodsThe Caraga One Health Initiative employs a mixed-methods implementation research design integrating: (1) cross-sectoral action research to establish and evaluate OH governance mechanisms; (2) six catalytic research projects (agrochemical exposure, schistosomiasis and zoonoses surveillance, food–water–NCD nexus, environmental and climate risk modelling, digital dog registry and rabies surveillance, and mining dust with health-social impacts); and (3) embedded coalition-building at LGU and regional levels. A Regional Technical Advisory Group (RTAG) and Technical Working Group (TWG) were established to coordinate governance, surveillance integration, capacity development, and knowledge translation across health, agriculture, environment, higher education, and local government sectors. At the LGU level, phased stakeholder mapping, co-design workshops, joint field activities, evidence-to-action sessions, and formalization of OH working groups linked to UHC coordination bodies were conducted. Mixed-methods

process and outcome indicators tracked governance institutionalization, capacity gains, surveillance integration, and early evidence use in decision-making.

ResultsFrom August 2025 to April 2026, the initiative supported formal establishment of the multisectoral RTAG and TWG with regular meetings and agreed terms of reference, and facilitated the creation or strengthening of OH working groups in six LGUs. Around 100 personnel across health, agriculture, veterinary, environment, academe, and local government sectors underwent ongoing training in OH governance, integrated surveillance, and risk communication, with documented pre–post knowledge gains. Early implementation of strategic research projects catalyzed joint planning, coordinated fieldwork, and shared data initiatives, including initial development of a digital dog/pet registry and rabies surveillance integration in pilot municipalities, and preparatory work for agrochemical exposure mapping, zoonoses surveillance, and food–water–NCD nexus studies in priority sites. RTAG and LGU deliberations have begun incorporating OH framing, risk perspectives, and cross-sector actions into local plans and draft ordinances, signaling early institutionalization within UHC processes.

ConclusionsThe Caraga One Health Initiative shows that subnational OH governance can advance when anchored in UHC reforms and supported by strategic research, coalition-building, and digital innovation. Early gains in governance, capacity, and surveillance provide actionable evidence on operationalizing OH in resource-constrained, climate- and zoonosis-vulnerable settings. The Caraga model offers a transferable, systems-oriented approach for embedding One Health within routine subnational governance and UHC implementation in the Philippines and similar contexts.

2470 – Silent Circulation of Rift Valley Fever Virus: Seroprevalence and Risk Factors Across Three Contrasting Ecosystems in Uganda

Teddy NAMAGGA (1), Phionah KATUSHABE (1), Ssali R. OGWAL (2), Gladys K. NAKANJAKO (1,3), Babi NACKSON (1), Joseph MUTYABA (1), Mercy HAUMBA (1), Wilber SSEMBAJJWE (4), Collins AGABA (4), Eric M. ENYEL (5), Gibb RORY (8), Elise RINGWALDT (8), Laura FERGUSON (9), Deo B. NDUMU (3), Musa SEKAMATTE (6), Gladys K. ZIKUSOKA (2), Dennison KIZITO (1), Janet SEELEY (7), Field NIGEL (8), Julius J. LUTWAMA (1)

1: UGANDA VIRUS RESEARCH INSTITUTE, Uganda; 2: Conservation Through Public Health (CTPH), Entebbe, Uganda; 3: National Animal Disease Diagnostics and Epidemiology Centre (NADDEC), Ministry of Agriculture, Animal Industry and Fisheries (MAAIF), Uganda; 4: Medical Research Council, Uganda Virus Research Institute & London School of Tropical Medicine and Hygiene, Entebbe-Uganda; 5: Uganda Wildlife Authority (UWA), Kampala Uganda; 6: National One Health Platform (NOHP), One Health Coordination Office (OHCO), Ministry of Health, Kampala, Uganda; 7: London School of Hygiene & Tropical Medicine (LSHTM), University in London, United Kingdom; 8: University College London, United Kingdom; 9: University of Southern California, United States of America

Background: Despite causing explosive outbreaks across East Africa, Rift Valley Fever (RVF) quietly causes infections between epidemics, affecting herders, farmers, and families without detection. Uganda is located at a unique ecological crossroads: arid pastoral rangelands in the northeast, highland farming communities in the southwest, and fertile pastoral savannah across key wildlife reserves in the Centre. However, there has been little research comparing RVF transmission across these three different ecosystems, which hampers surveillance efforts to identify where the burden truly lies and who is most at risk. This study aims to address that gap.

Methods: We conducted a cross-sectional study involving 667 adults from three ecologically diverse districts: Amudat (arid pastoral, Pian-Upe Wildlife Reserve; n=297), Kanungu (highland farming, Bwindi-Mgahinga; n=234), and Kyankwanzi (moderate pastoral savannah, Murchison Falls; n=136). Participants were recruited from community settings. All provided written consent, and blood samples were taken to test for RVF IgG antibodies via ELISA. Structured interviews gathered data on demographics, animal contact, food practices, water sources, and vector control behaviors. Fisher's exact tests were used for bivariate analysis, followed by multivariate logistic regression with district-stratified models to determine independent predictors, with significance set at p0.05. The study was approved by the relevant institutional review boards.

Results: 5.73% (37/646; 95% CI 4.18-7.79%) tested positive for RVF antibodies, indicating silent transmission. The risk varied markedly across regions: in Kyankwanzi, a moderate pastoral zone, the prevalence was 13.39% (95% CI 8.53-20.39%), 15 times higher than the 0.87% (95% CI 0.24-3.10%) found in Kanungu's highland farming areas. Amudat showed a prevalence of 6.25% (95% CI 3.99-9.66%). These differences were statistically significant (p0.001). Participants aged 35 or older had nearly three times the

odds of seropositivity (aOR 2.81, 95% CI 1.33-5.94, p=0.007), likely reflecting cumulative exposure. In Kyankwanzi, living in a community with a recent animal disease outbreak increased the odds of infection more than fivefold (aOR 5.41, 95% CI 1.57-18.66, p=0.007). Notably, personal behaviors such as contact with animals, consuming raw milk, or game meat did not independently predict infection across districts. These results imply that geographic location, rather than individual behaviors, mainly influences risk. However, the cross-sectional design precluded establishing causality; the consistent ecological gradient across zones, though, supports the biological plausibility of these findings.

Conclusion: RVF is spreading undetected in Uganda's most ecologically diverse districts. Ecological zone proves to be a stronger predictor of exposure than individual behaviors, challenging the usual emphasis on personal prevention. Highland farming communities seem naturally protected, whereas pastoral lowlands experience ongoing transmission. We suggest incorporating ecological zoning into national RVF surveillance, conducting joint veterinary-human investigations in pastoral areas, and establishing local seroprevalence monitoring at ecological boundaries. These insights are crucial for One Health preparedness across East Africa.

2484 – 1.HOW TO ACHIEVE SUSTAINABILITY OF ONE HEALTH PROGRAMS IN AFRICA: LESSONS LEARNED FROM GLOBAL HEALTH SECURITY IMPLEMENTATION

Luis Filipe L DE J LOUREIRO

Consultant OH GHS / Professor Universidade lusofona, Portugal

Background

Sustaining One Health (OH) programs remains a major challenge in many low- and middle-income countries despite increasing global recognition of the interconnectedness between human, animal, and environmental health. This presentation examines the development and implementation of One Health and Global Health Security (GHS) programs across several African countries, highlighting key achievements, operational challenges, and lessons learned. Particular emphasis is placed on identifying practical approaches that support long-term sustainability, multisectoral coordination, and institutional ownership of OH initiatives. The presentation also explores the role of national coordination platforms, regional economic communities, and continental structures such as the African Union in strengthening sustainable OH governance, and collaboration with European Union and other international stakeholders.

Methods

This work is based on field experience accumulated through the implementation and management of GHS programs in multiple African countries between 1997 and 2025. The analysis draws on lessons learned from major public health events, including Highly Pathogenic Avian Influenza (HPAI), the West Africa Ebola outbreak, COVID-19, and Mpox. Experiences from the establishment of national OH coordination mechanisms, Joint External Evaluations (JEE), and National Action Plans for Health Security (NAPHS) were reviewed to identify factors influencing sustainability. Particular attention was given to governance approaches, stakeholder engagement, multisectoral collaboration, capacity building, sustainable financing, and community participation using a bottom-up implementation approach.

Results

Countries that integrated OH programs within existing national governance structures demonstrated stronger coordination, ownership, and continuity of interventions. In countries where OH platforms did not previously exist, the establishment of formal coordination mechanisms and governance instruments facilitated multisectoral collaboration and policy alignment. The use of JEE findings and NAPHS priorities contributed to more targeted program implementation and resource mobilization. Key success factors included equitable engagement of the human, animal, and environmental health sectors; involvement of academia, security institutions, and communities; and integration of OH activities into broader national development and health security agendas. Cross-sectoral collaboration improved preparedness and coordinated response to emerging epidemics and antimicrobial resistance (AMR). Community engagement and complementarity of interventions were also identified as critical drivers of program sustainability and operational efficiency.

