

One Health  
Platform

International  
**One Health  
Symposium**

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# Book of Abstracts

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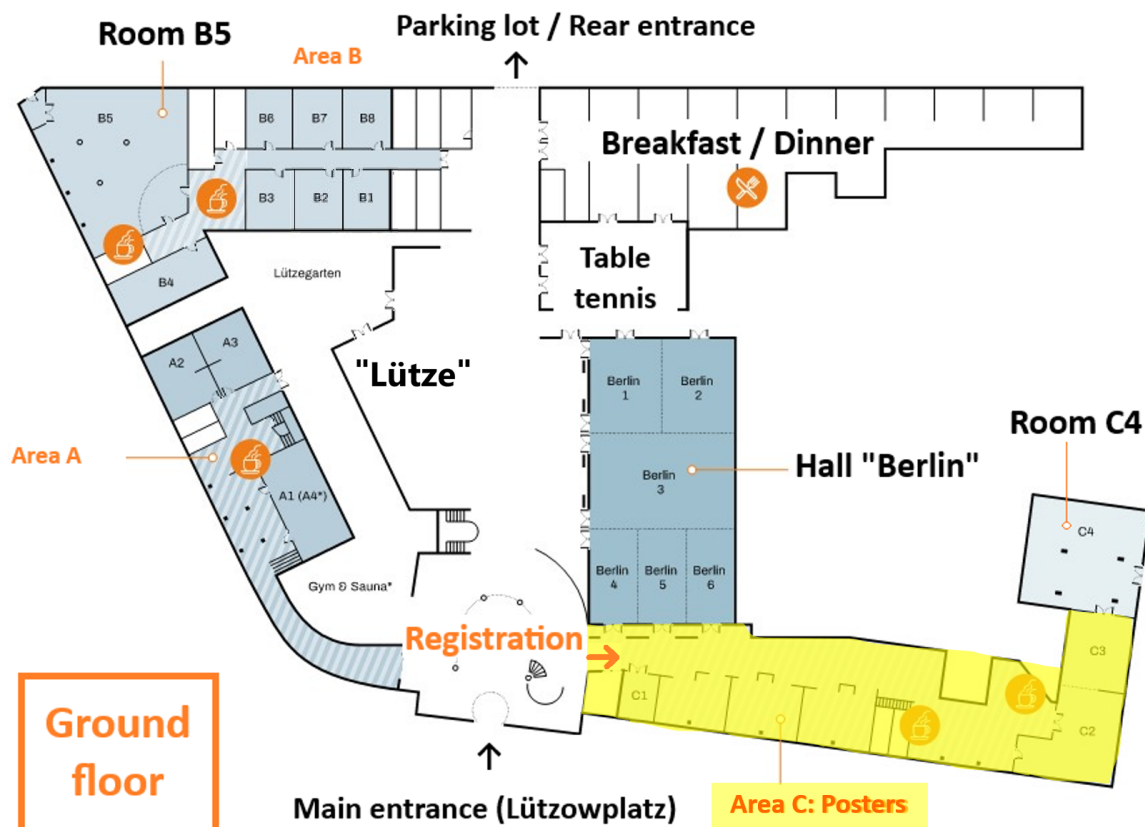
# Floor plan

Hotel Berlin, Berlin

<https://www.hotel-berlin.de/en>

Lützowplatz 17, 10785 Berlin

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- Hall "Berlin" = Plenary sessions
- Room B5 = Parallel sessions
- Room C4 = Game Night
- Restaurant / Bar "Lütze" = One Health Career Get-Together
- Breakfast / Dinner room = Conference Dinner
- Table tennis room = Party (aka "Music, Table Tennis & Drinks")

**Welcome Note / 543**

## **Welcome Note: One Health Platform**

**Author:** Sascha Knauf<sup>1</sup>

<sup>1</sup> *One Health Platform Greifswald-Insel Riems*

### **Corresponding Author:**

Dear Parliamentary State Secretary Dr. Kippels  
Dear Co-chair of the OHHLEP Prof. Markotter,  
Dear Representatives of the six Ministries (BMFTFR, BMG, BMVg, BMZ, BMUKN and BMLEH) that signed the One Health research agreement,  
Dear OHP Scientific Advisory Board Members,  
Dear Scientists, Practitioners,  
Ladies and Gentlemen,

My name is Sascha Knauf, and I head the One Health Platform office at the Friedrich-Loeffler-Institut. Together with our partner offices at the University of Muenster and the Helmholtz Institute for One Health, it is my great pleasure to welcome you to the International One Health Symposium 2026.

For the first time, and as part of our internationalisation strategy, this year's symposium has a regional focus. So let me extend a special ¡Bienvenidos! and Sejam muito bem-vindos to our guests from Latin America. Five of our six keynote speakers have strong ties to the region, and we are especially proud to welcome ten early-career colleagues from Latin America who received travel grants to join us.

Things are changing quickly. We are living through a time of enormous challenges, but also of opportunities. The challenges are obvious to most of us. Think of the Bundibugyo virus disease epidemic in the Democratic Republic of the Congo and Uganda, a Public Health Emergency of International Concern, with around 8000 confirmed cases and close to 4000 deaths. Think of the ongoing H5N1 clade 2.3.4.4b panzootic, which has cost millions of poultry, caused mass mortality in wild birds and, since 2022, killed tens of thousands of marine mammals. And beyond these, we face antimicrobial resistances, climate change, global inequity and, not least, rising nationalism, populism and political tensions that no longer stop at words.

The opportunities come more quietly, but they matter even more if we want sustainable answers to these challenges. The One Health Platform Germany is one of them. Over the past year, we have run 9 workshops and seminars, launched two funding calls, awarded numerous travel and training grants and presented the platform internationally, at the World One Health Congress in Lisbon and at the 1st Congresso Brasileiro de Saude Unica/ Uma Só Saúde.

Have you ever asked yourself what difference this platform makes, at home and abroad? Consider this: six federal ministries, around 2000 members across all sectors and one shared commitment to One Health research. That is rare, and it gives us the opportunity to lead by example.

This year's programme brings together interdisciplinary research built on observation, experimentation and evidence, on ideas that can be tested and revised. In this room, we do not need to explain the One Health concept; that would be carrying coals to Newcastle. Instead, let us go deeper and connect our research across sectors, continents and mindsets, to unlock the full potential of collaboration, communication and capacity strengthening.

Looking beyond Germany, the platform has recently started a discussion on better coordination and alignment of One Health initiatives across Europe. The aim is to break down national silos and to open doors for our young researchers to work across borders.

The One Health Platform is your platform! Our governance is community-driven, which means that all of you, from senior scientists to early-career researchers, are invited to engage, contribute and help shape it. So please join the Members' Assembly and the election of the Scientific Advisory Board. Look at the candidate profiles, and consider standing for election yourself.

Finally, a few announcements:

First, we warmly welcome the newly established research consortia on “Pandemic Prevention and Response within a One Health Framework,” funded by the BMFTR under the umbrella of the platform. Please join their session.

Second, as every year, we offer several activities for early-career scientists. Take part in the poster slams and the poster prize and join the One Health Career Get-Together. Most of all: network!

Third, we have scheduled a late-breaking session on the recent emergence of Shamonda virus in Central Europe.

Finally, my sincere thanks to Dana Thal, Friederike Jansen, Sebastian Sprengel, Anett Wagemann and the team at Orgalution GmbH for their tremendous work in keeping the platform and this symposium running.

Thank you all for being here. Enjoy the symposium!

**Welcome Note / 542****Welcome Note: Federal Ministries**

**Authors:** Federal Ministry of Health; Federal Ministry of Research, Technology and Space; Federal Ministry of Agriculture, Food and Regional Identity; Federal Ministry for Economic Cooperation and Development; Federal Ministry for the Environment, Climate Action, Nature Conservation and Nuclear Safety; Federal Ministry of Defence

Ladies and Gentleman,

I am delighted to welcome you to this year's International One Health Symposium on behalf of the Federal Ministry of Health as well as the five other Federal Ministries that support the German One Health research Platform – namely the Federal Ministry of Research, Technology and Space, the Federal Ministry of Agriculture, Food and Regional Identity, the Federal Ministry for Economic Cooperation and Development, the Federal Ministry for the Environment, Climate Action, Nature Conservation and Nuclear Safety and the Federal Ministry of Defence.

As many of you may know, inter-ministerial research collaboration in Germany has a long tradition in the field of zoonotic diseases. Recent events such as the Ebola out-break in Central Africa, the outbreak of Hantavirus on a cruise ship earlier this year or the wave of Avian Influenza outbreaks affecting wild birds and poultry last autumn vividly demonstrate the ongoing need for research in this field. Those outbreaks were caused by rare or novel strains of the viruses – reminding us that we need to expect the unexpected. New questions regarding the prevention and management of zoonotic diseases continue to emerge. The challenges are far from resolved.

However, in order to promote health, the need for cross-sectoral collaboration extends far beyond the field of zoonoses. More than ever, we are facing a complex web of challenges. The acceleration of climate change, biodiversity loss, habitat changes and the persistent rise of antimicrobial resistance are not isolated crises. They are disruptions of a delicate balance between all living beings. In order to promote health, we therefore need to promote One Health!

To this end, our Federal Ministries joined forces in 2022. Aiming to strengthen bridges between different scientific communities, a research agreement was set up to coordinate and advance scientific research at the intersection of human, animal and environmental health. The annual One Health Symposium which is funded by the Federal Ministry of Research, Technology and Space is part of this initiative. Looking at the agenda, one notices an impressive range of topics including agriculture, environmental pollution, education and artificial intelligence. This diversity is what we need in order to address the complex, interconnected health threats that cannot be solved by one sector alone.

We are delighted that so many participants from different parts of the world have come together to share their expertise. This is especially important, as many of the topics addressed have a strong international dimension.

Earlier this year, the international dimension of One Health was recognised at the highest political level. The president of France, Emmanuel Macron, invited the world to a One Health Summit in Lyon as a contribution to the countries G7 presidency. For the first time ever, the event brought together heads of states, scientists and many other relevant stakeholders under the One Health umbrella. It culminated in several deliverables aimed at cross-sectional governance and proactive risk prevention, which demonstrates that the unifying approach has been adopted by global leaders and politicians.

An initiative of the German government that is directly aimed at fostering international collaboration under the One Health approach is the Global Health Protection Programme, which was launched in 2016 by the Federal Ministry of Health. As an important pillar of the German health and security policy, the programme forms a key interface between policy-making and the scientific community. Earlier this year, more than 30 projects were launched as part of the third programme phase. One Health is one of the three key thematic areas addressed in various projects that are implemented by German institutes such as the Friedrich-Loeffler-Institute and the Robert Koch Institute.

Germany's international engagement in One Health is also driven by the Federal Ministry for Economic Cooperation and Development which promotes cross-sectional preventive and system-oriented approaches in partnerships with institutions in Africa and beyond.

At the EU level, the Federal Ministry of Research, Technology and Space is participating as a funder in

two European partnerships embracing the One Health approach. Covering antimicrobial resistance and pandemic preparedness, they will run for the next 7-10 years and centre around yearly transnational calls with varying topics. Starting this year, the researchers among you will be invited to submit suitable project proposals on an annual basis.

In addition, the Federal Ministry of Research, Technology and Space is currently funding seven national research networks on pandemic prevention and response with a One Health approach. They focus on different topics including influenza, tick-borne diseases, West Nile virus and antimicrobial resistance. On the second day of the symposium, the network coordinators will present their work programme in a dedicated session.

Other initiatives at the national level include the German Antimicrobial Resistance Strategy, which coordinates activities across multiple sectors in the fight against AMR. This year, a new action plan was adopted. With the adjusted strategies we aim to achieve the agreed targets on reducing resistance by 2030.

Many people already support the One Health approach. However, translating a theoretical framework into practice remains a challenge. It requires continuous dialogue between scientists, policymakers, other stakeholders and the general public. The previous examples demonstrate that we have already come a long way towards integrating One Health not only into the scientific but also into the political agenda. However, there is still a lot of work ahead of us.

I am grateful for such a strong and vibrant One Health research community that continuously generates critical insights on some of the most pressing questions of our time, and I would like to thank all of you for your invaluable contributions. Last but not least, I would also like to offer special words of thanks to the organisers of this symposium. I am sure the excellent programme will inspire many rewarding discussions in the coming days.

Presented by Parliamentary State Secretary Dr. Georg Kippels

**Session 1: Vectors I / 402****Temperature-driven mortality in *Aedes aegypti* and its role in modulating dengue outbreaks: an ecological time-series analysis**

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**Background:** Temperature influences dengue transmission, but the direction and magnitude of extreme heat effects on vector populations remain unclear. This study quantifies how cumulative heat-induced mortality in adult *Aedes aegypti* contributes to dengue incidence under real conditions, adopting a One Health perspective linking climate variability, vector biology, and human disease risk.

**Methods:** We combined a thermal tolerance landscape with a dynamic thermal tolerance model to predict mosquito mortality under variable temperatures, using laboratory heat tolerance data on *A. aegypti*. Daily survival probabilities are being aggregated into weekly cumulative measures and incorporated into a negative binomial regression within a distributed lag non-linear model, estimating the exposure-lag-response between predicted mortality and dengue incidence across three Brazilian municipalities, using ERA5 reanalysis data, adjusting for humidity and precipitation, with 1-3 week lags reflecting dengue's incubation period.

**Findings:** The thermal tolerance landscape yielded a CTmax of 49.9°C and  $z = 5.88^\circ\text{C}$  ( $r^2 = 0.993$ ): survival time decreases one order of magnitude for every 5.88°C increase in temperature. Predicted mortality varied among municipalities, peaking during sustained thermal accumulation, coinciding with the warmest periods rather than isolated spikes. The DLNM analysis linking mortality to dengue incidence is underway, and full results will be presented at the symposium.

## Session 1: Vectors I / 466

**An experimental field approach to study climate warming effects on container-breeding mosquitoes****Author:** Felix Sauer<sup>1</sup>**Co-authors:** Simon Bendig<sup>2</sup>; Kristopher Nolte<sup>1</sup>; Leif Rauhöft<sup>1</sup>; Renke Lühken<sup>1</sup><sup>1</sup> *Bernhard Nocht Institute for Tropical Medicine*<sup>2</sup> *Universität Hamburg***Corresponding Author:** felix.sauer@bnitm.de

Climate change and urbanization facilitate the spread of container-breeding mosquitoes, increasing the risk of mosquito-borne disease outbreaks in previously unaffected regions. However, most knowledge of mosquito thermal biology is based on laboratory studies. Here, we present the first results of a novel field experiment assessing climate warming effects on urban mosquito populations. Using low-cost, open-source Arduino hardware, we developed an automated heating system to warm water in experimental containers relative to unmanipulated controls. At eight sites in Hamburg (Germany), four 90-L containers were installed: one control and three treatments maintained at +1.5°C, +3.0°C, and +4.5°C above the control, reflecting projected IPCC warming scenarios. From June to September 2025, weekly measurements included water level, pH, electrical conductivity, *Culex* egg rafts, and insect emergence. Approximately 40,000 insects emerged from the 32 containers. *Culex pipiens* s.s. and *Cx. torrentium* accounted for ~95% of specimens. *Culex* productivity was ~20% higher in the +1.5°C and ~10% higher in the +3.0°C treatments than in the control and +4.5°C treatment. In addition, the wing size of the emerging mosquitoes decreased significantly with increasing water temperature, suggesting fitness-related effects. This cost-effective field approach enables ecologically realistic experiments to assess climate change impacts on urban mosquitoes and other aquatic insects.

**Session 1: Vectors I / 391****Human presence shapes mosquito community composition and virus abundance in a Savannah ecosystem****Author:** Hannah Munzel<sup>1</sup>**Co-authors:** Tuan Huy Truong<sup>2</sup>; Leo Tileni Lucas<sup>3</sup>; John K E Mfuné<sup>4</sup>; Christian Borgemeister<sup>5</sup>; Sandra Junglen<sup>2</sup><sup>1</sup> *Institute of Virology, Charité - Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Berlin, Germany.*<sup>2</sup> *Institute of Virology, Charité - Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Berlin, Germany*<sup>3</sup> *Department of Preclinical Veterinary Studies, School of Veterinary Medicine, Faculty of Health Sciences and Veterinary Medicine, University of Namibia, Windhoek, Namibia*<sup>4</sup> *Department of Environmental Sciences, University of Namibia, Windhoek, Namibia*<sup>5</sup> *Center for Development Research (ZEF), Ecology and Natural Resource Management, University of Bonn, Bonn, Germany***Corresponding Author:** hannah.munzel@charite.de

Anthropogenic land-use change reshapes mosquito communities with implications for arbovirus ecology. However, joint assessments of mosquito and virus communities across land-use types remain rare, particularly in African savannah ecosystems. We characterized both communities along an anthropogenic disturbance gradient in the Kavango Zambezi Transfrontier Conservation Area in Namibia.

In 2023, 7,727 mosquitoes (54 species) were collected across six land-use categories (national park, communal conservation area, rangeland, agriculture, village, town), using BG-Sentinel, CDC light and gravid traps. Urban sites showed the highest abundance and lowest diversity of mosquitoes, accompanied by a pronounced shift towards anthropophilic vector species, particularly *Culex quinquefasciatus*. Human presence was identified as a key driver for variations in mosquito community composition. *Mansonia uniformis*, common in intermediately disturbed habitats, harbored twice the virus richness and much higher infection rates than the more abundant *Cx. quinquefasciatus*, highlighting mosquito species identity as a major determinant of virus abundance. Virus communities, comprising mostly insect-specific viruses, were closely linked to mosquito community patterns.

Our results demonstrate that land-use change influences virus abundance primarily through restructuring mosquito communities, with anthropophilic vector species dominating in human settlements suggesting elevated arbovirus transmission risk.

**Session 1: Vectors I / 446****Behavioral Plasticity in *Ixodes ricinus*: Linking Energy Reserves to Host-Seeking Activity and Infection Transmission Potential****Author:** Paula Hornauer<sup>1</sup>**Co-authors:** Ard Nijhof<sup>2</sup>; Stefanie Becker<sup>3</sup><sup>1</sup> *Stiftung Tierärztliche Hochschule Hannover*<sup>2</sup> *Institut für Parasitologie und Tropenveterinärmedizin, FU Berlin*<sup>3</sup> *Vektor-assoziierte Biodiversität und Infektion (VABI), TiHo Hannover***Corresponding Author:** paula.hornauer@tiho-hannover.de

The seasonal dynamics of tick-host interactions are critical for the transmission of vector-borne pathogens, yet the physiological drivers of behavioral plasticity in *Ixodes ricinus* remain poorly understood. In this study, we investigated how seasonal changes in energy reserves influence host-seeking behavior and infection transmission potential. Monthly flagging of *I. ricinus* across a full year revealed significant seasonal shifts in questing activity, with peak host-seeking behavior observed in spring and autumn. To assess the impact of infection on behavior, we artificially infected ticks with the Jingmenvirus Alongshan virus strain Harz Mountain (ALSV\_HM), recently identified in *Ixodes ricinus* ticks collected from game animals in Lower Saxony, Germany. Seven days post-infection, we re-evaluated their host-seeking behavior. Infected ticks exhibited altered behavioral patterns, including increased questing height and decreased sensitivity toward repellents, particularly during peak seasonal windows. To elucidate the underlying physiological mechanisms, we quantified lipid, protein, and carbohydrate levels in ticks collected at different time points and across infection states. This study provides a mechanistic link between seasonal physiology, infection-induced behavioral changes, and vector competence, highlighting the importance of integrating metabolic and behavioral data to predict and mitigate disease risk.

**Session 1: Vectors I / 396****Hidden interactions in ticks: Co-infection patterns of *Borrelia* spp. as indicators of TBEV microfoci****Author:** Katrin Fachet-Lehmann<sup>1</sup>**Co-authors:** Rebecca Vogt<sup>1</sup>; Karsten Schweikert<sup>2</sup>; Ute Mackenstedt<sup>1</sup>; Alexander Lindau<sup>1</sup><sup>1</sup> University of Hohenheim, Department of Parasitology, Stuttgart<sup>2</sup> University of Hohenheim, Core Facility Hohenheim, Stuttgart**Corresponding Author:** fachet@uni-hohenheim.de

The ecological mechanisms underlying the spatial restriction of tick-borne encephalitis virus (TBEV) foci remain poorly understood. As *Ixodes ricinus* frequently carries multiple pathogens, interactions between *Borrelia* spp. and TBEV may contribute to focal virus persistence. Therefore, co-infection patterns and *Borrelia* species composition were investigated in relation to TBEV, in different hotspots in southern Germany. Between 2023 and 2025, 5,585 *I. ricinus* ticks from TBEV hotspots and adjacent TBEV-free sites in Stuttgart, Flappach, and Wangen in South Germany were screened using PCR methods. Overall, *Borrelia* spp. were detected in 23.4% of ticks, whereas TBEV prevalence in hotspots was low (0.4%; 15/3,535). *Borrelia afzelii* was the predominant species. Ticks collected from TBEV hotspots showed a significantly higher probability of *Borrelia* infection compared to TBEV-free sites ( $p = 0.034$ ;  $n = 3,535$ ). While the presence of *B. afzelii* significantly increased the probability of TBEV detection ( $p = 0.034$ ), *B. burgdorferi* s.s. showed a positive but insignificant association ( $p = 0.095$ ). Co-infections occurred in six of fifteen TBEV-positive ticks. Although these associations are consistent with shared reservoir hosts and overlapping transmission cycles, they provide valuable insights into the ecological structure of TBEV microfoci. *Borrelia* composition may represent an ecological indicator of environmental conditions supporting long-term TBEV persistence.

This project was funded by Pfizer Pharma GmbH.

**Session 1: Vectors I / 412****The Role of Raccoons in Tick-Borne Disease Ecology**

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Understanding the contribution of wildlife species to the maintenance and spread of zoonotic pathogens is a key component of the One Health concept. However, the role of raccoons in the epidemiology of tick-borne encephalitis virus (TBEV) has remained unexplored. In this study, raccoons from Baden-Wuerttemberg, one of the main endemic TBE areas in Germany, were screened for TBEV infections using molecular and serological methods.

TBEV RNA and neutralizing antibodies were detected in a substantial proportion of the examined animals. Overall, 40.9% (38/93) of raccoons tested positive for TBEV as first evidence of TBEV infections in raccoons in Germany, with prevalences ranging from 20.0 – 66.6%. Positive raccoons clustered in eastern Baden-Wuerttemberg, where 15 of 24 raccoons from district Ostalbkreis tested positive. A second hotspot was identified in the urban district of Heidelberg-Wieblingen, with 11 of 22 animals tested positive. In total, 18 individuals were positive by both PCR and virus neutralization assay.

Given their high tick infestation rates, wide-ranging movements and increasing adaptation to urban environments, raccoons may represent an epidemiologically relevant bridge linking wildlife reservoirs, tick populations, domestic animals and humans. Our findings highlight the importance of including invasive wildlife species in TBEV surveillance and the need for a One Health approach to better understand pathogen circulation at the human–animal–environment interface

**Session 2: Novel and Emerging Pathogens / 409****Establishing One Health surveillance across human, domestic animals, wildlife and arthropod vectors in two different Brazilian biomes.**

**Author:** Tomas Moutinho<sup>1</sup>

**Co-authors:** Danilo Kluyber; Expedito Luna<sup>1</sup>; Julio Benavides

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**Background:** Integrated field data from Brazil's biodiverse, fast-changing biomes are scarce. We will investigate the human-animal-environment interface in two different Brazilian biomes: the Pantanal and the Cerrado.

**Methods:** In a cross-sectional One Health survey, following ethical approval for both human and animal research, 147 rural residents underwent a sociodemographic questionnaire and dermatoneurological examination with active leprosy screening. In parallel, samples were obtained from domestic dogs (sentinels), free-ranging six-banded armadillos (*Euphractus sexcinctus*) captured by a specialised veterinary team, and *Amblyomma sculptum* ticks; whole blood, serum, nasal swabs and ticks were cryopreserved under a standardised protocol. Animal and vector samples will be analysed by untargeted next generation metagenomic sequencing, with host depletion and phylogenetic assignment of divergent viruses.

**Results:** Ten leprosy cases were clinically diagnosed, illustrating the burden of a neglected disease with recognized zoonotic host/reservoir at the study sites. We assembled a paired, cross-biome biobank of 124 canine, 34 armadillo and 62 tick samples alongside the human cohort forming an integrated One Health biobank.

**Conclusions:** By coupling wildlife and vector virome discovery with paired host sampling across both biomes, this platform provides a foundation to detect emerging infectious agents and anticipate spillover in threatened Brazilian ecosystems.

**Session 2: Novel and Emerging Pathogens / 424****Rethinking arboviral risk in malaria-endemic Africa**

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**Co-authors:** Jeannot Fréjus Zinsou<sup>2</sup>; Jumafr P. Koumba<sup>4</sup>; Gael D. Maganga<sup>4</sup>; Natacha Pougou<sup>5</sup>; Grace Cherile Ongouta<sup>2</sup>; Rodrigue Mintsa Rodrigue Mintsa<sup>6</sup>; Julien Z. B. Zahouli<sup>3</sup>; Akim Adegnika<sup>2</sup>; Steffen Borrmann<sup>7</sup>; Mario Recker<sup>8</sup>; Stefanie Becker<sup>9</sup>

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We conducted a prospective multicentre seroepidemiological study including 2,283 febrile patients from Côte d'Ivoire and Gabon between 2022 and 2024. IgG antibodies against dengue virus (DENV), Zika virus, West Nile virus, and Rift Valley fever virus were assessed using a novel high-specificity ELISA platform designed to reduce flaviviral cross-reactivity. Plasmodium infection was determined by routine diagnostics, and questionnaire-derived Exposure and Socioeconomic Indices were used to assess environmental and structural risk factors. Our findings redefine current assumptions of arboviral circulation in both regions. In Côte d'Ivoire, we provide the first broad assessment of arboviral exposure beyond dengue outbreak surveillance, while in Gabon improved serological specificity revealed a less heterogeneous arboviral landscape than previously suggested. Despite different ecological and epidemiological backgrounds, both countries showed similar patterns dominated by DENV exposure, with limited circulation of other arboviruses. Importantly, DENV IgG seropositivity and Plasmodium infection were strongly linked to cumulative exposure and socioeconomic conditions, particularly in children, identifying early life as a critical window of combined vector exposure.

These results highlight the need for integrated One Health surveillance approaches combining human diagnostics, vector ecology, and environmental risk assessment to better anticipate emerging vector-borne disease threats.

**Session 2: Novel and Emerging Pathogens / 410****Bats Are Susceptible to H5N1 Infection but Rapidly Control Virus Replication****Author:** Arthur Wickenhagen<sup>1</sup>**Co-authors:** Anthony McBain<sup>2</sup>; Claude Kwe Yinda<sup>2</sup>; Franziska Kaiser<sup>2</sup>; Jonathan E Schulz<sup>2</sup>; Julianne Bullock<sup>2</sup>; Reshma Mukesh<sup>2</sup>; Sarah van Tol<sup>2</sup>; Shane Gallogly<sup>2</sup>; Vincent Munster<sup>2</sup>

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Highly pathogenic avian influenza A virus (H5N1) continues to circulate globally in wild birds and is increasingly detected in mammals, highlighting the risk of cross-species transmission. Serological evidence of exposure in South American vampire bats and reports of H5N1-positive flying foxes in Bangladesh suggest that bats are susceptible to infection. However, their role in H5N1 ecology remains unclear. We investigated H5N1 susceptibility in bats using in vitro and in vivo models. Bat-derived cell lines from diverse species supported H5N1 replication, demonstrating permissiveness to infection. We then developed an experimental infection model in Jamaican fruit bats (*Artibeus* spp.) and inoculated animals via intranasal and oral routes. Infected bats showed productive infection, with viral RNA and infectious virus detected in respiratory and intestinal samples. Virus shedding was transient and declined within five days. Despite infection, bats exhibited no clinical signs, morbidity or mortality, suggesting effective control of viral replication and limited disease progression. These findings demonstrate that Jamaican fruit bats are susceptible to H5N1 infection and can transiently shed virus without developing severe disease. The results identify bats as potential incidental hosts and raise important questions about their role in H5N1 maintenance and transmission at the wildlife–livestock–human interface. This work was supported by the Intramural Research Program, NIAID,NIH.

**Session 2: Novel and Emerging Pathogens / 422****Full genome sequencing of Ekpoma Virus 2 from human sera, Uganda****Author:** Peter Z. Sabakaki<sup>1</sup>**Co-authors:** Yea-Seul Lee<sup>2</sup>; Selina L. Graff<sup>2</sup>; Sandra Junglen<sup>2</sup>; Lisa Biber-Freudenberger<sup>3</sup>; Maureen Nabatanzi<sup>3</sup>; Erick E. K. Bigala<sup>4</sup>; Anthony M. Nsubuga<sup>1</sup>; Teddy A. Tindyebwa<sup>1</sup>; Innocent B. Rwego<sup>4</sup>; Julius J. Lutwama<sup>5</sup>; James R. Ochieng<sup>6</sup><sup>1</sup> *Department of Plant Sciences, Microbiology and Biotechnology, Makerere University, Kampala, Uganda*<sup>2</sup> *Institute of Virology, Charité – Universitätsmedizin Berlin, corporate member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, 10117 Berlin, Germany*<sup>3</sup> *Center for Development Research (ZEF), University of Bonn, Germany*<sup>4</sup> *Department of Biosecurity, Ecosystems and Veterinary Public Health, Makerere University, Kampala, Uganda*<sup>5</sup> *Department of Arbovirology, Uganda Virus Research Institute (UVRI), Entebbe, Uganda*<sup>6</sup> *Department of Zoology, Entomology and Fisheries Sciences, College of Natural Sciences, Makerere University, Kampala, Uganda***Corresponding Author:** selina.graff@charite.de

Ekpoma virus 2 (EKV-2) is a human-associated rhabdovirus first detected in a febrile case in Nigeria. Seroprevalence studies from Nigeria and the Democratic Republic of Congo (DRC) reported EKV-2 reactivity rates ranging from 4 – 94%. EKV-2 is closely related to Mundri virus (MUNV), identified in the cerebrospinal fluid of a girl with nodding syndrome in South Sudan, and to Bas-Congo virus (BASV), which has been linked to severe cases of haemorrhagic fever in the DRC.

In a cross-sectional study, we collected 2,062 human serum samples from 20 locations across the Albertine Rift region of Uganda and tested them for acute viral infections using next-generation sequencing. We identified EKV-2 in two samples: a 39-year-old woman from an urban centre who reported febrile symptoms, and an asymptomatic 22-year-old man from a rural village 55 km away. Full genomes were obtained from both samples sharing 99% nucleotide (nt) with each other, and 89% nt identity with the Nigerian prototype strain. Phylogenetically, both strains clustered with EKV-2 and formed a clade with MUNV and BASV. To investigate human exposure to EKV-2 in the Albertine Rift region, we established a recombinant immunofluorescence assay as virus isolation in cell culture was not successful. The analyses are ongoing and will provide insights into the geographic distribution of EKV-2, potential regional differences and sociodemographic characteristics associated with EKV-2.

**Session 2: Novel and Emerging Pathogens / 471****Decoding Vascular Responses to Disparate Hemorrhagic Viruses: Andes and Ebola Viruses**

**Authors:** Isabel von Creytz<sup>1</sup>; Anastasiia Masaltseva<sup>2</sup>; Angelika Lander<sup>1</sup>; Lay Teng Ang<sup>2</sup>; Kyle M Loh<sup>2</sup>; Joseph B Prescott<sup>1</sup>

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Andes virus (ANDV) and Ebola virus (EBOV) are zoonotic pathogens that cause related severe vascular disease despite belonging to distinct virus families. So far, it is poorly understood whether unrelated viral hemorrhagic fevers elicit common or divergent host responses in the human vasculature.

To address this, we generated highly pure artery and vein endothelial cells (ECs) from human pluripotent stem cells, providing a physiologically relevant model of the human vasculature. Comparative infection studies revealed strikingly different host responses to ANDV versus EBOV. In artery ECs, ANDV induced robust antiviral and inflammatory programs, e.g. interferon- $\alpha/\beta$ , interferon-stimulated gene pathways, ISGylation, and cytokine storm signaling. Contrastingly, many of these pathways were suppressed during EBOV infection, indicating fundamentally different strategies of host immune modulation. A comparison of artery versus vein ECs showed mainly similar responses, with a few vessel-specific responses: COPII-mediated vesicle transport was increased in artery but reduced in vein following both infections, while EBOV selectively induced artery-specific activation of interleukin-1 family signaling and SUMOylation pathways.

These findings demonstrate that endothelial responses are both virus-specific and, to a lesser extent, vessel-type dependent. This highlights the utility of human stem cell-derived vascular models for understanding the mechanisms of viral vascular disease.

**Session 2: Novel and Emerging Pathogens / 485****Monkeypox virus in the wild: new insights into animal hosts and between species transmission**

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Mpox is an emerging zoonosis caused by the monkeypox virus (MPXV) which is endemic in West and Central Africa. Most zoonotic MPXV spillovers cause isolated cases or short transmission chains, but lineages showing sustained human-to-human transmission have recently spread. Rodents are thought to be MPXV reservoirs, but conclusive evidence linking human mpox cases to these animals is lacking. The spectrum of potential animal hosts as well as zoonotic transmission routes of MPXV are unknown. Here, we present novel insights into MPXV in wildlife. We traced the origin of an mpox outbreak in wild sooty mangabeys in Tai National Park (TNP), Côte d'Ivoire, to the consumption of an MPXV-infected fire-footed rope squirrel, suggesting these squirrels are MPXV reservoirs. Infected mangabeys contaminated fruit with viable MPXV, and the detection of an MPXV-infected strictly herbivorous red colobus monkey suggests that environmental contamination may play a role in between-species transmission. We also identified orthopoxvirus-positive duikers, including an MPXV-infected Maxwell's duiker in TNP. Camera traps and diet metabarcoding revealed duikers as frequent scavengers, including on known MPXV hosts, which may expose them to MPXV. While duikers likely represent accidental MPXV hosts, they are frequently consumed by humans and other animals, and may therefore play a role in MPXV emergence. Indeed, duiker consumption may have led to an mpox outbreak in a wild chimpanzee community in TNP.

**Session 3: Pandemic Preparedness & Prevention / 364****Can Wastewater-Based Epidemiology and Artificial Intelligence Predict Nosocomial Infections?**

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Early detection and prediction of nosocomial infections remain major challenges for hospital infection control and antimicrobial stewardship programs. In this study, we evaluated the potential of wastewater-based epidemiology (WBE) combined with shotgun metagenomics and artificial intelligence (AI) to predict the occurrence of antibiotic-resistant pathogens in a large tertiary-care hospital located in the Ruhr metropolitan region of Germany.

Over a two-year period, hospital effluent was sampled weekly, resulting in a total of 104 wastewater samples. In parallel, clinical microbiology records were collected, including isolates and associated antibiotic resistance profiles identified in routine diagnostics.

Our results demonstrate that hospital wastewater contains substantial predictive information regarding the emergence and prevalence of antibiotic-resistant pathogens. Depending on the organism and resistance phenotype, wastewater-derived signals provided an early warning window of approximately one to three weeks before corresponding increases were observed in clinical isolates. This lead time could support targeted infection prevention measures, enhanced surveillance activities and proactive antimicrobial stewardship interventions.

A One Health AI approach linking environmental monitoring with clinical microbiology and public health can successfully support clinical infection control.

**Session 3: Pandemic Preparedness & Prevention / 447****Immune function and Coronavirus prevalence in straw-coloured fruit bats (*Eidolon helvum*) at the Human-bat Interface in Nigeria****Author:** Chinedu I. Ngene<sup>1</sup>**Co-authors:** Marina Reyne<sup>2</sup>; Gábor Á. Cziráj<sup>2</sup>; Kristofer M. Helgen<sup>3</sup>; Temidayo Adeyanju<sup>4</sup>; Taiye Adeyanju<sup>5</sup>; Alex D. Greenwood<sup>6</sup><sup>1</sup> *Leibniz Institute for Zoo and Wildlife Research Berlin. Free University Berlin, Germany*<sup>2</sup> *Leibniz Institute for Zoo and Wildlife Research Berlin, Germany*<sup>3</sup> *Australian Museum, Australia*<sup>4</sup> *BatLife, Nigeria*<sup>5</sup> *University of Ibadan, Nigeria*<sup>6</sup> *Leibniz Institute for Zoo and Wildlife Research Berlin, Germany. Free University Berlin, Germany***Corresponding Author:** [ngene@izw-berlin.de](mailto:ngene@izw-berlin.de)

Straw-coloured fruit bat (*Eidolon helvum*) is a widely distributed African tropical bat species. They are a known reservoir for coronaviruses and well-adapted to anthropogenic environments, both in urban and rural areas. Despite their reservoir role, there is lack of information how anthropogenic activities could influence bat physiology and viral shedding. In this study we investigated the immunological and coronavirus prevalence differences between urban and rural environments in Nigeria. We measured innate and adaptive humoral and cellular immune makers, and calculated stress parameters such as Neutrophil-to-Lymphocyte Ratio (NLR) and Systemic Inflammation Response Index (SIRI). We found that basophil and eosinophil levels are higher in the urban environment, triggered by the habitat rather than the sex or coronavirus status. Similar results were found for immunoglobulin G, lysozyme and body condition, with urban bats showing higher values than rural conspecifics. The other parameters measured were not associated with the environment, NLR and SIRI tended to be higher in females. Furthermore, we also found higher coronavirus prevalence in the urban bats. Our study suggests that urbanization contributes to alteration in immune function and the coronavirus prevalence in *Eidolon helvum* have higher significant in the urban environment. This pattern also suggest that human activities, resources and high population density could be important factor in *Eidolon helvum* physiology.