Conclusions

Sustainable One Health programs require strong national ownership, institutionalized multisectoral coordination, and alignment with national, regional and international health security priorities. Findings from this experience suggest that sustainability is strengthened through evidence-based planning using JEE and NAPHS processes or other available tools such as PVS, equitable engagement of OH sectors (including international stakeholders), long-term capacity building, and integration of community-driven approaches. Enhanced collaboration between national, regional, and continental / international structures is also essential to ensure continuity, resource optimization, and resilience of African OH systems.

2506 – Operationalizing and Financing One Health Preparedness in a Cross-Border Region of Guinea: Building an Integrated Platform for Crimean-Congo Hemorrhagic Fever Readiness

Sona SIDIBE (1), Alpha Mahmoud BARRY (1), Claire STANDLEY (2), Mame Maryam SARR (1), Fassou KOUROUMA (3), Hassane DIALLO (3), Mohamed Idriss DOUMBOUYA (3)

1: Santé Plus Organisation, Guinea; 2: Georgetown University; 3: Direction Nationale de la Santé Vétérinaire

Background

Emerging zoonotic diseases require preparedness systems that integrate human, animal, and environmental health before outbreaks occur. In West Africa, increasing cross-border livestock movement and tick vectors heighten the risk of Crimean-Congo Hemorrhagic Fever (CCHF) emergence. Although Guinea has not reported confirmed human CCHF cases, its proximity to affected areas in neighboring Senegal underscores the importance of proactive preparedness. A One Health initiative was implemented in Koundara, a high-risk border district, to operationalize multisectoral collaboration while examining financial efficiencies that could support integrated surveillance and preparedness for zoonotic threats.

Methods

A multisectoral implementation approach was developed from May 2024 to July 2025 through collaboration among the Ministries of Health and Livestock, Georgetown University (FEVER Project), and Santé Plus Organisation. Activities included a community Knowledge, Attitudes and Practices (KAP) survey among high-risk occupational groups, livestock and tick sampling, and entomological surveillance. Program expenditures and resource allocation approaches were reviewed to assess the financial sustainability of combining international donor and academic funding with local non-governmental organization (NGO)-led field implementation. An internal financial analysis was conducted to estimate operational efficiencies associated with integrated One Health implementation.

Results

The initiative established an operational cross-border One Health platform before the occurrence of confirmed national CCHF cases. Community assessments involving 993 participants revealed a critical knowledge gap: only 4.3% of human healthcare workers had previously heard of CCHF, despite 48% of respondents identifying public health facilities as their first point of care for suspected zoonotic illnesses. Entomological surveillance identified a predominance of Amblyomma variegatum (84.40%) and confirmed the presence of Hyalomma truncatum (5.44%), a recognized vector of the CCHF virus. An internal financial analysis estimated that integrating human, animal, entomological field missions, and community outreach through a shared NGO logistics platform reduced operational deployment costs by approximately 25% compared with parallel sector-specific implementation. Despite these operational efficiencies, all core surveillance activities implemented under this initiative remained dependent on external international donor funding, highlighting ongoing challenges for long-term financial sustainability.

Conclusions

This experience demonstrates that operationalizing and financing One Health before disease emergence is both feasible and cost-efficient for strengthening epidemic preparedness in resource-constrained border settings. Building joint coordination mechanisms across sectors enhanced institutional readiness while creating a practical framework for integrated surveillance, shared financial accountability, and collaborative decision-making. The Guinea experience suggests that transitioning from disease-specific financing toward integrated and pooled One Health investments may strengthen the sustainability of

national preparedness systems and contribute to more resilient health security in high-risk cross-border settings.

2517 – Knowledge Gaps and Occupational Risk Perceptions of Crimean-Congo Hemorrhagic Fever among High-Risk Communities in a Cross-Border District of Guinea

Sona SIDIBE (1), Alpha Mahmoud BARRY (1), Claire STANDLEY (2), Mame Maryam SARR (1), Fassou KOUROUMA (3), Hassane DIALLO (3), Mohamed Idriss DOUMBOUYA (3)

1: Santé Plus Organisation, Guinea; 2: Georgetown University; 3: Direction Nationale de la Santé Vétérinaire

Background

Crimean-Congo Hemorrhagic Fever (CCHF) is an emerging tick-borne zoonosis of increasing concern in West Africa, particularly in border areas characterized by livestock mobility and close human-animal interactions. Although Guinea has not reported confirmed human or animal CCHF cases, neighboring Senegal has documented recent outbreaks, highlighting the need for preparedness before disease emergence. Understanding community knowledge, occupational risk perception, and health-seeking behaviors is essential for designing effective One Health preparedness strategies. This study assessed knowledge, attitudes, practices, and perceived risks among populations at highest occupational risk of CCHF in Guinea's border region.

Methods

A cross-sectional Knowledge, Attitudes and Practices (KAP) survey was conducted in May 2024 in four sub-prefectures of Koundara, Guinea (Guingan, Kamaby, Termesse, and Youkounkoun). Using a structured questionnaire, data were collected from 993 participants, including livestock keepers, farmers, butchers, hunters, and human and animal health professionals. The survey was complemented by community engagement activities involving local guides and community health workers to facilitate participation. Descriptive analyses assessed disease awareness, occupational exposure, perceived transmission routes, health-seeking behaviors, and preferred communication channels for zoonotic disease prevention.

Results

Important preparedness gaps were identified despite widespread occupational exposure to livestock and ticks. Among respondents familiar with CCHF, 49% were livestock keepers and 31.6% had only Quranic education, while only 4.3% were human healthcare workers, revealing limited awareness among frontline professionals responsible for early detection. Nevertheless, 48% of respondents reported public health facilities as their preferred first point of care for suspected zoonotic illnesses, demonstrating strong community confidence in the health system despite limited institutional preparedness. Respondents identified livestock as the species most affected by ticks and recognized tick bites as the principal route of disease transmission. Radios, community health workers, local leaders, veterinary services, and health professionals emerged as the most trusted communication channels for disseminating health information, providing practical opportunities to strengthen community-based preparedness.

Conclusions

Preparedness for emerging zoonotic diseases requires strengthening both community awareness and frontline health system capacity before outbreaks occur. This study demonstrates that high community trust in formal health services is not matched by adequate disease awareness among frontline professionals, creating a critical preparedness gap in a high-risk border setting. Integrating locally adapted One Health risk communication with continuous training of human and animal health professionals and community-based surveillance could substantially strengthen early detection, reporting, and preparedness for CCHF and other emerging zoonotic threats in Guinea.

2536 – Strengthening One Health Surveillance through Community Engagement: Evidence from the FEVER Project on Zoonotic Febrile Diseases in Guinea

Kadia DOUMBOUYA (1), Alpha Mahmoud BARRY (1), Claire STANDLEY (2), Maciré SYLLA (1), Sona SIDIBE (1), Mame Mariam SARR (1)

1: Santé Plus Organisation, Guinea; 2: Georgetown University

Background

Emerging zoonotic diseases require surveillance systems that extend beyond health facilities and actively involve communities. The FEVER Project implemented an integrated One Health surveillance approach to identify zoonotic pathogens while documenting community-level exposure to febrile disease risks.

Methods

A cross-sectional One Health study was conducted in Dalaba and Guéckédou. Community-based surveys included 954 participants and assessed occupations, contact with domestic and wild animals, visits to wildlife areas, handling of bushmeat and other behavioural risk factors. Human and animal sampling was conducted simultaneously, involving 1,258 animals from multiple species. Surveillance activities were implemented through collaboration between communities, health facilities, veterinary services and national laboratories.

Results

Community surveys documented frequent human–animal interactions and behavioural practices associated with potential zoonotic exposure. Integrated human and animal surveillance identified multiple infectious pathogens while strengthening local surveillance capacity. The project demonstrated the feasibility of combining epidemiological surveillance with community participation and multisectoral collaboration. Engagement of local authorities, health workers and community stakeholders improved implementation and reinforced acceptance of surveillance activities.

Conclusion

Community participation is a critical component of integrated zoonotic disease surveillance. One Health strategies that combine laboratory capacity, community engagement and risk communication can strengthen preparedness for emerging infectious diseases in Guinea.

2540 – From Advocacy to Action: Strengthening Community Engagement and Multisectoral Collaboration for Neglected Tropical Diseases Control in Guinea

Kadia DOUMBOUYA (1), Alpha Mahmoud BARRY (1), Papa Djibril FAYE (2), Maciré SYLLA (1), Sona SIDIBE (1)

1: Santé Plus Organisation, Guinea; 2: Speak Up Africa

Background

Neglected Tropical Diseases (NTDs) continue to disproportionately affect vulnerable populations in Guinea and require coordinated action beyond the health sector. While preventive interventions have expanded, achieving sustainable control and elimination depends on effective advocacy, community engagement and multisectoral collaboration. This study describes the implementation and outcomes of a national advocacy initiative designed to strengthen stakeholder commitment to NTD control within a One Health approach.

Methods

A participatory advocacy strategy was implemented by Santé Plus Organisation in collaboration with the National Programme for the Control of Neglected Tropical Diseases (PNLMTN), the National Directorate of Epidemiology and Disease Control (DNELM), government ministries, civil society organizations and technical partners. Activities included a national advocacy forum, a multisectoral roundtable, stakeholder consultations and the dissemination of advocacy materials. Process indicators and stakeholder commitments were documented to assess engagement and collaboration.

Results

The initiative convened **30 representatives** from government institutions, the national NTD programme, civil society and technical partners during a national advocacy event. A total of **29 commitment statements** were signed by participating stakeholders, while **eight institutional recommendations** were

developed to strengthen NTD control. Advocacy messages were disseminated through **100 communication materials**, including **60 advocacy stickers displayed across 16 government institutions and partner organizations**, promoting visibility and ownership of the NTD agenda. The initiative strengthened multisectoral dialogue, encouraged commitments to integrate NTD activities into institutional action plans and identified community engagement, intersectoral coordination and continuous advocacy as critical drivers for sustainable NTD control in Guinea.

Conclusion

Advocacy can serve as a catalyst for transforming institutional commitment into coordinated action for NTD control. The Guinea experience demonstrates that sustained community engagement, strategic communication and multisectoral collaboration strengthen national ownership and support the integration of One Health principles into NTD programmes. These lessons provide a practical model for accelerating progress toward the WHO 2030 NTD Roadmap in endemic settings.

2541 – Imported OXA-244- and NDM-5-Producing Escherichia coli ST167 Reveals a One Health International Lineage with Distinct Acquisition of OXA-48-like Carbapenemase

Carlos Henrique CAMARGO (1), Taise C.D.M. BARBOSA (2), Amanda Y. YAMADA (2), Daniel S. MIRANDA (1), Pedro S.P. FERRARO (2), Erica de Lima ORI (1), Marisa de Jesus Castro LIMA (1), Karoline R. CAMPOS (1), Claudio T. SACCHI (1), Stephani Zagui RUIVO (3), Marcela Grispino Vieira Torres de LOLO (4), Autor do CAISM (5), Monique R. TIBA-CASAS (1)

1: Instituto Adolfo Lutz, São Paulo (Brazil); Avenida Dr Arnaldo 355, CEP 01246-000, São Paulo, SP, Brazil; 2: Universidade de São Paulo, São Paulo (Brazil); Avenida Dr Arnaldo 355, CEP 01246-000, São Paulo, SP, Brazil; 3: Grupo de Vigilância Epidemiológica de Campinas (GVE XVII), Avenida Orosimbo Maia, 75, CEP 13024-045, Campinas, SP, Brazil; 4: Setor de Serviços Relacionados à Saúde - Departamento de Vigilância em Saúde - Secretaria Municipal de Campinas; Rua Afonso Pena, 1380, Vila Nova São José, CEP 13100-440, Campinas, SP, Brazil; 5: CAISM

Background:

The successful multidrug-resistant *Escherichia coli* lineage ST167 has been increasingly reported from humans, animals, food, and environmental sources worldwide, frequently carrying New Delhi metallo-β-lactamases (NDM). In contrast, OXA-48-like carbapenemases remain uncommon within this lineage, particularly in South America. We investigated the genomic context of an imported ST167 isolate recovered in Brazil after travel to Egypt, focusing on its phylogenetic relationship with international One Health genomes.

Methods:

A carbapenem-resistant *E. coli* was recovered from an admission rectal surveillance swab from a traveler returning from Egypt. Species identification, antimicrobial susceptibility testing, real-time PCR, conjugation assays, and PacBio whole-genome sequencing were performed. A core-genome SNP phylogeny including publicly available ST167 genomes representing human, animal, food, and environmental sources was reconstructed to evaluate the evolutionary context of the isolate.

Results:

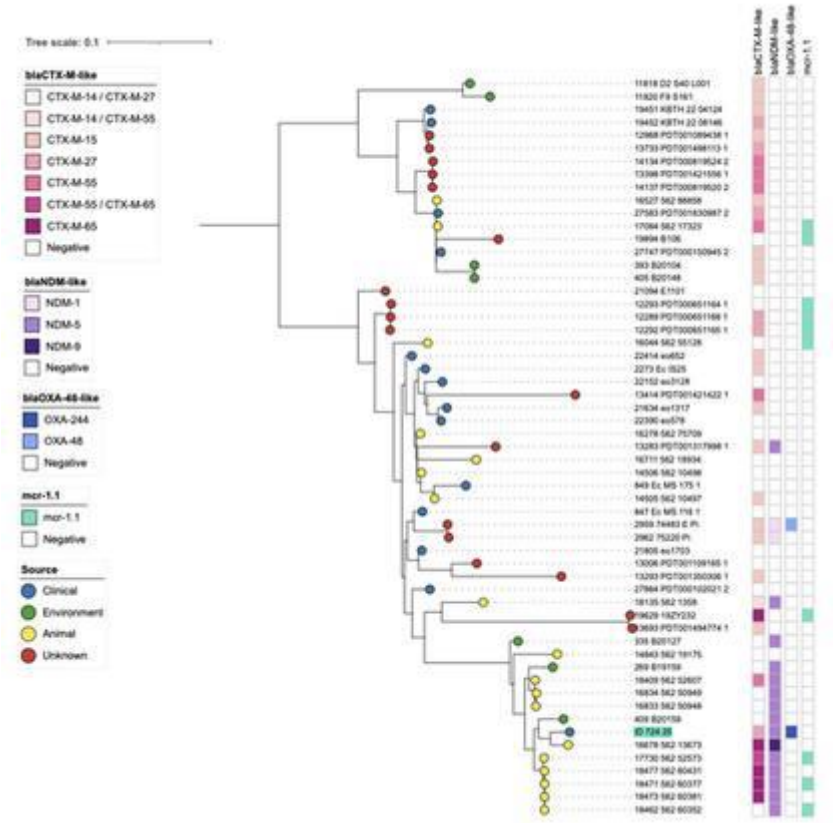
The isolate belonged to ST167, serotype O89:H9, and carried plasmid-borne blaNDM-5 together with chromosomal blaOXA-244, an OXA-48-like carbapenemase. The transferable IncF plasmid also harbored blaCTX-M-27 and additional resistance determinants. Active screening of 815 additional individuals detected no further OXA-48-like-positive carriers.

Phylogenomic analysis demonstrated that the Brazilian isolate clustered within the globally disseminated ST167 lineage, whose members originated from diverse ecological niches including humans, companion animals, livestock, wildlife, wastewater, and environmental samples. Several genomes within this international lineage carried blaNDM, confirming widespread dissemination of metallo-β-lactamases across multiple reservoirs. In contrast, none of the available non-human genomes carried an OXA-48-like determinant, suggesting that acquisition of blaOXA-244 represents a more recent evolutionary event superimposed on an already successful One Health lineage. Although the patient had recently traveled to Egypt, the closest genomes were predominantly from China and Europe, while limited genomic

representation from North Africa precluded definitive inference regarding the geographic origin of the strain.

Conclusions:

This study illustrates how globally disseminated One Health lineages can acquire additional carbapenemases during international circulation. The broad ecological distribution of ST167 contrasts with the restricted occurrence of OXA-48-like enzymes within this lineage, suggesting independent acquisition rather than long-term dissemination of this determinant. Continuous genomic surveillance integrating human, animal, and environmental sectors is essential for detecting emerging resistance combinations before their establishment in multiple reservoirs.



2564 – Socio-cultural and Institutional Determinants of Knowledge, Attitudes and Practices Related to Rabies Risk in the Kaffrine Health District, Senegal

Abou DIOP (1), Andrée Prisca Ndjoug NDOUR (1), Saila-Ngita DIAFUKA (3), Mamadou Makhtar Mbacké LEYE (2), Bruno Enagnon LOKONON (4)

1: Ecole inter-états des sciences et médecine vétérinaire de Dakar; 2: Université Cheikh Anta DIOP de Dakar; 3: Cummings School of Veterinary Medicine, Department of Infectious Disease and Global Health, Tufts University - MA-USA.; 4: Laboratoire de Biomathématiques et d'Estimations Forestières, Université d'Abomey-Calavi, Benin

Background:

Rabies is a neglected disease in developing countries, heavily burdening poor rural communities and disproportionately affecting children. In Senegal, reported data underestimate reality, with one case for every six unreported. The Kaffrine region is particularly alarming, with several fatal cases. While some studies on knowledge, attitudes, and practices (KAP) exist, socio-cultural, economic, and institutional determinants remain underexplored. This study examines factors influencing rabies-related knowledge, attitudes, and practices among community members and health providers in Kaffrine, Senegal.