**Session 3: Pandemic Preparedness & Prevention / 380****BTN3A3 resistance of emerging influenza A viruses is shaped by Mx1 of mammalian intermediate host species.****Author:** Jamina Molsen<sup>1</sup>**Co-authors:** Katharina Schmitz<sup>1</sup>; Martin Schwemmle<sup>1</sup>; Peter Reuther<sup>1</sup>; Kevin Ciminski<sup>1</sup><sup>1</sup> *Institute of Virology, Medical Center University of Freiburg, Freiburg, Germany***Corresponding Author:** jamina.molsen@uniklinik-freiburg.de

Zoonotic infections with influenza A viruses (IAVs) of animal-origin are typically self-limiting but can occasionally give rise to pandemics provided human host barriers are overcome. The recently identified human BTN3A3 (butyrophilin subfamily 3 member A3) is a potent restriction factor for zoonotic IAVs. Human-adapted IAVs overcome BTN3A3 restriction through adaptive residues 52 (N, H, Q) or 313 (Y, V) in the viral nucleoprotein (NP). Notably, these residues are associated with resistance to myxovirus resistance 1 (Mx1) proteins from human, swine, and bats. We thus hypothesized that BTN3A3 resistance might emerge as a result of Mx1-mediated selection pressure in intermediate hosts expressing antivirally active Mx1. To test this, we generated reassortant viruses carrying NP of different mammalian-derived IAVs and assessed viral replication in BTN3A3-expressing cells. Combining comparative mutagenesis with polymerase reconstitution assays, we found that NP residues conferring resistance to bat or swine Mx1 proteins also confer BTN3A3 resistance. Because bats and swine lack antivirally active BTN3A3, these adaptive residues emerged under Mx1-mediated selection pressure. Our findings demonstrate that resistance to the human restriction factor BTN3A3 can evolve in Mx1-competent intermediate hosts, providing new insight into the zoonotic potential of animal IAVs and the role of BTN3A3 in limiting zoonotic transmission.

**Session 3: Pandemic Preparedness & Prevention / 408****Community-Centred One Health Preparedness for Ebola Virus Disease in a Transboundary Biodiversity Hotspot: Evidence from the Greater Virunga Landscape (GVL), Uganda****Author:** mugisha kwiringira<sup>1</sup>**Co-author:** Jenifer Nancy Alaba<sup>2</sup><sup>1</sup> *Worldwide Fund for Nature (WWF), Uganda Country Office*<sup>2</sup> *WWF Uganda Country Office***Corresponding Authors:** jalaba@wwfuganda.org; mkwiringira@wwfuganda.org

The Greater Virunga Landscape (GVL), spanning Uganda, Rwanda, and DRC, is a biodiversity hotspot where wildlife-human-livestock interactions and fragile health systems drive zoonotic risk. In May 2026, Uganda confirmed an Ebola Bundibugyo outbreak imported from DRC; by 2 June, 15 cases were confirmed, prompting a WHO PHEIC. No vaccine or treatment exists.

Between 1-9 June 2026, the SOH-PPR-GVL project (GVTC, Gorilla Doctors, WWF Uganda; World Bank Pandemic Fund via FAO, WHO, UNICEF) deployed a rapid One Health response across seven border districts: Bundibugyo, Ntoroko, Bunyangabu, Kabarole, Kanungu, Kasese, Rukungiri. Teams trained VHTs/CHEWs, ran risk communication at schools, markets, facilities, radio talk shows, Point of Entry assessments, and One Health meetings.

The intervention reached 5,000+ people, including 700 VHTs/CHEWs, 1,903 pupils in Kanungu, and 100 cultural leaders.

Four findings emerged: misinformation undermined trust in three districts; risk perception was low community-wide; IPC infrastructure was inadequate everywhere; porous border crossings remained unmonitored. One district's O.H team had not met since November 2025.

This shows that pre-existing community infrastructure enables swift outbreak pivoting. Preparedness in transboundary biodiversity hotspots is fundamentally social, not only technical. Sustained investment in community health workers, coordination, and border surveillance is the most cost-effective path to preventing zoonotic spillovers

**Session 3: Pandemic Preparedness & Prevention / 524****One Health Systems Readiness Assessment in Croatia, Ghana and Nigeria: Development of an Assessment Tool for Evidence-informed Policy Making**

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While One Health (OH) principles are widely recognized, countries have yet to fully embed them into operational governance systems, slowing progress on coordinated efforts to address zoonotic transmission, AMR, and environmental health. The “KOHSRA” tool was developed to assess national readiness for OH implementation and to identify governance and policy gaps, and piloted in Croatia, Ghana, and Nigeria.

KOHSRA’s protocol includes the following steps: desk review of legal and policy frameworks and stakeholder mapping; multisectoral deliberative workshops; consensus-based scoring across five domains; and consolidation through SWOT analysis and priority setting.

All pilot countries showed a certain level of OH integration, but institutionalization remained uneven. Nigeria had a strategic plan and coordinating unit but still faced coordination challenges. Ghana had an active technical working group and draft policy, but limited legal mandates and data integration. Croatia had strong surveillance and EU-aligned regulations but lacked a formal OH policy and coordinating body. Common gaps included absent OH policies and budgets, fragmented data, weak knowledge translation, limited community engagement, and inadequate evaluation.

Strengthening OH governance requires formalized policies, sustainable financing, interoperable data systems, and institutionalized coordination. KOHSRA offers a practical framework for diagnosing system gaps and guiding policy dialogue and investment.

**Session 3: Pandemic Preparedness & Prevention / 516****Stigmatization in the context of a pandemic: Implications for pandemic preparedness****Author:** Samuel Tomczyk<sup>1</sup>**Co-authors:** Dafina Danqa<sup>1</sup>; Jule Menzinger<sup>2</sup>; Rena Stranzky<sup>2</sup>; Marlene Mühlmann<sup>2</sup>; Isabel Kuhlmann<sup>2</sup>; Carlotta Alpers<sup>2</sup><sup>1</sup> *Universitätsmedizin Rostock*<sup>2</sup> *Universität Greifswald***Corresponding Author:** samuel.tomczyk@med.uni-rostock.de

**Background:** The COVID-19 pandemic was not only a global health crisis but also a catalyst for stigmatization processes. In the BMFTR-funded “StiPEX” project, we integrate qualitative and quantitative methods to conduct a comprehensive analysis of these stigmatization processes and develop anti-stigma guidelines and toolkits for pandemic preparedness.

**Methods:** Through systematic reviews, we compiled existing measurement tools for assessing stigmatization related to COVID-19, infectious diseases as well as interventions in this context.

To evaluate individual experiences of stigmatization during the pandemic, we conducted interviews with various target groups: 1) healthcare workers, 2) psychotherapists, 3) the general public, and 4) patients with Long COVID. The interviews were analyzed using qualitative content analysis.

In addition, we conducted a representative population survey in three waves to assess public and internalized stigma regarding COVID-19-related topics (e.g., COVID-19 infection, Long COVID).

**Results / Discussion:** Based on our findings, we derive practical recommendations for action and communication aimed at policymakers and public health professionals. The goal is to shape and promote anti-stigma efforts and stigma research in the context of infectious diseases over the long term and foster pandemic preparedness.

**Session 4: Climate Change, Ecosystems, Environmental Pollution / 468****Wastewater based surveillance of fungi and mycotoxins****Author:** Christian Wurzbacher<sup>1</sup>**Co-authors:** Anna Uchaikina<sup>1</sup>; Sarah Devliegere<sup>2</sup>; Siedrid De Baere<sup>2</sup>; Siska Croubels<sup>2</sup><sup>1</sup> *Technical University of Munich*<sup>2</sup> *Ghent University***Corresponding Author:** c.wurzbacher@tum.de

Wastewater and environmental surveillance (WES) has emerged as a powerful tool for monitoring population-level health and environmental exposure. Although WES is widely used for viruses, bacteria and chemical biomarkers such as pharmaceuticals and illicit drugs, its potential for tracking fungal communities and associated mycotoxins within a One Health framework has not been fully realized.

This study surveys the mycobiome and mycotoxins in urban wastewater. Over the course of one year, composite wastewater samples were collected from wastewater treatment plants serving three German cities of different sizes. The composition of the fungal community was characterized through high-throughput sequencing. In parallel, a SPE-UHPLC-MS/MS method was used for the targeted quantitative analysis of selected mycotoxins.

The wastewater mycobiome across all sites showed low seasonality and a dominance of yeasts and yeast-like members. Fungal pathogens and mycotoxin producers were rare if present at all, and most of the mycobiome members were derived from human or environmental sources. Thirteen out of the 35 screened mycotoxins were detected, with several being identified consistently across all seasons, including enniatins, tenuazonic acid, and more site-specific toxins. Combining wastewater mycobiome with targeted mycotoxin quantification provides a promising approach for environmental surveillance of fungal risks in urban ecosystems.

**Session 4: Climate Change, Ecosystems, Environmental Pollution / 386****ZOOM: A glimpse into antimicrobial resistance in Berlin through wastewater surveillance****Author:** Víctor Hugo Jarquín-Díaz<sup>1</sup>**Co-authors:** Alexander Bartel<sup>2</sup>; Marie Bartels<sup>2</sup>; Julia Bitzegeio<sup>2</sup>; Uta Boeckelmann<sup>3</sup>; Sofia Kirke Forslund-Startceva<sup>4</sup>; Sonja Garske<sup>2</sup>; José Horacio Grau<sup>5</sup>; Sebastian Hoppe<sup>2</sup>; Markus Landthaler<sup>4</sup>; Nico Linzner<sup>3</sup>; Ulrike Löber<sup>4</sup>; Martin Meixner<sup>5</sup>; Claudia Ruscher<sup>2</sup>; Daniel Sagebiel<sup>2</sup>; Vera Schumacher<sup>3</sup>; Emanuel Wyler<sup>4</sup>; Frederik Zietzschmann<sup>3</sup><sup>1</sup> *Max-Delbrück-Center for Molecular Medicine in the Helmholtz Association (MDC), Berlin, Germany*<sup>2</sup> *Unit for Surveillance and Epidemiology of Infectious Diseases, State Office for Health and Social Affairs (SOHSA)*<sup>3</sup> *Laboratory of Berliner Wasserbetriebe, Berliner Wasserbetriebe*<sup>4</sup> *Max-Delbrück Center for Molecular Medicine in the Helmholtz Association (MDC)*<sup>5</sup> *Amedes Medizinische Dienstleistungen GmbH***Corresponding Author:** vhjarquind@gmail.com

Antimicrobial resistance (AMR) is a growing threat to public health, and the European Union has introduced AMR monitoring regulations for wastewater (WW). Here, we implemented a multi-method approach to assess prevalence and circulation of antibiotic resistance genes (ARGs) in the Berlin metropolitan area. In October 2025, we collected samples from the Schönerlinde WW treatment plant. We profiled the resistome using two methods: i) metatranscriptomic molecular assessment and ii) culture-enriched metagenomics. Metatranscriptomic profiles revealed ARGs conferring resistance to various antibiotics in the influent samples. While these genes were co-abundant with environmental bacteria, they were also detected in plasmids common to clinically relevant bacteria. Although ARGs profiles showed a marked reduction following treatment, bacteria such as *Escherichia coli* and *Pseudomonas* could be enriched in selective media in samples taken before and after WW treatment, indicating their persistence in a viable state after treatment. The abundance of *E. coli* matched the overall occurrence of ARGs, while different *Pseudomonas* species correlated with clinically relevant genes. We demonstrate the potential of metagenomic approaches in AMR surveillance and the value of culture-enriched metagenomics in assessing the dissemination of clinically relevant ARGs through wastewater. This information is crucial for developing strategies to limit the spread of AMR in urban and suburban areas.

**Session 4: Climate Change, Ecosystems, Environmental Pollution / 518****Epidemiology of malaria in Germany, 2017 to 2025: insights from statutory surveillance data, air traveller incidences and time series analysis**

**Authors:** Achim Doerre<sup>None</sup>; Franziska Hommes<sup>None</sup>; Julia Enkelmann<sup>None</sup>; Stefanie Bovermann<sup>None</sup>

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Malaria is mainly imported into Germany from endemic areas abroad, despite available chemoprophylaxis. We describe notified *Plasmodium* infections from 2017–2025 to identify epidemiological patterns and inform prevention.

We analysed notified infections in Germany (2017–2025) and describe demographics, species, exposure countries and travel purpose. Incidence/100,000 air travellers was estimated using German Federal Statistical Office air passenger data. Temporal trends and seasonality were assessed using negative binomial regression with Fourier terms, adjusting for the COVID-19 pandemic phases.

In total, 7,439 cases were reported (366 in 2020–1,001 in 2023). Median age was 38 years, 69% were male, 12% were children and 84% had *P. falciparum*. Among cases with travel purpose, 64% were visiting friends and relatives (VFR), 19% tourists and 7% occupational travellers. Most infections were acquired in Sub-Saharan Africa (95%), mainly Nigeria, Cameroon and Ghana. Traveller incidence was highest for Sierra Leone (1,038), Cameroon (666) and Guinea (605). No overall temporal trend was observed ( $p=0.56$ ), but annual and semi-annual seasonality were identified. Case counts declined during the COVID-19 pandemic. Among VFR-travellers, case counts increased over time ( $p=0.041$ ).

The majority of malaria cases notified in Germany occur among travellers returning from West Africa and VFR-travellers, highlighting the need for targeted prevention and improved uptake of chemoprophylaxis.

**Session 4: Climate Change, Ecosystems, Environmental Pollution / 384****The pollen microbiome at the interface of air pollution and allergic sensitization: Genomic and NO<sub>x</sub>-responsive traits of *Pantoea agglomerans*****Author:** Lisa-Marie Streb<sup>1</sup>**Co-authors:** Andrea Ghirado<sup>2</sup>; Silvia Gschwendtner<sup>1</sup>; Jörg-Peter Schnitzler<sup>2</sup>; Michael Schlöter<sup>1</sup><sup>1</sup> *Research Unit Comparative Microbiome Analysis, Helmholtz Munich*<sup>2</sup> *Research Unit Environmental Simulation, Helmholtz Munich***Corresponding Author:** lisamarie.streb@helmholtz-munich.de

Pollinosis is a significant public health burden, with its rising prevalence linked to environmental factors like traffic-related air pollution (e.g. Nitrogen Oxides (NO<sub>x</sub>)) and climate change. The ability of pollen allergens to induce allergic sensitization depends on the co-delivery of non-allergenic adjuvants like bacterial lipopolysaccharides (LPS) and virulence factors, that promote Th2 polarization over allergy-protective Th1 responses. However, the genetic basis of this process is unknown. While NO<sub>x</sub> itself acts as an adjuvant by enhancing inflammation, it remains unclear whether frequent NO<sub>x</sub> exposure additionally enhances the adjuvant activity of pollen-associated bacteria by altering microbial traits related to LPS and virulence. We performed genomic characterization of *P. agglomerans* 11\_6 isolated from *Artemisia vulgaris* pollen. Genome analysis detected several virulence factors, incl. proteases, T6SS effectors and hemolysin that might contribute to allergic sensitization. Except for two T6SS effectors and three LPS/EPS biosynthesis genes, virulence factors are highly conserved among *P. agglomerans* from different habitats. Transcriptome analysis of NO<sub>x</sub>-treated *P. agglomerans* 11\_6 showed induction of RpoE-mediated envelope stress response pathways and altered expression of LPS, EPS and biofilm genes. This work provides a first basis for a One Health perspective on the link between air pollution, pollen microbiomes and allergic sensitization in urban environments.

**Session 4: Climate Change, Ecosystems, Environmental Pollution / 515****Improved Climate Characterisation and Persistence of West Nile Virus Risk in Europe based on regional climate model projections and Machine Learning****Author:** Fuseini Yakubu<sup>1</sup>**Co-author:** Laurens M. Bouver<sup>2</sup><sup>1</sup> *Climate Service Center Germany, Helmholtz-Zentrum Hereon*<sup>2</sup> *Climate Service Center Germany (GERICS), Helmholtz-Zentrum Hereon***Corresponding Author:** fuseini.yakubu@hereon.de

West Nile virus is expanding across Europe under climate change, yet continental projection studies largely focus on outbreak probability while providing limited information on suitability persistence or geographic velocity. We use an XGBoost framework to predict WNV outbreak probability at NUTS3 resolution across Europe using E-OBS observations, ECDC outbreak records (2010-2024), and a bias-adjusted EURO-CORDEX CMIP6 ensemble under SSP1-2.6 and SSP3-7.0. Unlike previous studies relying primarily on regional climate means, our framework represents climate using transmission-relevant thermal indices together with percentile-based spatial descriptors that better characterize intra-regional climate distributions. Prospective validation on unseen outbreak seasons (2023-2024) demonstrates strong temporal generalization, yielding ROC-AUCs of 0.87 to 0.91. Future projections indicate substantial northward expansion under SSP3-7.0 but limited expansion under SSP1-2.6. Beyond conventional probability maps, we introduce a persistence classification distinguishing sporadic, emerging, persistent, and endemic hotspot regions. This reveals increasing suitability across central Europe, while some southern hotspots exhibit reduced persistence consistent with temperatures exceeding thermal optimums. Under SSP3-7.0, the northern suitability frontier advances by ~43 to 55 km per decade vs. near-stable conditions under SSP1-2.6, providing an interpretable framework for public health adaptation.

**Session 5: Public Health I / 477****Watching the buzzzz: Public, media and knowledge attention to mosquito-borne disease risk in Europe****Author:** Maria Eugenia Degano<sup>1</sup>**Co-authors:** Isabelle Marie Kramer<sup>2</sup>; Aidin Niamir<sup>1</sup><sup>1</sup> *Senckenberg Gesellschaft für Naturforschung*<sup>2</sup> *Goethe University Frankfurt***Corresponding Author:** eugenia.degano@senckenberg.de

Mosquito-borne disease risk is becoming increasingly visible in Europe, but countries are not experiencing or communicating this risk in the same way. Understanding how this risk is reported and framed matters because media coverage can shape public awareness, information-seeking behaviour, and support for preparedness. Here, we investigate how public, media and knowledge-seeking attention differs between countries with locally acquired mosquito-borne diseases (France, Italy and Spain) and countries where risk is emerging (Germany, Austria and Switzerland). The analysis focuses on two systems: the invasive tiger mosquito/Aedes-borne disease system and native Culex-borne disease system. We use Google Trends to assess public search interest, Media Cloud to examine media attention and framing, and Wikipedia pageviews to capture knowledge-seeking behaviour. The window covers January 2010 to December 2025, enabling comparison of seasonal patterns, attention peaks and cross-country differences. We expect to identify how attention varies across countries, whether peaks align across data sources, and how mosquitoes and mosquito-borne diseases are framed in relation to public health, climate change, invasive species, nuisance, surveillance, control, prevention and governance. By analysing attention as part of preparedness, this work contributes to a One Health understanding of mosquito-borne disease risk in Europe and may inform targeted communication and policy responses.