Methods:

The study was conducted in the Kaffrine health district among 600 community members (Two-stage cluster random sampling) and healthcare providers (44 in human health and 10 in animal health). Data were collected using structured questionnaires. Associations between response variables (knowledge, attitudes, and practices) and socio-demographic or institutional characteristics were first assessed using Chi-square tests. Variables with significant associations were subsequently included in multivariate logistic regression models performed using RStudio.

Results

In the community, although 520(86.67%) of respondents were aware of rabies, only 271(45.16%) had actual knowledge about risks associated with animal bites, preventive measures, notable signs of rabies, progression of declared rabies, and modes of transmission. There was a marked contrast between attitude with 598(99.67%) indicating they would go to a health facility in the event of a bite while in actual practice only 38 (46.25%) of 80 bite victims had sought medical care. The determinants of "sufficient knowledge" include *marital status* (widowers are better informed with OR=3.20 and p-value=0.01), *occupation* (employees and traders are better informed than the unemployed with OR=25.61 and 2.98 respectively and a p-value of less than 0.001 for both) and *socio-economic status* (respondents with low socio-economics status are better informed compared to those with an average socio-economic status with OR=2.43 and p-value=0.001, whilst those with a high socio-economic status are less well informed than the latter with OR=0.26 and p-value=0.02). Belonging to the Bambara ethnic group is associated with poorer attitude than to the Wolof (the majority ethnic group) with OR= 0.04 and p-value=0.01. There was a notable disparity among service providers with 90% of animal health workers having sufficient knowledge, compared to only 15.91% of human health providers. Nurses showed more appropriate attitudes than doctors with OR=97.13 and p-value=0.04, probably due to their proximity to rural realities. Finally, only 26.92% of the 78 dog owners had vaccinated their animals, with lower accessibility in rural areas.

Conclusions/Outlook

Rabies control in Kaffrine is hindered by insufficient knowledge and unfavourable practices that limit effective prevention and elimination of the disease. We recommend strengthening the training of human healthcare providers, enhancing community awareness through inclusive approaches, revising the regulatory framework, and strengthening intersectoral collaboration in line with the One Health approach.

2567 – Post-Pandemic SARS-CoV-2 Landscape in Georgia (2023–2026): Integrating Epidemiological Surveillance, Laboratory Monitoring and Public Health Insights

Olgha TARKHAN-MOURAVI, Irakli KARSELADZE, Khatuna ZAKHASHVILI, Ketevan SIDAMONIDZE, Davit PUTKARADZE, Paata IMNADZE

National Center for Disease Control and Public Health, Georgia

Background: Following the transition from the acute phase of the COVID-19 pandemic, SARS-CoV-2 has evolved from a global emergency pathogen into a continuously circulating respiratory virus. Understanding its post-pandemic epidemiological patterns and maintaining sustainable laboratory-based surveillance are essential for monitoring changes in viral activity, assessing disease burden, and supporting public health preparedness. This study aimed to characterize SARS-CoV-2 circulation in Georgia during the post-pandemic period through integrated analysis of laboratory surveillance data and epidemiological indicators.

Methods:SARS-CoV-2 surveillance data were analyzed from Influenza-like Illness (ILI) and Severe Acute Respiratory Infection (SARI) sentinel surveillance sites in Georgia during the 2023/2024, 2024/2025, and 2025/2026 respiratory seasons (weeks 40–20), as well as the 2025 inter-seasonal period (weeks 21–39). Respiratory specimens collected through the national sentinel surveillance system were tested for SARS-CoV-2 using real-time RT-PCR within the national laboratory network. Laboratory findings were evaluated alongside epidemiological indicators, including respiratory illness activity, ILI incidence, and SARI-associated hospitalizations.

Results: Across the three respiratory seasons, SARS-CoV-2 demonstrated sustained but relatively low-level circulation, accounting for 3.0% (98/3304) of laboratory-confirmed respiratory viral infections in

2023/2024, 4.0% (59/1452) in 2024/2025, and 4.2% (38/910) in 2025/2026 among specimens collected through ILI and SARI surveillance. Compared with influenza and respiratory syncytial virus (RSV), which showed clear seasonal predominance during the winter months, SARS-CoV-2 maintained persistent circulation at lower detection levels throughout the surveillance period. During the 2025 inter-seasonal period, SARS-CoV-2 activity increased, with 14% (269/1867) of tested specimens testing positive, demonstrating a gradual rise during the summer months and reaching peak detection levels in August. Periods of increased SARS-CoV-2 detection coincided with changes in respiratory illness activity, including variations in ILI incidence and SARI-associated hospitalization patterns.

Conclusions: The post-pandemic surveillance experience in Georgia demonstrates that SARS-CoV-2 continues to circulate as an important respiratory pathogen despite reduced predominance compared with influenza and RSV. Sustained laboratory-based monitoring within established national surveillance systems enables timely detection of changes in viral activity and supports evidence-based public health decision-making. The study highlights the value of national laboratory capacity developed during the COVID-19 response and its contribution to long-term respiratory pathogen surveillance and pandemic preparedness.

2619 – Leveraging community intelligence for better disease surveillance and safer practices: the case of wildlife-human interface communities in Ifanadiana district, southeastern Madagascar

Katerina ALBRECHTOVA (1), Samuel RANDRIAMANANTSOA (2), Volatiana RANDRIAFARANIAINA (2), Sévérine THYS (3), Ninon CREMER (4), Daouda KASSIE (1,5), Elliot FARA (1), Guillaume PARIZET (2), Veronique CHEVALIER (1,5,6)

1: Institut Pasteur de Madagascar (IPM), Madagascar; 2: Agronomes & Vétérinaires Sans Frontières (AVSF), Madagascar; 3: CIRAD, UMR ASTRE, Vientiane, Lao PDR; 4: Université Paris Cité, France; 5: CIRAD, UMR ASTRE, Madagascar; 6: ASTRE, Université de Montpellier, CIRAD, INRAE, France

Background

Madagascar is a recognized hotspot for zoonotic disease emergence due to the convergence of exceptional biodiversity, rapid environmental change, wildlife consumption and persistent socio-economic vulnerability. In rural districts such as Ifanadiana, livelihoods depend on agriculture, livestock keeping, hunting, and other interactions with forest ecosystems. The risk of pathogen spillover is shaped not only by ecological conditions (proximity of protected forest area) but also by everyday practices, local beliefs, and unequal access to health information and services. Community knowledge is essential for designing disease surveillance and prevention systems that are both effective and locally legitimate.

Methods

As part of the Africam Madagascar project, this study explored community perceptions, and behavior related to zoonotic risk in Ifanadiana district between July 2023 and May 2025, using a participatory science approach. We conducted a series of 9 focus group discussions complemented by participatory mapping, proportional piling, pairwise ranking, and simplified theory-of-change exercises. A total of 81 participants were purposively selected to reflect diversity in gender, age, occupation, and positions of public or traditional authority. A thematic analysis was applied to the transcripts of all data collections and emerging themes were coded by two independent coders with the support of Excel-based analysis grid.

Results

Participants demonstrated an intuitive understanding of the distinction between hazards and risks, as defined in epidemiology, despite being unfamiliar with the formal concepts. They identified multiple pathways of zoonotic exposure associated with wildlife hunting, free-ranging and close cohabitation with domestic animals, the presence of pests, unsafe water sources, and the consumption of animals that were sick or found dead. Participants also showed a clear ability to prioritize hazards and rank risks, leading to the identification of both feasible behavioral changes and institutional interventions, such as the construction of community latrines.

At the same time, participants acknowledged that their prioritization of risks does not always translate into corresponding practices, which are shaped not only by perceived health risks but also by other competing priorities, including food/economic security, social obligations, traditions, and local taboos.

Consequently, known hazards are assessed within a broader social and economic context in which health considerations represent only one of several decision-making factors. For example, meat from a zebu that has died of disease may still be purchased and consumed by neighbors of the animal's owner as an expression of social solidarity, despite the recognized health risks.

Conclusions

The richness of community knowledge provides a strong foundation for reducing zoonotic risks at the wildlife-human interface in rural Madagascar. Meaningful community participation in the design of risk communication, integration into formal surveillance systems, and active involvement in public health interventions are likely to strengthen community ownership of and adherence to inevitable top-down recommendations.

2651 – An innovative public health approach in Senegal: deployment of mobile laboratories for early detection of Rift Valley fever (RVF) and dengue (DENV) in remote settings during epidemics.

Abdou PADANE (1), **Seyni NDIAYE** (1), **Rokhaya DIONE** (2), **Marièma SARR** (1), **Mamadou NDAO** (1), **Marilyne AZA GNANDJI** (1), **Etienne Moussa SARR** (1), **Aminata MBOUP** (1), **Abdoulaye Leye SARR** (1), **Mariama DIALLO** (1), **Aissatou Nogaye DIENG** (1), **Bassirou DIAW** (2), **Papa Alassane DIAW** (1), **Badara CISSE** (1), **Boly DIOP** (5), **Hubert BASSENE** (3), **Cheikh SOKHNA** (3), **Mourtada SOW** (6), **Abass SARR** (7), **Papa Daouda MAR** (2), **Rokhaya DIAGNE** (2), **Bécaye FALL** (4), **Souleymane MBOUP** (1)

1: IRESSEF : Institut de Recherche en Santé, de Surveillance Epidemiologique et de Formations, Senegal; 2: 2- LNSP (Laboratoire National de Santé Publique); 3: 3-IRD (Institut de Recherche et de Développement); 4: 4- DL (Direction des Laboratoire); 5: 5- DP (Direction de la Prévention); 6: 6- Laboratoire de Kaffrine; 7: 7- Laboratoire de Tambacounda

Background / Objectives

Since 21 September 2025, Senegal has been experiencing an outbreak of Rift Valley fever (RVF), alongside a concurrent increase in dengue (DENV) cases across several regions of the country.

Both RVF and DENV constitute a public health emergency due to their potential to cause severe illness and death, necessitating rapid investigation and a coordinated response. The regions of Kaffrine and Tambacounda have been identified as high-risk areas for active transmission, driven by frequent human–animal interactions in environments conducive to vector-borne viral spread.

Following directives from the Minister of Health and Public Hygiene (MSHP), the Directorate of Laboratories (DL) deployed two mobile laboratories to these regions on 9 November 2025 to strengthen early detection and case management.

Our objectives during this intervention were:

- Deploy and position mobile laboratories in the targeted regions;
- Ensure molecular detection of suspected human cases of Rift Valley fever (RVF), dengue (DENV).
- Strengthen the capacity of local technical staff in molecular diagnostics of diseases with epidemic potential;
- Perform genomic sequencing of samples to better characterize circulating strains;

Samples tested positive for DENV by PCR and had Ct values below 25 were subjected to whole-genome sequencing. The Rapid PCR Barcoding kit was used, and the final library was loaded onto the portable MinION sequencer from Oxford Nanopore Technologies. The generated FASTQ data were then analyzed using bioinformatics tools to identify the circulating DENV lineage.

In conclusion, this intervention enabled real-time genomic sequencing of DENV and RVF during the 2025 outbreak in Senegal. The findings highlight the urgent need to invest in genomic surveillance, tailor prevention and control strategies to the Senegalese context, and adopt an integrated approach to better anticipate and manage future outbreaks.

2692 – Economic analysis of a pilot mass dog vaccination campaign using four delivery strategies in Kyegegwa district, Uganda

Rabina GHIMIRE (1,2), Adrian HERRERA (3), Terence ODOCH (4), Samuel George OKECH (3,4,5), Dickson AKANKWATSA (6), Paul TORGERSON (2), Andrew LARKINS (7), Salome DUERR (3), **Sonja HARTNACK** (1,2)

1: Centre for Veterinary Public Health & One Health, Clinical Department for Farm Animals and Food System Transformation, University of Veterinary Medicine Vienna, Vienna, Austria; 2: Section of Epidemiology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland; 3: Veterinary Public Health Institute, Vetsuisse Faculty, University of Bern, Bern, Switzerland; 4: College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala, Uganda; 5: Graduate School for Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland; 6: 6. Department of Global Health Security, Infectious Disease Institute, Makerere University, Kampala, Uganda; 7: School of Veterinary Medicine, Murdoch University, Murdoch, Western Australia, Australia

Background: Dog-mediated rabies, a paradigmatic One Health issue, remains endemic in Uganda, imposing public health and economic burdens through human deaths, disability-adjusted-life-years (DALYs) and post-exposure prophylaxis (PEP) costs. Mass dog vaccination (MDV) is central to rabies elimination, as it prevents transmission at animal source, reducing human exposures and PEP demand. However, MDV campaigns in Uganda are sporadic, cost evidence is limited, and alternative MDV delivery models have not been compared. We estimated and compared the cost per dog vaccinated across four MDV strategies in Kyegegwa district, Uganda and projected cost and benefits of reaching 70% vaccination coverage.

Methods: We conducted a cost-minimization analysis from implementer perspective of an MDV pilot campaign. Twelve parishes in Kyegegwa were selected, covering 32 villages and 40 vaccination points (VPs). Four delivery strategies were evaluated: static-point (SP), livestock-integrated (Li), human-health integrated (HHi), and school-based (SB). Costs were classified as fixed and variable costs and categorised into human resources, vaccine and consumables, transport, and cold chain, valued in 2023 USD. The primary outcome was weighted cost per dog vaccinated by strategy. The association between VP throughput (dogs vaccinated per VP) and unit cost was assessed using Spearman's rank correlation. The apparent least-cost strategy was scaled to estimate the cost of reaching 70% dog vaccination coverage. Health benefits, PEP costs averted, DALYs averted, and cost-effectiveness ratio (CER) were estimated against a no-vaccination counterfactual using Hampson et al., 2015 incidence estimates scaled to district population.

Results: Overall, 1008 dogs were vaccinated (9.6% of estimated dog population), at a total standardized cost of USD 6042.6. Transport was the primary cost driver (~------43% to ~54% of expenditure), followed by human resources (~30%); cold chain contributed to ~1%. SP was the apparent least-cost strategy, at USD 5.00 per dog vaccinated, followed by HHi at 5.73 USD, SB at 6.10 USD, and Li at 7.60 USD. Throughput, rather than strategy, was the dominant cost determinant and was strongly and negatively correlated with unit cost ($\rho = -0.89$; 95% CI −0.98 to −0.72; p 0.001). The estimated annual counterfactual burden was ~198 bite exposures and ~1.95 rabies deaths. Each dog vaccinated averted 0.0108 DALYs and USD 1.72 in PEP costs. CER was USD 303 per DALY averted, below Uganda's GDP per capita of USD 1,002, indicating cost-effectiveness. Reaching 70% dog population coverage in Kyegegwa using SP was projected to cost USD 37,044.93.

Conclusion: SP appeared apparently least costly, but throughput was a stronger determinant of unit cost than delivery strategy. Throughput-sensitive campaign design could therefore improve efficiency. Despite its small scale, the pilot MDV campaign was cost-effective using GDP-based benchmark, and achieving 70% coverage appears financially feasible at district level. Sustained annual campaigns could support elimination of dog-mediated rabies in Uganda.

2695 – A One Health approach to vaccination: timing is key, especially with a Super El Nino forecast for 2026-2027

Woutrina SMITH (1), Brian BIRD (1), Robert SUMAYE (2), Grace MWANGOKA (2), Ana PEROLA-BRANDOA (1), Sharif ALY (1), Mwokozi MWANZALILLA (2), Michael WILKES (1), Sonja MONTANUS (1), Rosemarie SCHARF (1), Ally OLUTU (1), Ali HAMAD (1)

1: University of California, Davis, United States of America; 2: Ifakara Health Institute, Tanzania

Background: Shifting weather and climate patterns globally will link to a Super El Nino event in 2026-2027. Our research focused on Rift Valley fever (RVF) as a zoonotic viral disease transmitted by mosquitoes, that causes significant impacts on animal health, public health, and socio-economic wellbeing. Now that RVF vaccines for livestock are available and human vaccines are soon to be available, a coordinated One Health approach to vaccination is especially timely to plan for across sectors.

Methods: Through a narrative literature review, evidence on RVF vaccination strategies for animals and humans was analyzed. Modeling of RVF virus (RVFV) transmission in relation to the One Health vaccination strategies was also conducted. Recurring themes relevant to decision making were identified and categorized into six interconnected decision domains, establishing a “One Health vaccination strategies” (OHVS) framework used to structure the synthesis and discussion of the evidence. Based on the available literature, as well as on strategies implemented for livestock and mathematical modeling studies, six joint scenarios combining livestock and human vaccination were evaluated.

Results: Across One Health vaccination scenarios evaluated, RVF vaccination of humans and/or animals consistently reduced outbreak size and overall disease burden over a 20 year period compared with the baseline levels involving no vaccination. Integrated One Health strategies combining livestock and human vaccination delivered the strongest control, by protecting humans directly as well as suppressing transmission in the animal reservoir. Simulations indicated that human vaccination strategies combined with preventive livestock vaccination can reduce cases in human and livestock populations by over 90%.