## Session 5: Public Health I / 383

**When does forecasting become actionable? Real-time vs. seasonal prediction of *Aedes aegypti* abundance****Author:** Gaëlle Sehi<sup>1</sup>**Co-authors:** Solomon Birhanie<sup>2</sup>; Volodymyr Minin<sup>3</sup>; Michelle Brown<sup>2</sup>; Daniel Parker<sup>4</sup><sup>1</sup> University of California Irvine; Institute of Epidemiology and Social Medicine, University of Münster<sup>2</sup> West Valley Mosquito and Vector Control District<sup>3</sup> University of California Irvine Donald Bren School of Information and Computer Sciences, Department of Statistics<sup>4</sup> University of California Irvine, Joe C. Wen School of Population and Public Health; University of California Irvine, Epidemiology & Biostatistics, Public Health**Corresponding Author:** gsehi@uci.edu

*Aedes aegypti*, the primary vector of dengue, Zika, and chikungunya, has expanded its range globally, increasing demand for spatially granular forecasting tools to support vector control. Short-term forecasts can inform near-term surveillance and intervention planning; however, few studies evaluate real-time, site-level approaches operationally. Using weekly trap data from 2017–2023 across sites in Southern California, with Earth observation and meteorological predictors, we evaluated two forecasting problems: (1) out-of-sample prediction of the 2023 seasonal abundance trajectory using models trained on 2017–2022 data, and (2) two-week-ahead, site-level forecasts in a rolling framework. We compared a generalized additive model (GAM), Random Forest (RF), and spatial Random Forest (RFsp) against appropriate baselines. Seasonal models captured broad abundance patterns but failed to reproduce an unusually sharp late-summer peak; performance was sensitive to year-to-year variation poorly explained by environmental predictors. Rolling forecasts updated with recent observations substantially outperformed seasonal predictions; RFsp performed best, with spatial features improving accuracy and spatial coherence. Short-term forecasts using recent site-level data offer more reliable operational guidance than seasonal outlooks, particularly where *Ae. aegypti* is newly established. Findings inform the design of surveillance systems and forecast updating protocols for vector control.

**Session 5: Public Health I / 448****Emergence of Northern European TBE virus strains in Central Europe**

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Tick-borne encephalitis (TBE) is the most important tick-borne viral disease in Europe. The virus belongs to the family “Flaviviridae”. Using genetic analyses strains from different geographic origin can be identified and characterized.

During the last years TBE virus strains were isolated and genetically characterized. The whole genomes of the isolated virus strains were sequenced and compared to the comprehensive TBE virus data base of the National TBE Reference laboratory.

During 2012 to 2025 a total of >400 TBE virus strains from >100 TBE natural foci in Germany and Europe were isolated and genetically characterized. Among these up to 2017, the TBEV strains identified had their origin mainly in Eastern European countries. Since 2018, a total of nine TBE viruses from different foci could be detected and characterized which were genetically closely related to TBE virus strains from Scandinavia, Russia and Latvia.

Northern European TBE virus strains are increasingly detected in Central Europe. Reasons for their increased emergence may be changes in bird migration which finally establish new TBE natural foci. So far, only limited data on their pathogenicity and the efficacy of the commercially available TBE vaccines against these emerging strains are available. The new Northern European TBE virus strains might be one reason for the increase of reported human TBE cases in Central Europe.

**Session 5: Public Health I / 453****Burden and Awareness of Zoonotic Tuberculosis in Africa: A Systematic Review and Meta-analysis****Author:** Guash Abay Assefa<sup>1</sup>**Co-authors:** Olga Hovardovska<sup>2</sup>; Torben Heinsohn<sup>2</sup>; Lydiah Kisoo<sup>1</sup>; Yaw Awuku-Larbi<sup>1</sup>; Brit Häcker<sup>2</sup>; Berit Lange<sup>3</sup><sup>1</sup> *Department of Epidemiology, Helmholtz Centre for Infection Research, Braunschweig, Germany; PhD Programme "Epidemiology" Braunschweig-Hannover, Germany*<sup>2</sup> *Department of Epidemiology, Helmholtz Centre for Infection Research, Braunschweig, Germany*<sup>3</sup> *Department of Epidemiology, Helmholtz Centre for Infection Research, Braunschweig, Germany; German Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Braunschweig, Germany***Corresponding Author:** guashabay.assefa@helmholtz-hzi.de

Zoonotic tuberculosis (zTB), caused by animal-associated members of the *Mycobacterium tuberculosis* complex (MTBC), remains a public health problem in Africa. Understanding both the burden of zTB and community awareness is essential for zTB interventions.

Systematic reviews and meta-analyses were conducted following PRISMA guidelines. Studies reporting laboratory-confirmed MTBC species were included to estimate the proportion of zTB among confirmed TB cases, while studies reporting awareness of zTB were included to assess knowledge levels. Random-effects models were used to pool proportions, and subgroup analyses were performed by region and population group.

Fifty-seven studies were included in the proportion review and 38 studies in the awareness review. The pooled proportion of zTB among confirmed TB cases was 2.8% (95% CI: 1.8–4.3;  $I^2=88.8\%$ ). Higher proportions were observed in Northern Africa (15%) and occupationally exposed populations (11.8%) than in hospital-based populations (2.4%). Pooled awareness of zTB was 25.8% (95% CI: 16.7–37.7;  $I^2=96.7\%$ ). Awareness was highest among abattoir workers (57.5%) and lower among herdsmen (22.7%), smallholder farmers (20.9%), and pastoralists (18.0%). Regional awareness ranged from 12.9% in Southern Africa to 34.4% in Western Africa.

The coexistence of measurable zTB burden and low awareness among high-risk populations highlights the need for public education, strengthened surveillance, and improved species-level diagnostics.

**Session 5: Public Health I / 411****The TBE natural focus landscape structure in Eastern Bavaria as basis for computer-assisted surveillance in Monid-Habitrack**

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Tick-borne encephalitis (TBE) is the most important tick-borne viral disease in Europe. The TBE virus circulates in small areas, called natural foci, between ticks and small mammals. The exact dynamics of the transmission cycle are still not well known. Although the existence of natural foci was established 90 years ago, still no knowledge on the basic structural components of TBE natural foci exists.

During the last 15 years TBE foci were studied according to locations of infection of TBE patients in the two districts, Amberg and Schwandorf, in Eastern Bavaria. The locations were sampled for ticks and collected ticks were tested for TBE virus by PCR and in positive ticks virus isolation in cell culture was conducted. The landscape structure of confirmed TBE natural foci was documented.

A total of 25 TBE foci in the two districts could be identified. Most of the TBE foci have a size of about 50 × 100 m and have the structure of a forest meadow surrounded on three or four sides from mixed forest. In three-sided foci the open side was always to the north or to the west.

Based on these data in the Monid-Habitrack project the identified foci will be studied in detail using drone analyses and data will be transferred to develop KI based models for the identification of TBE natural foci independent of TBE infection of patients as a tool of improved surveillance of tick-borne infections.

**Session 5: Public Health I / 474****Contact heterogeneity in network reconstruction: evaluating synthetic graph generators for rabies transmission modeling****Author:** Inez Derkx<sup>1</sup>**Co-authors:** Mac Hyman<sup>2</sup>; Nakul Chitnis<sup>1</sup><sup>1</sup> *Swiss TPH*<sup>2</sup> *Tulane University***Corresponding Author:** inez.derkx@swisstph.ch

Canine rabies remains endemic across much of Africa and Asia, causing approximately 59,000 human deaths annually. Network-based models can capture the heterogeneous contact patterns driving rabies transmission, but generating synthetic networks that faithfully reproduce empirical contact structures and downstream transmission dynamics is non-trivial. We compared five network generators (Erdős-Rényi model (ERM), stochastic block model (SBM), degree-corrected stochastic block model (DCSBM), spatially explicit network construction algorithm (SENCA), and Newman clustered random-graph generator (NCRG)) against an empirical free-roaming dog contact network from N'Djamena, Chad, as well as four additional dog-proximity datasets. We evaluated each generator's reproduction of six topological summary measures and of outbreak dynamics under SEIR (Susceptible-Exposed-Infectious-Recovered) and SIS (Susceptible-Infectious-Susceptible) simulations. The DCSBM most consistently reproduced empirical topology across all networks. Under SEIR dynamics with a short infectious period, as in rabies, the DCSBM also most closely matched empirical case patterns, underscoring the joint importance of degree and community structure in shaping outbreak patterns. Under SIS dynamics with longer infectious periods, generator-specific differences in outbreak dynamics attenuated, suggesting that capturing network heterogeneity matters more for fast-burning pathogens like rabies than for slower-spreading ones.

**Session 6: Education, Implementation / 481****One Health Detectives: Gamification as a Strategy for Inclusive Zoonosis Education in Latin American Schools****Author:** LUCIANA PIRES<sup>1</sup>**Co-authors:** Bianca dos Santos Adão<sup>2</sup>; Carla Passinato Aldigueri<sup>2</sup>; Felipe Veloso Bazestão<sup>2</sup>; Giovana Fiori Gava<sup>2</sup>; Isabela da Silva Santos<sup>2</sup>; Jaqueline Klein do Amaral<sup>2</sup>; Jaqueline Ribeiro Urbanik<sup>2</sup>; Juliana Luiza Unger<sup>2</sup>; Kellyn Dal Lago Ferreira<sup>2</sup>; Lucas Mendes de Paula<sup>3</sup>; Lyohana Colere Fledler<sup>4</sup>; Marlise Lima Brandão<sup>2</sup>; Milena Irina Iaremenco Pscheidt<sup>5</sup>; Natasha dos Santos Osorio<sup>3</sup>; Renan Z. Raia<sup>2</sup>; Silvia Carina Gerzvolff<sup>6</sup><sup>1</sup> *Federal University of Parana (UFPR) and Centro Universitario Autonomo do Brasil -UniBrasil*<sup>2</sup> *Centro Universitário do Brasil - UniBrasil*<sup>3</sup> *Centro Universitario Autonomo do Brasil - UniBrasil*<sup>4</sup> *Centro Universitario Autonomo do Brasil - UniBrasil*<sup>5</sup> *Centro Univeristario Autonomo do Brasil - unIbarsil*<sup>6</sup> *Centro Universitario Autonomo do Brasil***Corresponding Author:** lucianasapires@gmail.com

**Introduction:** Giardiasis is a prevalent zoonosis in Latin America and a suitable model for teaching One Health. Integrating these concepts into primary education requires inclusive and active methodologies, particularly in vulnerable schools. **Objective:** To report a gamified educational intervention for giardiasis prevention and assess its feasibility and replication potential. **Methodology:** A 14-member interdisciplinary undergraduate team (Veterinary Medicine, Nursing, Environmental Sciences, and Education) conducted an intervention with 120 students aged 12–14 years, including students with Autism Spectrum Disorder (ASD). Activities included storytelling (“One Health Detectives”), a recycled-material quiz, treasure hunt, and a giant human board game designed for peer replication. Feasibility was assessed using SWOT analysis. **Results:** Inclusive strategies supported ASD student participation through sensory and collaborative activities. The peer-to-peer model increased engagement among participants. SWOT analysis identified interdisciplinarity and proactivity as strengths, while time limitations and school bureaucracy were challenges. Expansion opportunities and quantitative evaluation were highlighted. Low-cost materials demonstrated high cost-effectiveness. **Conclusion:** Gamification combined with peer education is an inclusive, affordable, and replicable approach for promoting One Health in vulnerable Latin American settings.

**Session 6: Education, Implementation / 464****Interdisciplinary collaboration as individual and institutional learning: results from an interdisciplinary qualitative study****Author:** Susanne Ress<sup>1</sup>**Co-authors:** Amelie Lisa Arnecke<sup>2</sup>; Nadja Kutschke<sup>3</sup>; Reiner Ulrich<sup>2</sup><sup>1</sup> *Technische Universität Berlin*<sup>2</sup> *Universität Leipzig*<sup>3</sup> *Charité - Universitätsmedizin Berlin***Corresponding Author:** [ress@tu-berlin.de](mailto:ress@tu-berlin.de)

This report is based on a research project on interdisciplinary learning in the context of One Health. Interviews with researchers in human and veterinary medicine, ecology, biology and social sciences were conducted to better understand how interdisciplinary collaborations are initiated, structured, and maintained, and to what extent researchers perceive their interdisciplinary collaboration experiences as opportunities for professional development and learning. Main findings show that individual motivations and communication skills are key to successful collaboration in the context of insufficient institutional structures, processes, and regulations. On the one hand, the imbalance between individual-level and institutional-level enabling factors reifies disciplinary and gendered hierarchies in science. At the same time, interdisciplinary collaborations contributed significantly to learning about these inequalities in generating crucial One-Health-related knowledge, particularly relevant for wildlife surveillance and protection projects. The findings also provide insights for transdisciplinary collaborations.

**Session 6: Education, Implementation / 514****Developing One Health Competencies Through Interprofessional Co-Design: A Community Case Study of Veterinary Doctoral Students Collaborating with Pre-Service Science Teachers****Author:** Ulrich Hobusch<sup>1</sup><sup>1</sup> *University College of Agricultural and Environmental Education***Corresponding Author:** ulrich.hobusch@haup.ac.at

Veterinary doctoral training equips researchers to produce specialized One Health knowledge, but rarely to communicate it to non-specialist audiences, collaborate across disciplines, or translate it into societal contexts—the capacities One Health requires. This community case study examines how five veterinary PhD students experienced a 13-week interprofessional course co-designing school teaching materials with pre-service science teachers, using a Two-Eyed Seeing-informed transfer framework. Qualitative content analysis of 114 segments from learning journals, a focus group, and videographic recordings combined deductive NEOH competency coding with inductive coding. Because scientific work is strongly shaped by English-dominated discourse, several participants found explaining their research in accessible native-language terms a substantive learning experience. Across all cases, seven situated communication practices developed, including conveying zoonotic risk without unnecessary alarm. Participants also described an epistemological shift, recognizing educational research as a legitimate knowledge system beyond “p-values and graphs.” Notably, 32.5% of coded material fell outside the NEOH framework, including 20 unprompted implementation proposals, suggesting current models underspecify the strategic action competence such co-design activates. Interprofessional collaboration can help researchers move from producing One Health knowledge toward enabling its use in society.

**Session 6: Education, Implementation / 500****One Health Educators, Practitioners, and Advocates: Engaging Veterinary Social Workers in Canadian Veterinary Care****Author:** Haorui Wu<sup>1</sup><sup>1</sup> *School of Social Work, Faculty of Health, Dalhousie University***Corresponding Author:** haorui.wu@dal.ca

As emerging interdisciplinary professionals, veterinary social workers (VSWs) integrate social work practice into veterinary medicine, addressing the interconnected health and well-being of humans, animals, and the environment. Although VSWs are gaining increasing attention worldwide, little empirical research has documented veterinary professionals' awareness and familiarity with VSWs, their perceived practice impacts of engaging VSWs in clinical settings, and their anticipated barriers to hiring VSWs. Focusing on Canadian veterinary care, this study aims to investigate the veterinary practitioner's necessities and challenges of engaging VSWs in clinical teams. An online survey with both quantitative and qualitative questions grounded in the One Health framework was completed by 110 veterinary professionals across Canada. While over 90% of participants are familiar with VSW's contributions and over 80% are willing to hire VSWs, financial challenges and professional reorganization are the primary barriers to implementation. From the perspectives of veterinary professionals, survey results highlight the VSW's contributions to occupational health, client grief-loss support, client-practitioner relations, and the prevention of animal abuse and family violence in clinic and public education settings. These contributions further illustrate the VSW's roles as One Health educators, practitioners, and advocates for building healthy and resilient human-animal bonds.

**Session 6: Education, Implementation / 350****An educational intervention to reduce mosquito breeding habitats: The PuMo pilot project**

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The number of locally transmitted infections caused by mosquito-borne diseases such as West Nile fever and dengue fever increase in Germany and Europe. Children are one of the vulnerable groups at risk from these diseases. The PuMo pilot project tests whether an educational campaign for children in schools reduces the number of mosquito breeding sites on school grounds. For this purpose, a face-to-face session with scientists is being planned, and a book containing materials is being developed, which pupils and their teachers can use independently to explore the topic in greater depth.

The educational campaign covers knowledge about insects, mosquitoes and their breeding habitats, as well as the One Health concept. The latter is used to illustrate to the children the dichotomy between the removal of small water bodies for the purpose of vector control and the provision of small water bodies as drinking water for other animals or for rainwater collection. Emphasis is placed on explaining to the children how mosquito breeding sites can be reduced and controlled whilst simultaneously providing drinking stations and water sources to animals such as other insects and birds.

The awareness campaign is accompanied by entomological surveys and the completion of socio-ecological questionnaires by the children to document the effectiveness of the intervention and the potential of the children to act as knowledge mediators within the school community and into their family environments.

**Session 6: Education, Implementation / 376****Strengthening One Health Governance through Transparent and Systematic Evidence-Informed Policy-Making: Lessons from Croatia, Ghana and Nigeria**

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Global health threats, including pandemics, AMR, zoonotic diseases, and climate change, underscore the interdependence of human, animal, and environmental health. Although the One Health (OH) approach is increasingly recognized, translating evidence into effective policies remains complex. The OH-EVI project aimed to strengthen knowledge translation capacities and support evidence-informed policymaking across diverse national contexts.

Using the WHO EVIPNet four-stage methodology, OH-EVI worked in Croatia, Ghana, and Nigeria, where multisectoral stakeholders identified priority OH policy challenges through situational analyses. Systematic reviews informed Evidence Briefs for Policy (EBPs) outlining policy options and implementation considerations. Policy dialogues were then convened to contextualize the evidence, assess feasibility, and identify implementation priorities.

Main topics addressed in the EBPs were strengthening zoonoses surveillance (Croatia), integrating surveillance and preparedness systems (Ghana), and addressing AMR (Nigeria). Common barriers identified were fragmented governance, weak coordination, siloed data systems and workforce. The EBPs discuss context-adapted options for strengthening these areas, providing an evidence base to support the countries' OH operationalization.

OH-EVI demonstrates how structured evidence synthesis, stakeholder engagement, and policy dialogue can advance OH governance and support implementation of evidence-informed solutions.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 538****AiRisk - A Network on the Risk Airborne Transmission of Infections**

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Livestock farming is a major source of antibiotic-resistant bacteria (AMR bacteria), which can be spread through the air, facilitating their transmission. However, it is not yet fully understood how these bacteria, as well as zoonotic pathogens such as *Staph aureus* or *Francisella tularensis*, are transmitted to humans, animals and plants. Current models do not adequately account for rising infection and resistance rates. This knowledge gap hinders effective prevention, surveillance and response to such threats. The AiRisk project aims to close this gap by investigating a new transmission route: dust. Dust could represent an important link between the various domains of human, animal and environmental health (One Health) and mediate the spread of antibiotic-resistant bacteria and zoonotic pathogens from agriculture into the environment, to wildlife and to humans. Dust particles from livestock farming represent a complex biological mixture containing microorganisms and their resistance genes (the resistome<sup>1</sup>). In recent years, it has become apparent that this dust is not merely a waste product of livestock farming, but a significant reservoir for antimicrobial resistance and potential pathogens. The spread of these dust particles, as well as the survival capacity of the microbes associated with them, are therefore of epidemiological relevance and have a direct impact on public health.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 427****FLUPREP: A National Early-Warning System for Emerging Influenza Threats**

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Influenza A viruses (IAVs) frequently breach species barriers, posing a persistent pandemic threat. Mitigating this threat requires systems capable of detecting high-risk strains at the animal–human interface and implementing targeted countermeasures before human spillover occurs. Although international frameworks like TIPRA or IRAT routinely assess IAV risks, data gaps and lengthy consensus-building can hamper national preparedness. Hence, Germany needs its own rapid early warning system for emerging influenza threats.