Conclusions: The expected synergistic benefits for affected communities, along with the balanced distribution of responsibilities and resources across sectors, make OHVS a valuable intervention framework. As RVF human vaccines become widely available, this unified vaccination approach can strengthen collaboration among public health, veterinary, and environmental sectors, leading to a more effective, equitable, and sustainable intervention landscape.

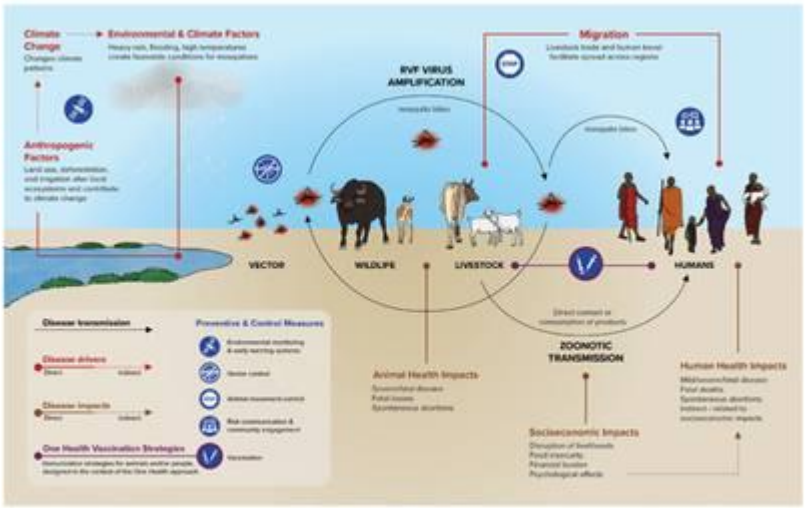


Fig. 1. One Health framework of Rift Valley fever (RVF), including the disease transmission cycle, drivers, impacts and main preventive and control measures.

Fig. 2. Decision domains to design One Health vaccination strategies (OHVS) for Rift Valley fever.

2707 – What if better biodiversity EU planning and decisions led to better health outcomes? One Health Knowledge Exchange Network to inform EU policy-makers through the Science Service for Biodiversity

Candice POUGET (1), Frauke ECKE (2), Julien CAPPELLE (3), Jan Felix DREXLER (4), Juliette YOUNG (5), **Lucinda KIRKPATRICK** (6), Marie VANDEWALLE (1), Nadja KABISCH (7), Ute JACOB (8)

1: Helmholtz Centre for Environmental Research - UFZ, Germany; 2: University of Helsinki, Finland; 3: CIRAD, France; 4: Charité - Universitätsmedizin Berlin, Germany; 5: INRAE, France; 6: Bangor University, Wales; 7: Leibniz Universität Hannover, Germany; 8: Helmholtz-Institut für Funktionelle Marine Biodiversität , Germany

Background: The One Health approach acknowledges the interconnectedness of human, animal, and environmental health, promoting interdisciplinary collaboration to address complex and emerging health and environmental challenges. Cross-sectoral and collaborative initiatives are essential to prevent, detect, and respond to health threats such as emerging infectious diseases, antimicrobial resistance, and food safety risk. A coordinated knowledge sharing, as proposed by the One Health Knowledge Exchange Network, proposes to strengthen cross-networks collaboration and governance, and support evidence-informed policymaking through the future Science Service for Biodiversity.

Methods: Based on the mechanisms developed by BioAgora to answer knowledge requests from the European Commission and engage with Knowledge Exchange Networks related to the EU's Biodiversity Strategy for 2030, the One Health KEN will contribute to the future Science Service for Biodiversity, as the scientific pillar of the Knowledge Centre for Biodiversity (EC-KCBD). Its development draws on recommendations and identified knowledge gaps from the Eklipse report "Biodiversity and pandemics: Interdisciplinary research and action priorities"(1) (2023) and the recently released position paper "Embedding Biodiversity within One Health Position Paper in the Strategy for European Life "(2) (end of May 2026) produced by four Horizon Europe projects working at the biodiversity–health interface (BCOMING, BEPREP, RESTOREID and ZOE). It will also explore innovative approaches to stakeholder mapping, community building, and engagement, with outputs tailored to the needs of diverse network members.

Results: After introducing the three core functions of the future Science Service for Biodiversity—supporting thematic knowledge exchange networks, strengthening science–policy processes, and responding to policymakers' knowledge requests—, we will demonstrate how the One Health KEN will contribute the on-going work to better connect One Health knowledge and research results in mapping knowledge gaps, and improving the uptake of biodiversity research in health and environmental policy and research agendas. The One Health KEN will strengthen science–policy dialogue between researchers, policymakers, practitioners, and relevant initiatives.

Conclusion: The official launch of the One Health Knowledge Exchange Network (KEN) will take place during the WOHC2026. By creating a space for exchange, collaboration and the co-development of capacity building activities and outputs, the network aims to help translate evidence into action and

supports more integrated approaches to the biodiversity–health interface. Through the Science Service for Biodiversity activities, networks and webplatform, alternative approaches for community building and engagement will be explored, in order to develop outputs tailored to the specific contexts and needs of its members.

(1)Biodiversity and pandemics: Interdisciplinary research and action priorities. https://eklipse.eu/wp-content/uploads/2024/02/EKLIPSE_Report-02-23_Biodiv-pandemics-REPORT_final.pdf

(2)Embedding Biodiversity within One Health Position Paper in the Strategy for European Life Sciences | Zenodo: https://zenodo.org/records/21031938

2711 – Antimicrobial use and resistance in marginalised small-scale farming communities: a multi-disciplinary approach to identify risk factors and create solutions.

Jude YATUWA (1), Victoria COLE (2), Nolwazi NDIMANDE (1), Siphelele PHILLIP (3), Setshaba TAUKOBONG (2), Ngazo SIGA (1), Nosiseko MTATI (4), Maya MARSHAK (1), Katie KRIEGLER FOSTER (1), Rachel WYNBERG (1), Mary-Ann DAVIES (1), Anastasia KOCH (1,5), Craig KINNEAR (2), Lumko MBOYI (3), Helen MCILLERON (1)

1: University of Cape Town, South Africa; 2: South African Medical Research Council; 3: Conservation Exposure Education and Training; 4: Meat Naturally - Africa; 5: Eh!woza

Background: There is a shortage of information about antimicrobial resistance (AMR) outside the formal health care sector. As marginalised communities own approximately half of the livestock in South Africa, understanding the development and transmission of AMR in these settings is critical for evolving policies against AMR.

Methods: We describe a proof-of-concept study in the Eastern Cape, South Africa. Metagenomic sequencing mapped bacterial species and AMR gene distributions in humans, livestock, and water. Livestock and water samples were screened for antibiotics using high-resolution mass spectrometry. Citizen surveys, community workshops, household questionnaires, transect walks, semi-structured interviews and focus group discussions were used to understand AMR's social dimensions. The research, in collaboration with conservation non-profit organisations, was combined with community engagement to raise awareness of AMR, and to co-design local solutions against AMR.

Results: A survey of 197 community members revealed low levels of knowledge about AMR and antibiotics. Adults with secondary schooling were 10 times more likely to know what antibiotics are than those without schooling. Based on questionnaires in 25 homesteads, 76% of households used antibiotics in livestock for prevention of disease or recent treatment, and 40% of adults interviewed had used antibiotics themselves in the 6 months before interview. Those with sufficient income to save, were more likely to use antibiotics. 74% of homesteads collect drinking water from rivers, which are largely unprotected from livestock traffic and other waste. Drinking water was frequently contaminated by faecal indicator organisms. AMR genes were found in all sample types, including those from humans, cattle, goats, sheep, chicken, water and retailed meat. All 50 human faecal samples had AMR genes, with extensive multiclass resistance patterns. In keeping with the most frequently used antibiotics in animals, tetracycline resistance was common in livestock rectal swab samples, and oxytetracycline was detected in drinking water and retailed meat.

Access to veterinary services was extremely limited. Unqualified local vendors supplying over-the-counter antibiotics and counterfeit medicines have become an influential source of advice to households and may contribute to overuse and misuse of antibiotics to prevent and treat livestock illnesses. A Herd Health WhatsApp system is under development to link farmers to animal health technicians, aiming to improve access to veterinary advice and reduce the overuse and misuse of antibiotics.

Conclusions: Antibiotics are widely used in this rural setting with weak animal health, water and sanitation services. Shared microbiome and resistome findings suggest ecological connectivity between reservoirs. Thus through AMR, the potentially global impact of marginalisation of rural communities is highlighted. Using a multidisciplinary approach and involving the community, allowed us to identify locally important factors linked to AMR and co-design solutions.