To fill this gap, we established FLUPREP, a national One Health consortium funded by the BMFTR. Uniting six core partners—RKI, Charité Berlin, FLI, University of Münster, University Medical Center Freiburg, and LGL—FLUPREP seeks to proactively characterize IAVs emerging at the human–animal interface to generate comprehensive risk profiles that drive evidence-based pandemic preparedness. Central to FLUPREP is an integrated experimental pipeline that evaluates pandemic potential by quantifying key risk factors, such as human-type receptor specificity, airborne transmissibility, and resistance to diverse immune barriers. The measured data are then converted into a pandemic risk score calibrated against contemporary and historical IAVs. Graded risk score thresholds will act as actionable triggers, enabling local, state, and federal authorities to scale response measures from routine surveillance to emergency protocols, securing Germany’s future pandemic resilience.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 540****GUARDIAN – One Health Surveillance for Predicting Antimicrobial Resistance: An AI-Based Pilot Project in Central Hesse**

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Antimicrobial resistance (AMR) is a global health challenge that requires collaboration across human, animal, and environmental health. Yet surveillance data are often collected and analysed separately, limiting the early detection of emerging resistance patterns and transmission pathways.

GUARDIAN is developing an AI-enabled One Health platform for the Central Hesse region. It integrates genomic, microbiological, clinical, epidemiological, environmental, and geospatial data to support predictive AMR surveillance.

The project focuses on two contrasting scenarios: colistin resistance, closely associated with veterinary antimicrobial use, and carbapenem resistance, which is particularly relevant in human healthcare and hospital settings. Analysing both scenarios across sectors will help identify genetic links, transmission pathways, and regional patterns of spread. Data-driven models will be used to assess potential future developments.

An interactive dashboard will visualise AMR trends and support public-health decision-making. By combining expertise from human and veterinary medicine, bioinformatics, public health, and environmental sciences, GUARDIAN aims to demonstrate how integrated One Health data and artificial intelligence can strengthen regional AMR surveillance.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 531****The Respiratory Mucus Barrier in Zoonotic Influenza Transmission****Author:** Maximilian Rohde<sup>None</sup>**Co-authors:** Fiona Riegel<sup>1</sup>; Cosmin Stefan Butnarusu<sup>2</sup>; Daniel Lauster<sup>3</sup>; Christian Sieben<sup>1</sup><sup>1</sup> *Helmholtz Center for Infection Research*<sup>2</sup> *University of Turin*<sup>3</sup> *Freie Universität Berlin***Corresponding Author:** maximilian.rohde@helmholtz-hzi.de

The spread of a highly pathogenic avian influenza virus (H5N1) in wild birds and poultry has increased global concern regarding the potential for zoonotic and pandemic spread of emerging influenza A viruses (IAV). Before viruses can infect epithelial cells, they must overcome the respiratory mucus barrier. Mucus in the airways can trap particles and promote their removal via mucociliary clearance. Beyond this physical barrier function, mucins can interact with viral surface proteins, influencing virus mobility, attachment, and infectivity. To study how respiratory mucus influences IAVs, we have collected native respiratory mucus from relevant host species. We have developed standardized biophysical and biochemical methods to quantify the penetration of IAVs through species-specific mucus. This allows us to analyze the penetration behavior and subsequent infection potential of multiple IAV strains. The findings indicate that mucus exerts a differential effect on the penetration efficiency and infectivity of avian- and human-origin influenza strains. These observations suggest that respiratory mucus plays a multifaceted role. Our research revealed that virus-mucus interactions enhance the efficacy of virus infection by potentially protecting against viral degradation. Research into the interaction between respiratory viruses and native mucus samples is crucial to understand how the mucus barrier influences the emergence and transmission of influenza viruses.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 541****Tracking and containing endemic and emerging tick-borne human and animal infections by integrating citizen science, knowledge-supported proactive surveillance, and AI-enhanced modelling in a changing climate (TAC-TICKS)****Authors:** Martin Pfeffer<sup>1</sup>; Martin Wikelski<sup>2</sup>; Lidia Chitimia-Dobler<sup>3</sup>; Sophie Schneitler<sup>4</sup>; Markus Scholz<sup>5</sup><sup>1</sup> *Institute of Animal Hygiene and Veterinary Public Health, Leipzig University*<sup>2</sup> *Max Planck Institute for Animal Behavior, Radolfzell*<sup>3</sup> *Fraunhofer Institute of Immunology, Infection and Pandemic Research (IIP), Penzberg*<sup>4</sup> *Institute of Medical Microbiology, Immunology and Hygiene, University Clinic Cologne*<sup>5</sup> *Institute for Medical Informatics, Statistics and Epidemiology (IMISE), Leipzig University***Corresponding Author:** pfeffer@vetmed.uni-leipzig.de

Increasing human and animal case numbers and geographical spread of ticks and tick-transmitted diseases show their pandemic potential in the Northern hemisphere due to changing environmental conditions. In TAC-TICKS, experts from human/veterinary medicine, Public Health, animal ecology and biomathematical modelling join forces to elucidate this development and improve pandemic preparedness. We extend our 15+ year database of monthly native tick activities and pathogens through hotspot sampling, stratified Citizen Science and comprehensive pathogen characterization. To study tick and pathogen spread, we utilize our extensive *Hyalomma*- and *Rhipicephalus* tick database, TBE virus genomes, bird and large mammal migration, and related tick pathogen burden. We evaluate the potential vaccination's impact on disease epidemiology and containment serologically with the example of TBE.

Combining newly generated and publically available data, we develop climate-aware prediction models for tick activity and disease prevalence that inform efficient surveillance concepts and strategies. Partnering with district and state health departments and empowering communities, we aim to establish effective pre-pandemic surveillance and countermeasures. Our proactive approach, encompassing known bacterial, viral and protozoal pathogens as well as emerging unknown pathogens (“Pathogen X”) using a suitcase lab and nanopore sequencing in the field, thus strengthens public health in the face of evolving environmental threats.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 431**

**\*TrophicHealth: Effects of fertilization on AMR and zoonotic pathogen accumulation along the trophic chain – towards a One Health perspective in circular agriculture\***

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TrophicHealth investigates how circular agriculture may facilitate the transmission of antimicrobial resistance (AMR) and zoonotic pathogens among livestock, environmental reservoirs, and agricultural systems, and how ecosystem resilience may interrupt these transmission cycles. Using a pan-microbiome framework combined with metagenomic analyses, we identify pathogens, AMR determinants, and antimicrobial peptide-producing microorganisms that may contribute to the stabilization of microbial communities and suppression of harmful microbes. We characterize microbial communities in the field across soil, wastewater, plants, and potential animal vectors, and experimentally assess the spread and mitigation of AMR and pathogens using controlled mesocosm systems. By elucidating the ecological mechanisms underlying microbial transmission and resilience in circular agriculture, TrophicHealth aims to improve surveillance of AMR and zoonotic pathogens in agricultural environments and food production systems, while identifying potential mitigation strategies. The project will contribute to a One Health approach by supporting evidence-based surveillance and risk assessment efforts by institutions such as the Robert Koch Institute and the Umweltbundesamt, and by providing knowledge to support veterinarians and farmers in the transition toward sustainable and safe livestock farming.

**Session 7: Research consortia on the topic of “Pandemic prevention and response within a One Health framework” / 539****WNVcombat - Combatting WNV through an integrated One Health approach**

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West Nile virus (WNV) is an emerging mosquito-borne virus that can cause neuroinvasive infections and death in humans. WNV has emerged as a growing concern in Europe, with its spread and the intensity of outbreaks being exacerbated by climate change. WNV is transmitted by mosquitoes that are native to Europe and occur in high densities in urban environments. Numerous bird species can amplify the virus and infect mosquitoes during their blood-meal acquisition. Berlin, as one of the largest metropolitan areas in Europe, is of particular concern due to the establishment of WNV and due to the urban heat island effect, with increasing heat extremes and an increasing number of tropical nights, which enhance WNV amplification.

WNVcombat seeks to understand local maintenance and amplification of WNV at fine temporal and spatial scales. Objectives include analyzing how urban bird species assemblages affect WNV infection rates in mosquitoes with consequences for human infection risk under current and climate change scenarios, assessing human exposure, and developing a web-based tool featuring an epidemiological model as a warning platform. The project will produce high-resolution risk maps and test nature-based interventions, refining strategies in other WNV-endemic regions. WNVcombat is crucial for public health, veterinary services, and environmental agencies, providing guidelines for public health responses and a comprehensive communication strategy.

**Session 8: Public Health II / 452****Salmonella Bochum outbreak in children caused by chocolate hazelnut spread, Germany 2026**

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In February 2026, the Robert Koch Institute (RKI) identified an outbreak in Germany caused by the rare *Salmonella* (*S.*) *enterica* subspecies *enterica* serovar Bochum. Descriptive epidemiology and exploratory patient interviews were performed. The RKI compared outbreak cases (n=12) and participants from the RKI panel “Health in Germany” aged 2–15 years (n=197) regarding consumption of chocolate hazelnut spreads in the 3 days before symptom onset or completing the questionnaire. Findings were shared with food safety authorities, prompting on-site inspections and food sample analyses. The outbreak involved 42 cases; predominantly children in eastern Germany. More males than females were affected (64 % vs. 36 %). The National Reference Center assigned all isolates with sequence data (n=27) to the same genomic cluster by cgMLST analysis. In exploratory patient interviews 12 of 14 cases (86 %) stated consumption of a specific brand of chocolate hazelnut spread. The case-control-study confirmed a strong association between consumption and being a case (odds ratio: 93 [95% confidence interval: 21-663]). Genome analysis proved the presence of the outbreak strain and other serovars in the product. In April 2026, the implicated product was recalled and the outbreak stopped. Trustful collaboration and rapid communication of findings between infection control and food safety authorities enabled fast identification of the infection vehicle and initiation of control measures.

## Session 8: Public Health II / 530

**Cross-species transmission of *Strongyloides fuelleborni* at the human–animal interface****Authors:** E. Nosková<sup>None</sup>; Barbora Pafco<sup>None</sup>**Co-authors:** B. Červená; F. S. S. Niatou; G. Nzayisenga; J. Nziza; K.J. Petrželková; L. Dumas; L. Ilík; R.M. Sá; V. Audrlický**Corresponding Author:** barafrikacar@gmail.com

Strongyloidiasis is a neglected tropical disease, yet the epidemiology of *Strongyloides fuelleborni* remains poorly understood despite its broad host range and evidence of zoonotic potential. We investigated parasite circulation among humans, domestic dogs, and non-human primates (NHPs) across African countries (Central African Republic, Guinea-Bissau, Uganda, and Rwanda). Samples were screened by qPCR, and positive samples were characterized using high-throughput sequencing. *Strongyloides fuelleborni* predominated in NHPs and was also frequently detected in humans and dogs. Identical parasite haplotypes were shared among sympatric hosts, providing evidence of parasite exchange at the human–animal interface. The high prevalence and genetic diversity of *S. fuelleborni* in dogs suggest they may act as important bridge hosts, while infections detected in breastfed puppies support vertical transmission. In contrast, mountain gorillas and dogs from Uganda and Rwanda showed low infection prevalence and no evidence of parasite sharing. Although *S. stercoralis* was absent from mountain gorillas, a fatal infection in a gorilla infant was associated exclusively with *S. fuelleborni*, highlighting its potential pathogenicity in endangered wildlife. Our findings demonstrate contrasting transmission patterns across African ecosystems and emphasize the importance of One Health surveillance to better understand parasite transmission at the wildlife–human–domestic animal interface.

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**Prevalence and associated factors of severe mpox in Mbarara City, southwestern Uganda, October 2024–May 2025****Author:** Justine Wobusobozi<sup>1</sup>**Co-authors:** Martha.D. Nalweyiso<sup>1</sup>; Michael Mutegeki<sup>1</sup><sup>1</sup> *Field epidemiologist***Corresponding Author:** justinewobusobozi@uniph.go.ug

**Background:** In October 2024, Mbarara City, Uganda, experienced sustained mpox transmission, with Nyamityobora Ward being disproportionately affected. Data on factors associated with severe disease were limited. We determined the prevalence and factors associated with severe mpox in Nyamityobora Ward during October 2024–May 2025.

**Methods:** We conducted a cross-sectional study using active case finding among suspected mpox cases in Nyamityobora Ward from April to May 2025. Disease severity was assessed using an adapted Mpox Severity Scoring System (MPSSS) and dichotomized as severe versus non-severe. Modified Poisson regression was used to identify associated factors.

**Results:** Of 106 mpox cases identified, 62 (59%) had severe disease. The median age was 29 years and 55% were female. HIV co-infection (adjusted prevalence ratio [aPR] 1.8, 95% CI 1.2–2.7), delayed care-seeking >5 days (aPR 1.5, 95% CI 1.1–2.1) and sex work (aPR 1.4, 95% CI 1.0–2.0;  $p = 0.045$ ) were independently associated with severe mpox.

**Conclusion:** Severe mpox was common and strongly associated with HIV co-infection, delayed care-seeking and sex work. Integrating mpox screening into HIV services and promoting early care-seeking and implementing targeted interventions for sex workers may reduce severe outcomes during outbreaks.

## Session 8: Public Health II / 476

**RBM-targeted amplicon sequencing coupled with the WasteCov pipeline for rapid surveillance of SARS-CoV-2 lineage groups in municipal wastewater**

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Wastewater-based epidemiology is a tool for population-level surveillance when clinical testing capacity is limited. We developed a rapid amplicon sequencing workflow targeting the spike RBM, together with WasteCov, our custom bioinformatic pipeline for SARS-CoV-2 lineage surveillance in wastewater. This method combines one-step RT-PCR amplification with targeted sequencing. Candidate assignments are constrained using contemporaneous epidemiological priors derived from clinical reports of globally circulating variants. WasteCov performs mapping, variant calling and lineage estimation using an updated UShER matrix operating through two modes: a Freyja-adapted mutation-centric approach and “sign\_mol”, a haplotype-aware mode that detects RBM molecular signatures, estimates their frequencies and assigns them to lineage groups. We applied the framework to 76 weekly composite wastewater samples from Thessaloniki, Greece, covering the Delta-to-Omicron transition (W47-2021 to W18-2022) and subsequent Omicron diversification (W48-2022 to W48-2023). Our approach captured major replacements, including the BA.1-to-BA.2 shift, the transition from BA.5/BA.2.75 to XBB descendants, and the rise of BA.2.86, while remaining informative at low prevalence. Wastewater-derived profiles were concordant with 28803 genomes from clinical surveillance and, in some cases, detected variant emergence earlier. This approach supports timely, cost-efficient variant surveillance, extendable to other viruses.

## Session 8: Public Health II / 469

## Transcriptomic Profiling of Intestinal Organoids Infected with *Mycobacterium avium* subsp. *paratuberculosis*

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*Mycobacterium avium* subsp. *paratuberculosis* (MAP) causes Johne's disease in ruminants and is a discussed zoonotic contributor to Crohn's disease, making it a key One Health target. However, epithelial responses to MAP remain poorly understood. We used human ileal organoids to characterize the epithelial transcriptomic response to MAP infection. Organoids were microinjected with MAP or PBS, treated with forskolin, or left untreated, and analyzed by RNA sequencing over 48 hours.

Culture-associated transcriptional drift was the dominant driver of gene expression, with patterns suggesting a progressive loss of metabolic and digestive programs and increased chromatin remodeling activity, likely masking pathogen-specific responses. Although forskolin facilitated microinjection, it transiently activated inflammatory and stress pathways, limiting its suitability as a neutral experimental aid. While MAP infection did not induce significant single-gene expression changes, pathway analyses suggested preservation of enterocyte-associated metabolic programs, indicating that MAP partially counteracts culture-induced drift. This may promote intracellular persistence and contribute to mucosal pathology in both Johne's disease and Crohn's disease.

These findings identify temporal drift and experimental perturbations as major confounders in organoid infection models and provide a framework for improving studies of enteric pathogens at the human-animal interface.

**Session 8: Public Health II / 393****Successes & Outlook of the Integrated Genomic Surveillance: importance of computational infrastructure for pandemic preparedness in Germany****Author:** Silver A. Wolf<sup>1</sup>**Co-authors:** André Götze<sup>1</sup>; Anne-Christine Schulz<sup>2</sup>; Benjamin Tittmann<sup>3</sup>; Caroline Roschek<sup>1</sup>; Felix Hartkopf<sup>1</sup>; Hanna Buck<sup>2</sup>; Hannah Maatsch<sup>1</sup>; Katrin Kremer-Flach<sup>3</sup>; Marie Lataretu<sup>1</sup>; Maximilian Driller Povill<sup>1</sup>; Nadine Litzba<sup>2</sup>; Paul Wolk<sup>1</sup>; Stephan Fuchs<sup>1</sup>; Torsten Houwaart<sup>1</sup>; Torsten Semmler<sup>2</sup>; Yusra Seyam<sup>1</sup>; the IGS system development group<sup>4</sup><sup>1</sup> *Genome Competence Centre (MF1), Robert Koch Institute, Berlin, Germany*<sup>2</sup> *Integrated Genomic Surveillance Coordination (IGS), Robert Koch Institute, Berlin, Germany*<sup>3</sup> *Surveillance and Electronic Reporting and Information System (FG32), Robert Koch Institute, Berlin, Germany*<sup>4</sup> *Robert Koch Institute, Berlin, Germany***Corresponding Author:** wolfs@rki.de

The Integrated Genomic Surveillance (IGS) enables monitoring of 30 prioritized pathogen groups with increased public health importance. Genomic information from notifiable cases detected throughout Germany are collected at the Robert Koch Institute (RKI). Here, sequences are integrated with case data of the German reporting system to provide a comprehensive overview on the national emergence, spread, outbreaks and evolution of pathogens, enabling the foundation for infectious disease monitoring and prevention.

Our results highlight multiple major successes of the IGS project, including establishing a centralized infrastructure for storing, analyzing and maintaining surveillance data. As part of this, the IGS Datawarehouse (IGS DWH) represents the basis for combined investigations of genomic and epidemiological data. Interacting with this are bioinformatic analyses, dashboards, interactive visualizations and automated reports. To provide these, we have developed specialized computational workflows (IGS Bioinformatics Toolkit & Omnifluss) for high-throughput genomic analyses of multi-pathogen data sets.

To date, the IGS has been used to analyze more than 1.2 million pathogen samples, including a majority of SARS-CoV-2 sequences, supporting infectious disease monitoring on a national scope. We hereby highlight the importance of establishing scalable, robust and maintainable infrastructure such as the IGS for pandemic preparedness and intersectoral One Health projects.

**Session 9: Biodiversity, Landuse & Food Systems / 445****Inactivation of pathogens in contaminated cattle manure by Lactic Acid Fermentation and in biogas plants****Author:** Hannah Halm<sup>1</sup>**Co-authors:** Sören Wölke<sup>1</sup>; Ines Lehnert<sup>2</sup>; Thorben Schilling<sup>2</sup>; Heike Köhler<sup>3</sup>; Charlotte Schröder<sup>1</sup>; Michael Eschbaumer<sup>1</sup>; Hendrik Scheinemann<sup>4</sup><sup>1</sup> *FLI Riems*<sup>2</sup> *Uni Hohenheim*<sup>3</sup> *FLI Jena*<sup>4</sup> *WIS Munster***Corresponding Author:** hannah.halm@fli.de

In case of a notifiable animal disease like paratuberculosis or salmonellosis, the manure is contaminated and a cause for spread of infections. Before it can be safely used as fertilizer it must be disinfected. This can be performed using heat measures, chemical disinfectants or long-term storage. All these measures entail economic, ecological and logistical problems. The aim of project was to evaluate lactic acid fermentation (LAF) on laboratory scale as an alternative disinfection method.

For this, cattle manure was spiked with different kinds of pathogens like *Salmonella Typhimurium*, *Mycobacterium avium* ssp. *paratuberculosis* (MAP) or Food-and-mouth disease virus (FMDV). Fermentation was initiated by adding different carbohydrate sources (CHO) to the manure and creating anaerobic conditions. The samples were incubated at 21 °C. The microbial shift was determined using culturing methods or titration.

All tested pathogens were inactivated by LAF dependent on the CHO-source within a few weeks. The combination of sucrose and oats revealed the best results in all cases. Altogether, LAF is a valuable option for disinfecting cattle manure.

Another issue is the retention time of pathogens in biogas plants. To investigate this, the contents of fermenters are spiked on lab scale with pathogens and their retention time is monitored. Results are still pending.

**Session 9: Biodiversity, Landuse & Food Systems / 513****Operationalising One Health in regional food systems****Author:** Hannah Schöneberg<sup>1</sup>**Co-authors:** Melanie Speck<sup>2</sup>; Stefan Stiene<sup>2</sup>; Julia Heinz<sup>2</sup>; Kirsten Reichardt<sup>2</sup>; Robin Becker<sup>2</sup>; Tim Stelzner<sup>3</sup>; Martin Atzmueller<sup>4</sup>; Antje Risius<sup>5</sup><sup>1</sup> *University of Göttingen*<sup>2</sup> *University of Applied Science Osnabrück*<sup>3</sup> *Osnabrück University*<sup>4</sup> *Osnabrück University & German Research Center for Artificial Intelligence (DFKI)*<sup>5</sup> *University of Göttingen & University of Applied Science Fulda***Corresponding Author:** hannah.schoeneberg@uni-goettingen.de

Food systems are central interfaces of human, animal and environmental health. They shape nutrition, food security, animal welfare, biodiversity, climate impacts and supply-chain resilience. Yet operationalising One Health in regional food systems remains difficult, as indicators, cross-stage relations and data gaps are often unclear. This work develops a conceptual, data-oriented, and relational modelling framework for applying One Health to the food system of Lower Saxony, Germany, using pesticide use as a case. It maps value chains from production to consumption and waste, and links actors, products, flows, infrastructures, governance and health- and sustainability-related outcomes. Domains include consumer and occupational health, animal health and welfare, nutrient flows, water quality, land use, biodiversity, greenhouse gas emissions and resilience. The methodology combines value-chain and indicator mapping, data assessment and ontology-based modelling. Statistical, administrative, spatial and qualitative data are assessed with respect to availability, resolution, accessibility, interoperability and modelling relevance. Entities and relationships are represented using an ontology-based model and formalised via a graph-based structure capturing complex network relationships. The framework translates One Health into a regional food-system model and supports scenario analyses, vulnerability assessments, policy information and decision support for sustainable food systems.

**Session 9: Biodiversity, Landuse & Food Systems / 425****Impact of oil palm plantation use on the gut microbiome of Malaysian macaques****Author:** Miriam Simon<sup>None</sup>**Co-authors:** Nurul Iza Adrina Binti Mohd Rameli; Ulrike Rolle-Kampczyk<sup>1</sup>; Norsyahida Arifin<sup>2</sup>; Martin von Bergen<sup>1</sup>; Nadine Ruppert<sup>3</sup>; Anja Widdig<sup>4</sup><sup>1</sup> *UFZ Helmholtz*<sup>2</sup> *Universiti Sains Malaysia*<sup>3</sup> *Southeast Asia Biodiversity Research Institute & Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences*<sup>4</sup> *Universität Leipzig***Corresponding Author:** miriam.simon@uni-leipzig.de

Some wildlife species in SE Asia have partly adapted to human-modified agricultural landscapes, including southern pig-tailed macaques (*Macaca nemestrina*) which regularly forage in oil palm plantations. Our previous research suggests that their plantation use is associated with adverse health effects, but the underlying mechanisms remain unclear. Because the gastrointestinal tract is a key interface between environment and host health, this project investigates how pesticide exposure through plantation foraging alters the gut microbiome of wild pig-tailed macaques. We hypothesize that microbiome composition and function is associated with plantation use and changes with pesticide treatments. To do so, we collected 287 faecal samples of 30 individuals from two groups over 12 months in Segari Melintang Forest Reserve, Peninsular Malaysia, including targeted sampling before and after two pesticide treatment events. Microbiome composition and function will be analysed using 16S rRNA gene and shotgun metagenomic sequencing. By investigating how agricultural practices shape the microbiome of a wildlife species living at the human–environment interface, this study adopts a One Health perspective, highlighting the gut microbiome as a potentially sensitive indicator of contamination and providing insights that can inform both wildlife conservation and more sustainable agricultural management.

**Session 9: Biodiversity, Landuse & Food Systems / 398****Trends and Geographical Distribution of Snakebite Cases in Uganda, 2020–2024: An Analysis of National Surveillance Data****Author:** Martha Dorcas Nalweyiso<sup>1</sup>**Co-authors:** Aminah Namwabira<sup>1</sup>; Benon Kwesiga<sup>1</sup>; Emmanuel Obuya<sup>2</sup>; Fred Isaasi<sup>1</sup>; Justine Wobusobozi<sup>1</sup>; Patricia Eyu<sup>1</sup>; Richard Migisha<sup>1</sup>; Rio Lexus Ario<sup>1</sup><sup>1</sup> *Uganda National Institute of Public Health*<sup>2</sup> *Ministry of Health***Corresponding Author:** nmartha@uniph.go.ug

Snakebites are a neglected public health challenge in Uganda. Adverse outcomes of snakebites include paralysis, disfigurement, limb amputation and death. Uganda's Neglected Tropical Diseases Master Plan, 2023-2027, aligns with WHO's target to reduce snakebite mortality and disability by 50% by 2030. We described trends and distribution of snakebite cases in Uganda from 2020–2024 to inform snakebite prevention and control strategies.

We analysed snakebite cases reported through DHIS2 from January 2020–December 2024 defining cases as snakebite injuries with puncture wounds regardless of envenomation status. Annual incidence per million population was calculated by age, sex, year, and district using UBOS projections. Trends were assessed using Mann-Kendall and rainfall-incidence associations using Spearman correlation.

A total of 50,011 cases were reported (mean incidence 250/million). Adults  $\geq 20$  years had the highest incidence (320/million), and females had slightly higher incidence than males (250 vs 240/million,  $p < 0.001$ ). Annual incidence ranged 210–260/million with no significant trend ( $p = 0.22$ ). West Nile and Acholi regions consistently exceeded 1,000/million. Rainfall showed a weak negative correlation with incidence, significant only in 2022 ( $\rho = -0.22$ ,  $p = 0.008$ ).

Snakebites disproportionately affect adults and females, with the highest burden in Northern Uganda. Strengthening community awareness and antivenom access could reduce morbidity and guide resource allocation.

**Session 9: Biodiversity, Landuse & Food Systems / 467****Landscape Change Shapes Bat Communities and Viral Dynamics in the Colombian Amazon****Author:** Gabriela Aliaga-Samanez<sup>1</sup>**Co-authors:** Marina Reyne<sup>1</sup>; Maricruz Jaramillo<sup>2</sup>; Luz Dary Acevedo-Cendales<sup>2</sup>; Erika García-Bonilla<sup>3</sup>; Mailyn González<sup>3</sup>; Sarah H. Olson<sup>2</sup>; Lucy Keatts<sup>2</sup>; German Forero<sup>2</sup>; Mathieu Pruvot<sup>4</sup>; Alex Greenwood<sup>1</sup><sup>1</sup> *Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany*<sup>2</sup> *Wildlife Conservation Society*<sup>3</sup> *Instituto de Investigación en Recursos Biológicos Alexander von Humboldt, Bogota, Colombia.*<sup>4</sup> *University of Calgary, Faculty of Veterinary Medicine, Calgary, Canada***Corresponding Author:** samanez@izw-berlin.de

Habitat degradation is a key driver of zoonotic disease emergence. In Colombia, deforestation along the Amazonian agricultural frontier is transforming ecosystems and potentially increasing pathogen spillover risk. Bats are important reservoirs of viruses with zoonotic potential, while also providing key ecosystem services. Within the Volkswagen Foundation-funded SIMPEL project, which investigates pathogen dynamics across land-use change gradients (objective 4), we sampled a subset of 431 bats across a deforestation gradient in Guaviare, Colombia, using ecological, molecular, and metagenomic approaches to evaluate the effects of environmental disturbance on diversity, viral prevalence, and virome composition. Preliminary results showed that habitat disturbance was associated with reduced bat richness, abundance, and occurrence probability. Hantavirus prevalence tended to be higher in recently deforested areas, whereas orthobunyavirus prevalence was highest in conserved forests, with no significant habitat-related difference. Metagenomic analyses revealed a diverse virome, including herpesviruses, papillomaviruses, adenoviruses, polyomaviruses, and coronaviruses, and ongoing analyses are evaluating virome patterns across gradients of habitat degradation. These findings suggest that land-use change influences both bat communities and viral circulation at the human-wildlife interface.

**Session 10: AMR I / 394****Biofouling in membrane bioreactors decreases the retention of free plasmid DNA carrying antibiotic resistance genes****Author:** Robin Starke<sup>1</sup>**Co-authors:** Arthur Leon<sup>2</sup>; Kristin Kerst<sup>2</sup>; Patric Wommer-Röhm<sup>2</sup>; Valentin Conrad<sup>2</sup>; André Lerch<sup>2</sup>; Thomas U. Berendonk<sup>2</sup>; Uli Klümper<sup>2</sup><sup>1</sup> *TU Dresden, Institute of Hydrobiology*<sup>2</sup> *TU Dresden***Corresponding Author:** robin.starke@tu-dresden.de

Membrane bioreactors (MBRs) effectively remove bacteria during wastewater treatment. Less is known about removal of extracellular DNA, including ARG-carrying plasmids, which are far smaller. If released into the environment, such plasmids can persist for months and be taken up by bacteria via transformation. During MBR operation, biofilm forms on membranes and may act as an additional barrier to free DNA. We hypothesized that thicker biofouling layers increase free-DNA retention.

To test this, we quantified retention of three ARG-carrying plasmids of different sizes using model MBRs at different biofouling stages. Biofilm thickness was continuously monitored by optical coherence tomography. At defined growth stages, free plasmid DNA was spiked into the feed and retention quantified by ddPCR.

Without biofouling, retention ranged from 95.4% to 99.9%, depending on the plasmid. Contrary to our hypothesis, plasmid passage increased up to 6.3-fold in MBRs with early biofilm formation. Retention declined further at later stages.

These findings suggest biofilm growth promotes preferential flow paths that facilitate plasmid migration through the membrane barrier by increasing local flux and reducing contact time. EPS may further reduce adsorption or electrostatic repulsion by occupying binding sites. Plasmid degradation and uptake did not play a significant role. This highlights that MBR anti-biofouling strategies, while increasing performance, also aid in retaining free AMR-plasmids.

**Session 10: AMR I / 433****Similar Wastewater Microbiomes, Distinct Resistomes: A Comparative Metagenomic Analysis of German and Nigerian Wastewaters from Diverse Sources****Author:** Chijioke Nsofor<sup>1</sup>**Co-authors:** Alan Elena<sup>2</sup>; Robin Starke<sup>2</sup>; Uli Klümper<sup>2</sup>

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Environmental contamination links antimicrobial resistance (AMR) across human, animal, and environmental compartments, but how wastewater source and infrastructure shape resistomes remains unclear. We used metagenomics to compare communities and resistomes in municipal wastewater in Germany and municipal, hospital, and slaughterhouse wastewaters in Nigeria. Bacterial communities showed limited separation (ANOSIM  $R=0.059$ ,  $p=0.278$ ), indicating a shared wastewater microbiome baseline. In contrast, resistomes differed significantly (PERMANOVA  $p=0.023$ ), showing that ARG profiles diverged more strongly than underlying communities. German samples showed a homogenized, diverse resistome ( $H'=2.15-2.25$ ), dominated by aminoglycoside, bacitracin, beta-lactam, and MLS genes. Nigerian samples showed greater heterogeneity and hotspots exceeding 2.0 log<sub>10</sub> relative abundance, driven by sulfonamide and tetracycline genes. Despite this divergence, 634 ARG subtypes (53.9%) formed a shared resistome core, while 375 variants were detected only in Nigerian samples. Co-occurrence networks linked *erm(B)* and *OXA-10* with opportunistic pathogen-containing genera such as *Acinetobacter*, *Klebsiella*, and *Pseudomonas*. These findings show that similar wastewater microbiomes can harbour distinct resistomes and identify wastewater source and infrastructure as determinants of environmental AMR distribution. Hotspots highlight the need for One Health surveillance that accounts for source-specific waste streams.

## Session 10: AMR I / 432

**Harmonized One Health surveillance of antimicrobial resistance and heavy metal tolerance in Baltic Sea surface waters and wild birds****Author:** Max Sittner<sup>None</sup>**Corresponding Author:** max.sittner@helmholtz-hioh.de

**Abstract.** Antimicrobial resistance (AMR) and heavy metal tolerance in aquatic and wildlife-associated bacteria are interconnected One Health challenges, yet harmonized cross-border data remain scarce. BALTIC-AMR addresses this gap through standardized longitudinal surveillance across Germany, Sweden, Estonia, and Poland, integrating surface-water and wild-bird sampling with culture-based isolation, phenotyping, genomics, and residue analysis. From 04/24–09/25, 1,346 isolates were recovered from water and wild birds, mainly comprising priority *Enterobacterales* and selected *Pseudomonadales*. Putative ESBL and arsenic tolerant phenotypes predominated, while carbapenem resistance was more frequent among water-derived isolates; zinc tolerance occurred rarely.

The same sampling framework also captured water-borne *Vibrio* spp. During the 2024 *Vibrio* season (06/24–10/24), 330 isolates were collected and sequenced to resolve phylogenetic diversity and screen for resistance and virulence determinants. Preliminary screening identified genes assigned to tetracycline and beta-lactam resistance classes, alongside efflux and lipid A modification markers. In parallel, residue analysis detected fluoroquinolone and tetracycline concentrations exceeding PNEC levels year-round in WWTP effluents.

Together, these data confirm environmental AMR occurrence and support phylogeny-aware One Health risk assessment in the Baltic Sea region.

**Session 10: AMR I / 501****Dual-Species Interactions with Intestinal Bacteria Drive Multi-Drug Resistance in Campylobacter****Authors:** Sangeeta Banerji<sup>1</sup>; Gudrun Holland<sup>2</sup>; Michael Laue<sup>2</sup>; Antje Flieger<sup>1</sup><sup>1</sup> Robert Koch Institut, FG11<sup>2</sup> Robert Koch Institut, ZBS4**Corresponding Author:** banerjis@rki.de

Campylobacter is a major foodborne pathogen. We investigated multidrug resistance (MDR) in clinical isolates from Germany (2010–2022) within the national surveillance program. A total of 6,950 single-colony isolates were phenotypically tested; 2,912 were genome sequenced and screened for antimicrobial resistance genes. MDR cultures were further analyzed for contaminating DNA and by scanning electron microscopy (SEM). We identified 451 (6.5%) isolates resistant to fluoroquinolones and macrolides; two *C. jejuni* isolates exhibited resistance to up to ten antibiotic classes. Unexpectedly, genome analysis revealed >10% *Enterococcus* DNA in these single-colony-derived samples. SEM confirmed coccoid bacteria interspersed with spiral Campylobacter. Subsequent purification separated fluoroquinolone-resistant but not macrolide-resistant Campylobacter from multidrug-resistant *Enterococcus*. Mixed-culture experiments demonstrated protection of Campylobacter against ribosome-targeting antimicrobials in the presence of *Enterococcus*. These findings indicate that apparent MDR in Campylobacter can arise from interspecies interactions rather than intrinsic resistance, highlighting the importance of a One Health perspective integrating microbial ecology into antimicrobial resistance surveillance.

**Session 11: Vaccines & Immunology / 369****Advancements in Chikungunya Virus Vaccines: Emerging Innovations and Future Directions****Author:** Jonas Schmidt-Chanasi<sup>None</sup>**Corresponding Author:** jonassi@gmx.de

Chikungunya virus (CHIKV) is re-emerging as a One Health threat at the human-vector-climate interface. WHO and ECDC data show major resurgence in 2025-2026, with large outbreaks in the Indian Ocean and the Americas and substantial autochthonous transmission in Europe, including 788 confirmed locally acquired cases in France and 384 in Italy in 2025. European evidence, indicates that once *Aedes albopictus* is established, transmission risk is shaped by vector distribution, seasonal abundance and mobility rather than temperature alone. Vaccine prevention has advanced rapidly. IXCHIQ, a single-dose live-attenuated vaccine, induces near-complete seroresponse, with neutralizing antibodies persisting in 95% of vaccinees 4 years after one dose; however, post-marketing safety signals, including serious neurologic adverse events and aseptic meningitis, have sharpened benefit-risk assessment, especially in older adults and people with chronic disease. VIMKUNYA, a single-dose recombinant virus-like-particle vaccine, achieved seroresponse in 98% of 12-64-year-olds and 87% of adults aged ≥65 years by day 22, with persistence for at least 6 months, offering a non-live alternative for adolescents and adults. Together, these data support risk-adapted vaccination embedded in integrated surveillance, vector control and climate-sensitive preparedness for travellers, outbreak-prone regions and newly exposed European settings

**Session 11: Vaccines & Immunology / 506****Zoonotic MPXV Clades Outpace Human-adapted Strain in Driving Disease and Shedding in a Nasal Respiratory-Infection Macaque model****Author:** Julia R. Port<sup>1</sup>**Co-authors:** Trenton Bushmaker<sup>2</sup>; Franziska K. Kaiser<sup>2</sup>; Heinz Feldmann<sup>2</sup>; Kyle Rosenke<sup>2</sup><sup>1</sup> *Laboratory of Transmission Immunology, Helmholtz Center for Infection Research, Braunschweig, Germany*<sup>2</sup> *Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, USA***Corresponding Author:** [juliarebecca.port@helmholtz-hzi.de](mailto:juliarebecca.port@helmholtz-hzi.de)

MPXV comparative biology after mucosal exposure remains unclear. We compared clades Ia (Zaire and Republic of Congo isolates), IIa, and IIb in a cynomolgus macaque respiratory infection model to assess disease, viral shedding, and immune responses. Mucosal infection caused milder, more localized disease than high-dose aerosol or intravenous models. Clade Ia (Zaire) and IIa produced stronger clinical symptoms and systemic immune activation, while clade IIb resulted in minimal illness and limited spread. Viral genomes persisted in skin lesions at later stages without evidence of active replication, suggesting tissue damage rather than long-term reservoirs. Presymptomatic shedding occurred across all clades, indicating potential transmission before lesion onset. However, clade IIb showed reduced shedding, with little to no oral or rectal virus detection. Clade IIb triggered the strongest dendritic cell activation, whereas clade Ia (Zaire) induced proliferating but functionally impaired antigen-presenting cells and weaker T-cell priming. Natural killer cell responses followed a similar pattern, with clade Ia (Zaire) showing weaker activation compared to other clades. A biomarker panel based on monocyte/eosinophil dynamics and cytokine ratios effectively distinguished clade IIb infections. These findings underscore the importance of clade-specific analysis for outbreak preparedness and One Health surveillance. Funding: intramural NIAID/NIH and INF of the Helmholtz Association.