2713 – A One Health perspective on West Nile virus transmission in Madagascar: integrating canine and human serology through multi-host serocatalytic modelling

Herilantonirina Solotiana RAMAROSON (1,2,3), Mauricianot RANDRIAMIHAJA (4), Soa Fy ANDRIAMANDIMBY (5), Harinirina Aina RABEMANANJARA (5), Lova Tsikiniaina RASOLOHARIMANANA (6), Solohery Lalaina RAZAFIMAHATRATRA (6), Jonathan BASTARD (7), Andres GARCHITORENA (4,8), Katerina ALBRECHTOVA (2), Julia GUILLEBAUD (1,2), Benoit DURAND (7), **Véronique CHEVALIER** (1,2)

1: Unité Mixte de Recherche (UMR) Animal, Santé, Territoires, Risques et Écosystèmes (ASTRE), Centre de coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), 34398 Montpellier, France; 2: Unité d'Epidémiologie et de Recherche Clinique, Institut Pasteur de Madagascar, Antananarivo 101, Madagascar; 3: Département de Recherches Zootechniques, Vétérinaires et Piscicoles, Centre National de la Recherche Appliquée au Développement Rural (FOFIFA), Antananarivo 101, Madagascar; 4: Organisation Non Gouvernementale (ONG) Pivot, Ranomafana, Ifanadiana 312, Madagascar; 5: Unité de Virologie, Institut Pasteur de Madagascar, Antananarivo 101, Madagascar; 6: Unité d'Immunologie des Maladies Infectieuses, Institut Pasteur de Madagascar, Antananarivo 101, Madagascar; 7: Épidémiologie des Maladies Infectieuses Multi-hôtes (EPIMIM), Laboratoire de Santé Animale, Anses, Ecole Nationale Vétérinaire d'Alfort, 94700 Maisons-Alfort, France; 8: Maladies Infectieuses et Vecteurs, Écologie, Génétique, Évolution et Contrôle (MIVEGEC), University of Montpellier, Centre National de Recherche Scientifique (CNRS), Institut de Recherche pour le Développement (IRD), 34000 Montpellier, France

Background: West Nile virus (WNV) is a mosquito-borne flavivirus of public health importance. Despite evidence of WNV circulation in Madagascar, its transmission dynamics remain poorly characterized, particularly in this resource-limited setting where human surveillance is challenging. In such contexts, domestic animals may provide valuable information on local virus circulation. Because dogs and humans share similar environmental exposures, we hypothesized that canine exposure to WNV would reflect human exposure risk. This study assessed the relationship between canine and human WNV force of infection (FOI) estimates in a tropical setting of southeastern Madagascar.

Methods: The study was conducted in Ifanadiana district, southeastern Madagascar, an area encompassing a marked altitudinal and ecological gradient, from humid high-altitude rainforest bordering Ranomafana National Park to lower-elevation agricultural landscapes dominated by rice fields. Two cross-sectional serosurveys were analyzed: a canine survey conducted in 2023 among 513 dogs from five communes, and a human survey conducted in 2021 among 530 individuals using archived dry blood spots samples collected from the same area. Samples were tested for antibodies against the WNV envelope protein (pr-E) and non-structural protein 1 (NS1) using a bead-based multiplex immunoassay. We analyzed this age-stratified serological data using Bayesian serocatalytic models, to estimate the FOIs and assess the relationship between canine and human exposure. We compared models that accounted for different hypotheses regarding the relationship between canine and human exposure and that included, or not, temporal and/or spatial variation in FOI.

Results: Widespread WNV exposure was observed in both dogs and humans, with seroprevalences of 60.6% (95% confidence intervals (CI): [56.2 – 64.9]) and 18.5% (95% CI [15.3 - 22.1]), respectively. Age-specific seroprevalence profiles were consistent with cumulative exposure in both species, indicating that dogs acquire infection early in life. Across all communes, dog seroprevalence ranged from 38.7% (95% CI [30.7 – 47.3]) to 75.0% (95% CI [62.6 – 85.0]), compared with 7.7% (95% CI [2.9 – 16.0]) to 24.8% (95% CI [18.5 – 32.2]) in humans. The best-supported serocatalytic model identified spatial heterogeneity in WNV FOIs across communes, with lower transmission intensity in Ranomafana (neighboring a rainforest national park) than elsewhere. The model also supported a proportional relationship between canine and human FOIs. Human FOIs followed the same spatial pattern as canine FOIs, with an estimated proportionality parameter of = 0.06 (95% credible intervals: [0.05 – 0.09]).

Conclusions: By showing a quantitative spatial relationship between canine and human WNV FOI, our results support the potential of young dogs as sentinels of WNV human exposure risk in Madagascar. Further studies are warranted to evaluate their integration into One Health surveillance systems for WNV and other zoonotic pathogens.

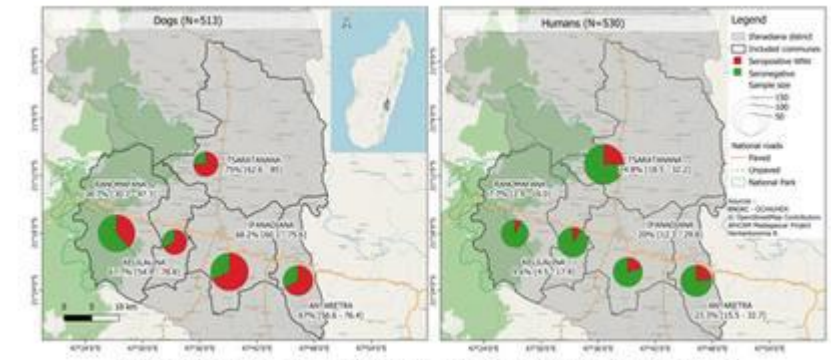


Figure 1 : Spatial variation in West Nile virus seroprevalence in dogs (2023) and humans (2021) in Ifanadiana district, Madagascar

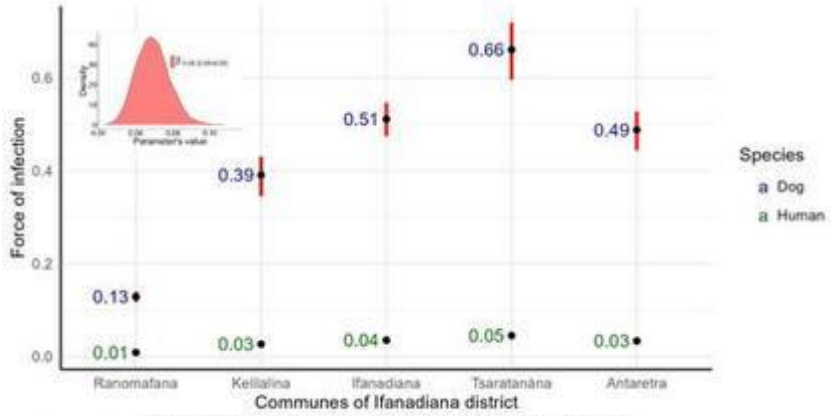


Figure 2: Estimates of the spatial variation of WNV FOI in dogs and humans from serological surveys of 2023 and 2021, respectively, according to the best fitting serocatalytic model assuming WNV FOI in dogs proportional to RVF FOI in humans and varying in space, Ifanadiana district, Madagascar

2727 – Mobile Genetic Elements as Drivers and Predictors of Antimicrobial Resistance in Enterococcus faecium Across the One Health Continuum

Jee In KIM (1), Athanasios ZOVOILIS (2), Gary VAN DOMSELAAR (3), Sani -e-Zehra ZAIDI (2), Robert BEIKO (4), Tim MCALLISTER (1), **Rahat ZAHEER** (1)

1: Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada; 2: University of Manitoba, Winnipeg, MB, Canada; 3: National Microbiology Laboratory, Public Health Agency of Canada; 4: Dalhousie University, Halifax, NS, Canada

Antimicrobial resistance (AMR) in enterococci represents a critical One Health challenge, driven by the dissemination of resistance determinants through mobile genetic elements (MGEs) and compounded by difficulties in accurately predicting resistance phenotypes from genomic data alone. To address these interconnected challenges, we integrated genomic, functional, transcriptomic, and machine-learning (ML) approaches to investigate both the mobility of clinically relevant AMR genes and the biological basis of ML-mediated genotype-to-phenotype predictions in *Enterococcus faecium*.