**Session 11: Vaccines & Immunology / 508****Impacts of Respiratory Mucus on Influenza Virus Stability, Transmission, and Immune Interactions****Author:** Jailene Castillo<sup>None</sup>**Corresponding Author:** jpcas021@gmail.com

The remarkable zoonotic competence of Influenza A virus (IAV) warrants dedicated One Health vigilance. As the cause of four disruptive pandemics in the last century, pervasiveness into previously unaffected regions, and elevated incidence of human and animal infections, IAV continues to circulate across multiple host species. Most of the research on IAV entry has investigated interactions between viral proteins and cellular receptors. Still, the role of respiratory mucus in IAV transmission remains underexplored. As part of the Respiratory Mucus as a One Health Interface (ONEMUC) project, this study investigates the environmental stability of avian, human, and swine IAV strains in respiratory mucus under varying temperature, relative humidity, carbon dioxide concentration, and light spectrum conditions. Viral infectivity will be determined over time using TCID<sub>50</sub> assays and analyzed via exponential decay kinetics, revealing how mucus composition and environmental variables interact to modulate IAV persistence and zoonotic spillover risk. By systematically evaluating virus–mucus interactions across environmentally relevant conditions, this work aims to determine how respiratory mucus influences IAV persistence and transmission potential. These findings will provide a foundation for developing standardized assays to evaluate the environmental stability and potential zoonotic risk of emerging influenza viruses and viral variants under changing climatic conditions.

**Session 11: Vaccines & Immunology / 441****Differential innate immune activation following Puumala virus infection of human or reservoir host cells****Authors:** Marie Demuth<sup>1</sup>; Daniel Bourquain<sup>1</sup>**Co-authors:** Laura Enke<sup>1</sup>; Linah Chibrac-Ahad<sup>1</sup>; Stefanie Schuerer<sup>1</sup>; Andreas Nitsche<sup>1</sup>; Christine Luttermann<sup>2</sup>; Rainer G. Ulrich<sup>3</sup>; Lars Schaade<sup>1</sup><sup>1</sup> Centre for Biological Threats and Special Pathogens (ZBS), Robert Koch-Institute, Berlin, Germany<sup>2</sup> Institute of Immunology (IfI), Federal Research Institute for Animal Health, Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany<sup>3</sup> Institute of Novel and Emerging Infectious Diseases, Federal Research Institute for Animal Health, Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany**Corresponding Authors:** demuthm@rki.de; bourquaind@rki.de

Hantaviruses maintain persistent and asymptomatic infections in their mammalian reservoir hosts but can cause severe disease when transmitted to humans. In Europe, Puumala virus (PUUV) is the most important cause of human hantavirus infections. To investigate if hantavirus disease in humans is driven by an overreactive immune response, we aimed to compare PUUV replication and innate immune responses in human cells and cells of its natural host, the bank vole (*Myodes glareolus*).

Bank vole MGN-2-R cells and human A549 cells were initially shown to mount a comparable immune response after stimulation with double-stranded (ds)RNA. Following PUUV infection, the expression of interferon-induced MX1 and the viral nucleocapsid protein were quantified to monitor the dynamics of the innate immune response and viral replication. While PUUV replication was relatively strong in MGN-2-R cells, the immune response remained remarkably weak, despite a high viral load. In contrast, we observed a lower rate of PUUV replication and a much stronger induction of innate immunity in the human A549 cells. These profound differences were neither caused by lower amounts of viral dsRNA in MGN-2-R cells nor by PUUV-induced inhibition of the type I interferon signaling pathway.

These observed differences between PUUV infections in human and reservoir host cells could provide a possible explanation for the mostly asymptomatic course of the disease in the reservoir host and the pathogenicity in humans.

**Session 12: AMR II / 428**

## **Predicting environmental susceptibility to antimicrobial-resistant bacterial invasion using biodiversity and phylogenetic structure**

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Antimicrobial resistance (AMR) can spread through freshwater systems when resistant bacteria enter river biofilms, yet predicting which communities resist such introductions remains difficult. Biotic resistance theory predicts lower invasion success in more diverse communities, but whether this applies to natural biofilms under change is unclear.

We collected epilithic biofilms from 30 river sites across seven European countries and transferred them into standardized flumes. A model antibiotic-resistant *E. coli* was introduced, and its persistence quantified over 14 days. Diversity was characterized at collection, after acclimation, and maturation.

Using leave-one-out cross-validated models, we tested whether resistance could be predicted from diversity, phylogenetic structure, and diversity change during ecosystem transfer. In established flume biofilms, resistance was best explained by Shannon diversity and mean phylogenetic distance to the invader, supporting niche saturation and phylogenetic limiting similarity. During river-to-flume transfer, resistance depended on initial diversity and proportional diversity loss, indicating that community stability shapes invasion outcomes.

These findings show that freshwater biofilm invasion is structured by measurable community properties. Biodiversity and phylogenetic structure may help identify systems vulnerable to resistant bacterial colonization, supporting One Health surveillance and environmental AMR risk assessment.

**Session 12: AMR II / 457****One Health Surveillance of Antimicrobial Resistance in Integrated Constructed Wetlands****Author:** Gaia Streparola<sup>1</sup>**Co-authors:** Caolan Harrington<sup>2</sup>; Aila Carty<sup>2</sup>; Gillian Madigan<sup>3</sup>; Finola Leonard<sup>4</sup>; Catherine M. Burgess<sup>5</sup>

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Antimicrobial resistance (AMR) is a major One Health challenge linking human, animal and environmental health. Wastewater systems are recognised as reservoirs of antimicrobial-resistant organisms (AROs), facilitating their dissemination into natural ecosystems. Integrated Constructed Wetlands (ICWs) are nature-based wastewater treatment systems that combine water treatment with biodiversity enhancement; however, their role in mitigating environmental AMR remains poorly understood. This study investigates the occurrence and reduction of AROs within seven ICWs in Ireland treating municipal, agricultural, industrial and companion animal wastewaters. A two-year monitoring programme involved monthly sampling of influent and effluent waters. Target organisms included ESBL-producing, carbapenemase-resistant and fluoroquinolone-resistant Enterobacterales, *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. Isolates were identified by MALDI-TOF, characterised by antimicrobial susceptibility testing, and a subset of *Escherichia coli* isolates underwent whole-genome sequencing. To date, over 660 target organisms representing 20 bacterial species have been identified, with *E. coli* predominating across all sectors. Preliminary findings indicate reduced ARO numbers in effluent compared with influent samples. Multiple multidrug-resistant phenotypes were detected, and AMR profiles differed between wastewater sectors. The findings support ICWs as One Health tools for mitigating environmental AMR.

**Session 12: AMR II / 475****Comparison of antimicrobial resistance in conventional and organic pig production in Germany**

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We compared antimicrobial resistance in *E. coli* and the prevalence of cephalosporin resistant *E. coli* in organic and conventional fattening pigs and their derived meat in Germany. Boot sock samples were collected from 368 conventional and 131 organic pig farms. At retail, 430 and 306 samples from fresh conventional and organic pork, respectively, were collected. *E. coli* were isolated using routine methods and a predefined selective procedure targeting *E. coli* resistant to 3rd generation cephalosporins. Minimum inhibitory concentrations of 15 antimicrobials for *E. coli* were tested using broth microdilution, and resistance genes of selectively isolated *E. coli* were identified using whole genome sequencing. The proportion of completely susceptible *E. coli* was higher among isolates from organic farms (77.8 %) than from conventional farms (49.8 %,  $p < 0.05$ ). Likewise, the prevalence of cephalosporin-resistant *E. coli* was lower in samples from organic farms (13.0 % vs. 36.7 %). Significantly lower resistance rates were observed to ampicillin, tetracycline, trimethoprim and sulfamethoxazole among isolates from organic farms. Significant differences were neither found in resistance rates nor in the prevalence of cephalosporin-resistant *E. coli* in pork. These differences likely arise during the final phase of the fattening period or from the subsequent production steps (i.e. slaughter and processing). Further research is needed to elucidate the underlying reasons.

**Session 12: AMR II / 349****Prevalence of antimicrobial resistance bacteria in dust from piglet farms.**

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Dust can contain microorganisms that are both pathogenic and resistant to antimicrobials (AMR), which can potentially transmit airborne human pathogenic bacteria. Agriculture is one of the largest producers of primary particle matter, accounting for approximately 20% of global fine dust emissions. While it is known that the use of antibiotics in agriculture often results in antibiotic-resistant bacteria, the extent to which environmental factors can alter the bacterial composition of AMR containing bioaerosols, and the associated risks to humans and the environment, remain open research questions. In this study aerosols from and inside animal barns were investigated and both the size and density of fine dust particles in pig barns was measured. During summer a higher abundance of fine particles was seen, compared to winter. The prevalence of pathogenic microorganisms on those airborne particles was visualized and showed mature biofilm. Those biofilms consisted of more than 500 species and both gram-negative and gram-positive bacteria were found on dust, independent of the seasonality. Interestingly there was a strong correlation between AMR gene abundance and ESKAPE bacteria in air during winter compared to summer.

This study provides a strong insight into the composition of dust associated bacteria and shows the potential risk for humans and the environment.

**Session 12: AMR II / 496****Syntheses of KAP surveys on AMU and AMR in livestock across Ethiopia: implications for one health and informed decision**

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**Introduction:** Knowledge, Attitudes, and Practices (KAP) of livestock farmers and animal healthcare providers (AHCPs) regarding antimicrobial use (AMU) and antimicrobial resistance (AMR) are critical for advancing One Health and monitoring interventions.

**Methods:** We synthesized cross-sectional KAP surveys, 2020–2024 livestock owners and AHCPs using structured questionnaires on AMU and AMR.

**Results and Discussion:** Analysis of 15 surveys revealed widespread misuse driven by limited awareness (50%–94%) and neither to substandard and falsified pharmaceuticals, and weak regulation. The frequently used antimicrobials (AMs) were tetracyclines, aminoglycosides, penicillin, trypanocides and anthelmintics. Farmers commonly use AMs over the counter (44%–60%), prophylactically, sharing not uncommon, used leftovers, or incomplete courses, and limited knowledge of withdrawal times which may lead residues in food. AHCPs showed better knowledge but >56% reported inadequate practices. Both groups relied unnecessarily on AMs fuelling AMR, varying by species; reduced effectiveness and increased mortality, food safety risks, and zoonotic transmission. These call for improved access to quality veterinary AMs and regulation on their management, rapid diagnostics, enhanced surveillance, prudent use, continuing education for AHCPs, and application of generic or evidence-based interventions such as good husbandry, biosecurity, and disease prevention practices to mitigate AMR threats.

**Session 12: AMR II / 492****Molecular Surveillance of Extended-Spectrum Beta-Lactamase- and Carbapenemase-Producing *Escherichia coli* from one health interface in Ado-Ekiti, Southwestern Nigeria**

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Carbapenem-resistant and ESBL-producing *Escherichia coli* at the human-animal-environment interface represent an escalating One Health threat. This study characterised ESBL- and carbapenemase-producing *E. coli* from five One Health source compartments in Ado-Ekiti, Nigeria. Five hundred samples (n=100 per group) were processed; MALDI-TOF MS confirmed identifications; EUCAST 2021 susceptibility testing was performed; ESBL production was confirmed by DDST and Brilliance ESBL/CRE agar; PCR targeted five ESBL and five carbapenemase genes. Ten isolates (five MDR/CRE, five non-MDR controls) underwent Illumina WGS with SPAdes assembly, ECTyper serotyping, PubMLST MLST, AMRFinderPlus, and ABRicate/VFDB profiling. Of 69 confirmed livestock *E. coli*, 32 (46.4%) were ESBL producers; blaCTX-M predominated (75.0%). Carbapenemase genes were detected exclusively in cattle: OXA-48 (27.5%), VIM (12.5%), and IMP (7.5%). WGS revealed four sequence types — ST10 shared between cattle and pig non-MDR controls, ST196 in cattle MDR, ST226 in environment MDR, and ST348 in an environment control harbouring five AMR genes despite a non-MDR phenotype. The clinical isolate carried the highest AMR burden (18 genes including blaCTX-M-15 and blaOXA-1). These findings provide the first One Health genomic AMR dataset from Southwestern Nigeria, demonstrating that phenotypic surveillance underestimates true resistance burden and highlighting the urgency of WGS-based AMR surveillance.

**Session 13: Vectors II / 421****Not all West Nile virus lineages behave alike: dose-response differences between lineages 1 and 2**

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The globally distributed arbovirus West Nile virus (WNV) is expanding across Europe, with rising numbers of human cases and an increasingly broad geographic distribution. Transmitted primarily by *Culex* mosquitoes, WNV lineages 1 and 2 are pathogenic to humans, yet their differences in transmission dynamics remain unclear. As vertebrate hosts develop varying viremia, mosquitoes encounter a wide range of viral doses, which may influence transmission. Here, we investigated the dose-response differences between the lineages in *Cx. pipiens* biotype *pipiens*, *Cx. torrentium*, and *Aedes albopictus*. Mosquitoes were fed increasing titers of one strain of either WNV lineage, and infection and transmission were assessed after 14 days at 24°C. Lineage 2 required lower infectious doses while causing higher transmission. Notably, *Cx. torrentium* was identified as a highly competent vector for lineage 2. These findings highlight important differences between WNV lineages, improve our understanding of dose-dependent transmission, and therefore support refined risk assessments in Europe.

**Session 13: Vectors II / 526****Does viral persistence shape virus–virus interactions in mosquitoes?****Author:** Mine Altinli<sup>1</sup>**Co-authors:** Bianca Weber; Derin Topaktas; Jorn Brink; Bernhard Zibrat; Esther Schnettler<sup>2</sup><sup>1</sup> *Friedrich-Loeffler-Institute*<sup>2</sup> *Bernhard-Nocht-Institute for Tropical Medicine***Corresponding Author:** mine.altinli@fli.de

Mosquitoes host a wide diversity of insect-specific viruses alongside medically important arboviruses. While insect-specific viruses have been proposed as potential modulators of arbovirus transmission, the mechanisms underlying these interactions remain poorly understood, particularly in the context of persistent infections (long-term infection without clearance) that characterise most mosquito–virus associations.

Here, we investigated interactions between insect-specific alphaviruses and arboviruses in mosquito cell lines. Insect-specific alphaviruses reduced the replication of related arboviruses, especially when they were persistently infecting cells. No strong interference was detected in sequential or simultaneous co-infection settings. To explore potential underlying mechanisms, we compared acute and persistent insect-specific virus infections. Differences were observed at multiple levels, including changes in host transcriptomic profiles and microRNA expression. In addition, small RNA sequencing revealed antiviral RNAi responses targeting ISVs, with differences between acute and persistent conditions.

Overall, our results indicate differences in host responses associated with persistent insect-specific virus infections, which may influence subsequent arbovirus infections. Further work will be needed to determine how these responses contribute to interference phenotypes and whether they can be leveraged to better understand or modulate arbovirus transmission.

**Session 13: Vectors II / 355****Virus detection in *Culicoides* biting midges during the BTV-3 outbreak in north-west Germany 2024****Author:** Sophie Zeiske<sup>None</sup>**Co-authors:** Anja Voigt<sup>1</sup>; Doreen Werner<sup>1</sup>; Dorothee Scheuch<sup>2</sup>; Franziska Sick<sup>2</sup>; Helge Kampen<sup>2</sup>; Kerstin Wernike<sup>2</sup>; Martin Beer<sup>2</sup><sup>1</sup> *Leibniz-Centre for Agricultural Landscape Research, Muencheberg, Germany*<sup>2</sup> *Friedrich-Loeffler-Institute***Corresponding Author:** [sophie.zeiske@fli.de](mailto:sophie.zeiske@fli.de)

Bluetongue virus (BTV), Schmallenberg virus (SBV) and epizootic haemorrhagic disease virus (EHDV) are arthropod-borne viruses transmitted by biting midges and primarily affect domestic and wild ruminants. In Central Europe, the importance of biting midges as vectors increased after the emergence of BTV-8 in 2006 and SBV in 2011. Furthermore, in 2022, EHDV was detected for the first time in southern European regions. Outbreaks of BTV, SBV, or EHDV in livestock populations may cause animal suffering and economic losses due to management and control measures such as vaccination and trade restrictions. The aim of this study was to monitor the viruses present in the biting midge population during the severe outbreak of BTV serotype 3 in Germany. Biting midges were caught from April to September 2024 on 14 farms in north-west Germany. Of the trapped midges, 337,359 females were selected and sorted into 7,549 pools, with up to 50 individuals per pool. The pools were tested by PCRs for the genomes of SBV, BTV and EHDV. BTV-RNA was detected in a total of 1,359 pools (18.0%) and SBV-RNA in 402 pools (5.3%). None of the tested pools was positive for EHDV. In this study, we confirmed the ongoing circulation of SBV, as well as an extensive BTV circulation in the *Culicoides* fauna in north-west Germany in 2024. Both viruses were first detected in the biting midges in early summer and reached their highest levels in August.