We characterized the abundance, diversity, and transferability of MGEs carrying key resistance genes, including *vanA*, *tet(M)*, and *erm(B)*, among enterococci originating from clinical, agricultural, and environmental sources. Replicon typing combined with reference-based and reference-free clustering identified diverse plasmid- and transposon-associated MGEs. Conjugation assays using *E. faecium* donor strains and *E. faecium*, *E. faecalis*, and *E. hirae* recipients, followed by long-read-based whole genome sequencing, confirmed both intra- and inter-species transfer. The *vanA* locus from *E. faecium* VRE0008 was embedded within a large RepA_N-type plasmid carrying a Tn1546-like transposon and demonstrated broad host-range transfer across all recipient species. Whole genome sequencing revealed that transfer frequently involved mobilization of an approximately 40-kb genomic region surrounding the *vanA* locus. Similarly, *erm(B)* in *E. faecium* NS0794 was located on a transferable RepA_N-type plasmid that also exhibited broad host-range transfer. In contrast, *tet(M)* in *E. faecium* Ent0189 resided on a Rep_Trans-like plasmid containing Tn916-associated integrative conjugative element features and displayed a comparatively narrower host range. Transfer events occurred among isolates originating from clinical,

wastewater, feedlot catchbasins, retail beef, and natural-water environments, highlighting the capacity of enterococcal MGEs to facilitate AMR dissemination across ecological and sectoral boundaries.

To evaluate the biological relevance of ML-based AMR predictions, we performed transcriptomic profiling of selected *E. faecium* isolates exhibiting vancomycin-, doxycycline-, and erythromycin-resistant phenotypes. Differential gene expression analyses under antibiotic exposure revealed transcriptional responses consistent with ML-predicted resistance determinants, including *vanA*, *tet(M)*, and *tet(L)*. Notably, genes involved in MGE maintenance and transfer, including conjugative transfer proteins, DNA relaxase NicK, type IV secretion system components, and the anti-restriction protein AardA, were consistently upregulated, supporting the mechanistic significance of ML-selected genomic features. In contrast, *erm(B)*-carrying erythromycin-resistant isolates exhibited limited transcriptional responses to antibiotic exposure, suggesting alternative regulatory or mutational mechanisms not captured by gene presence-absence models alone.

Collectively, these integrated findings demonstrate that MGEs serve as both primary drivers of AMR spread and informative biological signals for predictive modeling, and that coupling genomic, functional, and transcriptomic data can substantially improve interpretation of ML-based AMR predictions. This work strengthens the mechanistic foundation for predictive AMR analytics while providing actionable insight into the dynamic processes facilitating resistance dissemination across species and habitats.

2732 – Coupling Contact-Based and Environmental Transmission: A Mathematical Model of Canine Parvovirus in Free-Roaming Dogs in Uganda

Inez DERKX (1,2), Ayrin PIEPHOH (3), Salome DUERR (3), Lordrick ALINAITWE (4), Terence ODOCH (4), Nakul CHITNIS (1,2)

1: Swiss TPH, Switzerland; 2: University of Basel, Switzerland; 3: Veterinary Public Health Institute, University of Bern, Switzerland; 4: Makerere University, Uganda

Background

Canine parvovirus can cause acute haemorrhagic enteritis and myocarditis and remains a leading infectious cause of canine mortality worldwide. Free-roaming and unvaccinated dog populations across Africa and Asia, including Uganda, contribute to ongoing transmission, with consequences for canine wellbeing and mortality, spillover risk to wildlife, and the socio-economic security of underprivileged communities. Because parvovirus is highly persistent in the environment, transmission likely depends jointly on direct canine contact and indirect, environmentally mediated exposure. However, no existing model captures how these two pathways interact with contact-network structure and demography. We therefore developed a mathematical model of canine parvovirus transmission that incorporates both direct contact and environmental transmission pathways to identify which population characteristics and transmission routes are most amenable to intervention.

Methods

We studied free-roaming dog populations across six urban and rural sites in Uganda between January and March of 2026. Blood samples were tested for IgG antibodies by ELISA to generate age-stratified seroprevalence estimates at each site. Contact rates were derived from empirical contact networks collected over multiple days using GPS collars to determine an average daily interaction rate. We built an age-stratified compartmental model (SEAIR-W), distinguishing between asymptomatic and symptomatic infectious individuals and incorporating maternally derived antibody dynamics and environmental viral persistence. Environmental and contact-based transmission rates were calibrated by maximum-likelihood estimation against the serological data, followed by global convergence and local sensitivity analyses. We then used the calibrated model to simulate and compare the dynamic, population-level impacts of candidate interventions: environmental sanitation, vaccination, and quarantine.

Results

The calibration framework links population-level transmission dynamics to individual age-dependent seroconversion, showing that direct and environmental transmission pathways can be reconstructed from the age-stratified seroprevalence data. Multi-start optimization and convergence tests confirmed that the calibration pipeline is numerically stable. The estimated relative contribution of the two pathways was highly sensitive to assumptions about recovery rate and the rate of progression out of latency, but largely

insensitive to the environmental viral decay rate. The resulting simulation framework compares the population-level effects of vaccination, quarantine, and environmental sanitation.

Conclusions

By linking calibrated transmission parameters to population dynamics, this model provides a tool for evaluating parvovirus control strategies in endemic settings. Our framework highlights the relative importance of direct contact and environmental persistence when analyzing transmission in high-turnover, free-roaming dog populations. This framework is readily adaptable to other canine pathogens with similarly dual transmission routes, such as leptospirosis and canine distemper virus.

2733 – First recognized U.S. outbreak of Salmonella Woodinville linked to pet veiled chameleons: a One Health investigation enabled by genomic surveillance

Thai-An NGUYEN (1), Grace PEDERSON (1,2), Alexsandra DOLAN (3), Laura GIERALTOWSKI (1), Jessica HICKS (4), Taylor JONCKOWSKI (5), Tonya MACKIE (4), Oluwakemi ONI (6), Samantha SPENCER (7), Kathy BENEDICT (1), Kate VARELA (1)

1: U.S. Centers for Disease Control and Prevention, United States of America; 2: Great Hill Solutions, A Seneca Nation Group Company; 3: Nebraska Department of Health and Human Services; 4: U.S. Department of Agriculture, National Veterinary Services Laboratories; 5: Oklahoma State Department of Health; 6: Iowa Department of Health and Human Services; 7: Texas Department of State Health Services

Background

Reptile-associated salmonellosis (RAS) remains an ongoing zoonotic public health concern in the United States, particularly among children. Increased implementation of whole genome sequencing (WGS) through the U.S. Centers for Disease Control and Prevention's (CDC) PulseNet has improved detection of geographically dispersed, low-incidence RAS outbreaks that may previously have gone unrecognized. In recent years, several investigations identified rare *Salmonella* serotypes linked to pet reptiles, highlighting the importance of coordinated One Health surveillance and response activities. In 2026, PulseNet detected a cluster of human infections with closely genetically related *Salmonella* Woodinville isolates associated with pet veiled chameleon exposure. We describe epidemiologic, laboratory, and traceback investigation findings, highlighting the critical role of a One Health approach.

Methods

Cases were identified through PulseNet and defined as an isolate of *Salmonella* Woodinville related within 9 allele differences by core genome multilocus sequence typing (cgMLST). State and local public health agencies conducted epidemiologic investigations using standardized enteric illness questionnaires and a reptile exposure questionnaire. Traceback investigation identified animal retailers and suppliers. Public health agencies in 3 states collaborated with animal health and laboratory partners for animal and environmental sampling and WGS. Investigators also engaged industry partners to disseminate prevention messaging to reptile retailers, breeders, and suppliers. CDC collaborated with the United States Department of Agriculture's National Veterinary Services Laboratories to facilitate sequencing of banked *Salmonella* Woodinville chameleon isolates.

Results

A total of 5 cases were identified across 4 U.S. states, occurring among children ≤2 years of age. Illness onset dates ranged from 12 February to 10 April, 2026. Two of 5 patients were hospitalized and no deaths were reported. Parents or caretakers reported all cases had veiled chameleon exposure prior to illness onset.

All illnesses were associated with indirect household exposure, including contact with contaminated surfaces or caregivers handling reptiles. Traceback activities identified a shared chameleon supplier among all cases. Animal and environmental samples were related to the outbreak strain within 9 allele differences, confirming chameleon exposure as the source. Of 6 banked *Salmonella* Woodinville isolates from chameleons, 4 were related to the outbreak strain within 2-12 alleles, indicating this rare serotype has circulated among chameleons since at least 2021. A national pet industry advocacy organization disseminated reptile-associated salmonellosis prevention messaging in response to the investigation.

Conclusions

This was the first recognized multistate outbreak of *Salmonella* Woodinville infections in the United States. The outbreak highlighted the critical role of WGS-based surveillance in identifying RAS outbreaks and the value of One Health collaboration among public health, laboratory, animal health, and industry partners. Findings reinforce the importance of prevention messaging addressing indirect household exposure risks associated with pet reptiles, particularly for households with young children.