**Session 13: Vectors II / 395****Experimental BTV-3 and BTV-8 infection of *Culicoides sonorensis* biting midges****Author:** Franziska Sick<sup>1</sup>**Co-authors:** Bernd Hoffmann<sup>1</sup>; Helge Kampen<sup>1</sup>; Martin Beer<sup>1</sup>; Sophie Zeiske<sup>1</sup>; Kerstin Wernike<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut***Corresponding Author:** franziska.sick@fli.de

Bluetongue virus (BTV) is the causative agent of a major livestock disease and it is transmitted by *Culicoides* biting midges between the ruminant hosts. The first recorded outbreak in Central Europe was caused in 2006/2007 by serotype BTV-8, leading to a major epidemic. In 2023, serotype BTV-3 emerged in the Netherlands and spread rapidly to neighbouring countries. Compared to the BTV-8 outbreak in 2006, the BTV-3 epizootic had a more severe clinical course and spread faster. To explore the possible causes of the different epidemiologies, we compared the replication properties of BTV-8 and BTV-3 in a laboratory colony of *Culicoides sonorensis* biting midges. The midges were orally infected with BTV-3 or BTV-8 via an infectious blood meal. Engorged females were either processed immediately or incubated for six days. Viral genome copies per individual midge were quantified using BTV-specific RT-qPCR. Replication was assessed using a cut-off derived from day-0 viral loads. Overall, 4.39% of the midges infected with BTV-3 replicated the virus, whereas a smaller proportion of midges infected with BTV-8 replicated the virus (3.44%). Moreover, oral infection with BTV-3 resulted in a significantly higher viral load in infected midges with demonstrated replication than infection with BTV-8. This may be a factor contributing to the observed faster progression of the BTV-3 outbreak in comparison to the BTV-8 outbreak in 2006/2007.

**Session 13: Vectors II / 420****Sequencing complete mitochondrial genomes to solve *Culicoides* biting midge (Diptera: Ceratopogonidae) phylogeny**

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Accurate species identification of biting midges (Diptera: Ceratopogonidae) is essential for understanding pathogen transmission dynamics and developing effective vector control strategies. Traditional morphological identification is challenging and in many cases impossible due to the occurrence of cryptic species. Although sequencing of the mitochondrial cytochrome c oxidase subunit I (COI) gene is widely used for molecular species identification, this marker frequently lacks sufficient resolution within the genus *Culicoides*.

To overcome these limitations, we used sequence comparison of complete mitochondrial genomes (mitogenomes). Compared to single-locus markers, mitogenomes provide substantially greater phylogenetic signal. This approach is valuable for taxonomically challenging groups such as the subgenera *Avaritia* and *Culicoides*, in which morphological similarity and low COI divergence complicate species discrimination.

In this study, we generated 32 complete mitogenomes representing 17 *Culicoides* species. Specimens were collected from multiple locations across Germany during various monitoring programmes, pre-identified morphologically and, if possible, by COI barcoding. Complete mitogenomes were assembled from high-throughput sequencing data. Results indicate the presence of two distinct mitochondrial structures in the two subgenera. These, for example, confirm that *Culicoides dewulfi* does neither belong to the *Obsoletus* Group nor to the subgenus *Avaritia*.

**Session 13: Vectors II / 523****Interactions of insect-specific viruses (Bunyaviricetes) with *Aedes aegypti* and Rift Valley Fever Virus****Author:** Swati Jagtap<sup>1</sup>**Co-authors:** Mine Altinli<sup>1</sup>; Marlis Badusche<sup>1</sup>; Bernhard Zibrat<sup>1</sup>; Esther Schnettler<sup>1</sup> *Bernhard-Nocht Institute for Tropical Medicine***Corresponding Author:** schnettler@bnitm.de

Mosquitoes are important vectors of arboviruses but also harbour insect-specific viruses (ISVs), which replicate exclusively in insects. Although numerous ISVs have been identified, little is known about their interactions with arboviruses and mosquito hosts. ISVs closely related to arboviruses have been suggested to interfere with arbovirus replication, making them potential tools for vector control. In this study, we investigated the replication and dissemination of three Bunyaviricetes-class ISVs (Herbert, Gouléako, and Badu viruses) in *Aedes aegypti* mosquitoes and mosquito-derived cell lines. All three viruses successfully infected and replicated in mosquitoes, although differences in tissue tropism and dissemination were observed. Herbert virus was also detected in saliva, indicating its potential for horizontal transmission. Detailed analysis regarding in interaction In vitro, Herbert virus significantly reduced intracellular RNA levels of Rift Valley fever virus (RVFV); however no significant effects on RVFV infection or transmission were detected in co-infected mosquitoes. These findings provide the first in vivo characterisation of Bunyaviricetes ISVs in *Ae. aegypti*, improve our understanding of ISV–arbovirus interactions, and highlight the need for further studies to evaluate their potential for arbovirus and vector control.

**Snacks & Poster Viewing I / 348****Natural Ozone Covid-19 Infection Assessment by Zoologic Zones Investigation method to develop daily bulletins preventing the social behavior of virus outbreak****Author:** Dario Di Gangi<sup>None</sup>**Corresponding Author:** [dgangi@hotmail.com](mailto:dgangi@hotmail.com)

Few scientific studies tell about the relation between the activation of a virus and its environment and the most ones are published in the past decades until seventies. To prevent and control the pandemics is important to understand the mechanisms about the origins of the viruses spread and built a tool to warn the population in order to adopt the tempestive solutions. To design a new health emergency bulletin based on the Natural Ozone Covid-19 Infection Assessment by Zoologic Zones Investigation (NOCIAZZI method), studying main indicators that can affect the reproduction number (R) and growth rate (r) of the COVID-19 epidemic in order to develop a model reproducing the behaviors of the virus in the environment before its outbreak in different scenarios. In this context, natural variability of climate system can threaten health system functioning and the stability of ecosystems worldwide having direct and indirect impacts on public health. We can consider that tropospheric ozone concentrations (correlated stratospheric ozone, UV,...) are a good indicator to represent all the climatic/meteorological variations and give a solid base of available information (AQ monitoring stations, satellite data,...). To take account of all the environmental factors and the ecosystems interacting with human population, we can consider a good indicator the earthworms because of its important soil taxon as ecosystem engineers, providing a variety of crucial ecosystem functions and services.

**Snacks & Poster Viewing I / 352****BEYOND CARBON: A ONE HEALTH CONCEPTUAL FRAMEWORK FOR BIOCHAR PROJECTS IN TROPICAL AGRICULTURAL SYSTEMS****Author:** José Alejandro Martínez Sepúlveda<sup>1</sup><sup>1</sup> *Universidad Ean***Corresponding Author:** jamartinez@universidadean.edu.co

Biochar has gained global attention as a carbon dioxide removal technology, yet its broader contribution to One Health remains underexplored. This work proposes a One Health conceptual framework for assessing biochar projects in tropical agricultural systems, drawing on evidence from coffee production in Colombia and an emerging coffee biochar initiative in Andes, Antioquia.

Studies on coffee-based biochar have shown improvements in soil health, including reduced acidity, increased organic carbon and enhanced nutrient retention. These benefits translate into improved plant health through greater nutrient uptake, higher productivity and increased tolerance to water stress. In Colombian coffee systems, parchment coffee yield increased from approximately 0.21 kg tree<sup>-1</sup> to 0.41 kg tree<sup>-1</sup> under optimized biochar treatments, while international experiences have reported yield gains of 30–40%.

The Andes Coffee Biochar Project aims to transform coffee-processing residues into biochar as a pathway for regenerative agriculture and carbon removal. From a holistic and integral perspective, its value extends beyond climate mitigation by strengthening food systems, enhancing climate resilience and supporting human well-being. Accordingly, the framework proposes evaluating biochar projects through integrated indicators of soil and plant health, food security, climate adaptation and human well-being, providing a foundation for scaling biochar interventions across the Global South.

**Snacks & Poster Viewing I / 356****Data-Driven Development of Nanostructured Biodegradable Packaging Films as A One Health Strategy for Food Safety and Sustainability****Author:** Lizandra Viana Maurat da Rocha<sup>1</sup>**Co-author:** Maria Inês Bruno Tavares<sup>1</sup><sup>1</sup> *Federal University of Rio de Janeiro - UFRJ***Corresponding Author:** lizandramaurat@nano.ufrj.br

Food packaging is a strategic interface between human health, environmental quality and sustainable systems. Persistent plastic waste and microplastic formation are growing environmental concerns, while microbial contamination and food spoilage continue to challenge food safety and public health. This research investigates a One Health-oriented material proposal: nanostructured biodegradable active packaging films based on poly(butylene adipate-co-terephthalate) (PBAT), nanoencapsulated bioactive compounds and molybdenum trioxide as multifunctional nanofiller. This proposed system aims to combine active food protection, antimicrobial potential, enhanced material functionality and lower environmental persistence when compared with conventional plastics. The study integrates polymer science, nanotechnology and sustainability through structural, physicochemical, thermal, surface and microbiological characterization. Artificial intelligence and exploratory data analysis support experimental planning, data interpretation and more efficient use of resources. By connecting food safety, antimicrobial risk reduction, plastic pollution mitigation, climate-sensitive innovation and responsible scientific practices, this work offers a Latin American contribution to sustainable material development for One Health.

**Snacks & Poster Viewing I / 357****Circulation of the One Health Approach in Municipal SUS Management: An Interlocal Qualitative Study in the Canindé Micro-region, Ceará, Brazil.**

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**Background:** One Health emphasizes the interdependence of human, animal, environmental and ecosystem health, yet its appropriation at the municipal level of Brazil's Unified Health System (SUS) remains poorly understood in territories with socioenvironmental vulnerabilities. **Objective:** To analyze how managers in the Canindé micro-region (semiarid Ceará, Brazil) interpret and appropriate One Health in local SUS management, especially surveillance, and how related elements are institutionalized in Municipal Health Plans (MHPs). **Methods:** Qualitative multiple-case study grounded in social constructionism and knowledge circulation theory. MHPs (2022-2025) from six municipalities were analyzed via thematic content analysis, complemented by manager interviews and an exploratory ordinal matrix covering environmental surveillance, animal health, intersectorality, primary care-surveillance integration, socioenvironmental determinants and territorial governance. **Results:** No MHP used "One Health"/"Saúde Única" explicitly; indirect, fragmented, unequal approximations emerged. Itatira/Paramoti showed highest density of integrative elements; Canindé/Madalena were intermediate; Boa Viagem/Caridade reflected assistance-based rationalities. Animal health was least institutionalized, only in Paramoti (rabies vaccination). **Conclusion:** One Health circulates indirectly via existing SUS categories, indicating need to strengthen surveillance-territorial governance integration.

**Snacks & Poster Viewing I / 358****Serological and molecular surveillance of West Nile virus, tick-borne encephalitis virus and hepatitis E virus in wild carnivores from northeastern Germany****Author:** Lydia Kasper<sup>1</sup>**Co-authors:** Josefine Wassermann<sup>2</sup>; Jonas Heck<sup>3</sup>; Ute Ziegler<sup>1</sup>; Gereon Schares<sup>2</sup>; Kerstin Wernike<sup>3</sup>; Martin Eiden<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Novel and Emerging Infectious Diseases, Greifswald-Insel Riems, Germany*<sup>2</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Epidemiology, Greifswald-Insel Riems, Germany*<sup>3</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Diagnostic Virology, Greifswald-Insel Riems, Germany***Corresponding Author:** lydia.kasper@fli.de

Wildlife is considered a key driver of zoonotic disease emergence. Invasive carnivores such as raccoons or red foxes may facilitate disease transmission through close contact with humans. Wild carnivores are recognized as incidental hosts of vector-borne zoonotic flaviviruses, such as West Nile virus (WNV) and tick-borne encephalitis virus (TBEV), as well as the fecal-orally transmitted hepatitis E virus (HEV), but data on virus distribution in these animals in Germany remain scarce.

This study investigated the exposure of red foxes, badgers, raccoons and raccoon dogs to WNV, TBEV and HEV on the German Baltic Sea Island Rügen from 2023 to 2026. Blood collected from the body cavities of hunted animals was screened for virus-specific antibodies after centrifugation using a multiplex bead-based assay, with results verified by commercial ELISAs, Western Blots or virus neutralization tests. Organ or feces samples were tested for viral RNA.

No flavivirus RNA was detected, whereas HEV RNA was sporadically identified in red foxes and raccoon dogs. HEV- or flavivirus-specific antibodies were detected in all tested species, with seroprevalences below 10 %. These findings demonstrate exposure of wild carnivores to WNV, TBEV and HEV in northeastern Germany. The low serological and molecular detection rates suggest that wild carnivores are not involved in the transmission of WNV, TBEV or HEV but may serve as sentinels of virus circulation in wildlife populations.

**Snacks & Poster Viewing I / 361****Phenotypic and Genotypic Characterization of Porcine RNA Viruses isolated from diarrheic piglets highlights its zoonotic potential****Author:** Yassein Ibrahim<sup>1</sup>**Co-author:** Gebremeskel Mamu Werid<sup>2</sup><sup>1</sup> *Chongqing Academy of Animal Science, National Center of Technology Innovation for Pigs, Chongqing 402460, China, Faculty of Veterinary Science, University of Nyala, Nyala 155, Sudan*<sup>2</sup> *Davies Livestock Research Centre, School of Animal & Veterinary Sciences, University of Adelaide, Rose worthy Campus, Rose worthy, SA 5371, Australia***Corresponding Author:** yassin8322@gmail.com

**Background:** Swine harbor diverse viruses with zoonotic potential, necessitating continuous surveillance. This study investigated the prevalence and molecular characteristics of Parainfluenza Virus 5 (PIV5) and Enterovirus G (EV-G) in diarrheic piglets in northern China.

**Methods:** A total of 232 fecal samples from diarrheic piglets in Heilongjiang Province were analyzed by viral isolation, molecular characterization, phylogenetic analysis, and pathogenicity studies.

**Results:** A PIV5 strain was isolated and found to be closely related to strains previously detected in pigs and lesser pandas in China. The virus infected multiple mammalian cell lines, including human cells, indicating cross-species transmission potential. An indirect ELISA based on recombinant nucleocapsid protein showed high sensitivity (94.1%) and specificity (96.4%), while serological testing of 530 sera revealed a prevalence of 75.7%. EV-G was detected in 37.5% (87/232) of samples, and four G1-PLCP strains carrying a 639-nt papain-like cysteine protease insertion were isolated. These strains infected multiple cell lines and caused mild disease in piglets.

**Conclusion:** The broad host tropism of PIV5 and the circulation of recombinant EV-G strains highlight their importance to swine health and their potential implications for public health.

**Snacks & Poster Viewing I / 363****A One Health Perspective on a Histamine Fish Poisoning Outbreak in Fernando de Noronha, Brazil: Integrated Surveillance, Health Education and Lessons Learned****Author:** Camila Ferro<sup>None</sup>**Corresponding Author:** camila.ferro@fiocruz.br

**Introduction:** Histamine fish poisoning is a foodborne disease associated with failures in fish preservation and cold-chain maintenance. Island communities are particularly vulnerable due to geographic isolation, dependence on fisheries, and intense tourism. **Objective:** To describe the 2016 outbreak in Fernando de Noronha, Brazil, from a One Health perspective. **Methods:** A descriptive study was conducted using epidemiological and sanitary investigation reports from December 2015 to May 2016. **Results:** Sixty-six suspected cases were identified; 37 were confirmed. Histamine concentrations ranged from 3,120 to 13,411.5 mg/kg, far above Brazilian regulatory limits. Inspections revealed inadequate refrigeration, insufficient ice use, transportation failures, improper storage, and poor food handling practices. Educational gaps among fishermen and food handlers were also observed. In response, health authorities strengthened inspections and implemented educational and regulatory measures, including technical guidance and promotion of good practices. No further cases were reported after implementation of these measures. **Conclusion:** This outbreak demonstrates the importance of integrating surveillance, health education, and food safety actions within a One Health framework to prevent foodborne diseases in island communities. The findings highlight the need for monitoring, risk assessment, and health education to sustain prevention in island communities dependent on fisheries and tourism.

**Snacks & Poster Viewing I / 365****How innovative barn design and novel decontamination methods in high-welfare pig and poultry barns can contribute to pandemic preparedness****Authors:** Corinna Thomas<sup>1</sup>; Tina Kabelitz<sup>1</sup>**Co-authors:** Thomas Amon<sup>1</sup>; Ulrich E. Schaible<sup>2</sup><sup>1</sup> *Leibniz-Institut für Agrartechnik und Bioökonomie e.V. (ATB)*<sup>2</sup> *Research Center Borstel (FZB)***Corresponding Author:** tkabelitz@atb-potsdam.de

Due to increasing global interconnection, the steadily rising number of livestock and the increase in zoonotic diseases (e.g. avian influenza), it is becoming increasingly important to improve biosecurity and to align it with the One Health approach. Improving animal welfare, particularly through open housing systems, leads to healthier animals with lower susceptibility to diseases, but also increases the risk of interactions with wildlife and environmental reservoirs, which facilitates the transmission of pathogens. Within the framework of the Leibniz Lab Pandemic Preparedness, we studied innovative approaches for pig and poultry housing design and management to minimize pathogen spread, e.g. outdoor areas that minimise the contact with wildlife by 'internal' position or the temporary installation of nets and roofings. The use of digital monitoring systems for efficient pest control (rodents, insects), new technologies for wildlife deterrence, and the use of antimicrobial surfaces (nanomaterials or bio-inspired structures) can be important steps towards increasing biosecurity. Novel physical and biological decontamination measures, such as far-UVC and the use of cold plasma are promising approaches. This study provides a crucial framework for the integration of innovative biosecurity solutions for open housing concepts in order to address the specific risks of these systems and significantly increase the resilience of livestock farming against future pandemics.

**Snacks & Poster Viewing I / 370****FineInfect – Particulate Matter in Focus: Effects on molecular mechanisms during respiratory infections**

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Air pollution caused by fine particulate matter (PM) resulting from industry, traffic, and fossil fuel combustion is a major risk for respiratory diseases. Influenza A viruses (IAVs) are a leading cause of acute respiratory illness, and recent findings suggest that PM can influence the host responses during infection. While PM increases susceptibility to infection, the underlying mechanisms remain unclear.

Our *in vitro* data show that cell morphology remained intact in presence of PM of various sources and lactate-dehydrogenase release increased only slightly, whereas mitochondrial activity was reduced. Interestingly, PM modulated the host immune response in a cell-type- and time-dependent manner, with differences observed based on the specific composition of the PM. While IAV-induced type I IFN response was reduced, IL-6 and IL-8 were upregulated, indicating selective immune regulation toward inflammation. Although early stages of infection appeared to be unaffected in presence of PM, viral titers decreased in certain cell types, suggesting interference with post-entry steps. We also observed PM-induced alterations in cell cycle regulators, pointing to disrupted cell cycle progression that may be driven by the paradoxical immune modulation.

Future work will characterize these effects, resolve their temporal dynamics, and use more complex cell culture models to further elucidate their biological significance.

**Snacks & Poster Viewing I / 373****N6-methyladenosine modifications regulate hepatitis E virus infections****Author:** Pauline Wieczorek<sup>1</sup>**Co-authors:** Elene Loliashvili<sup>2</sup>; Daniel P. Depledge<sup>2</sup>; Eike Steinmann<sup>1</sup>; Mara Klöhn<sup>1</sup><sup>1</sup> *Department of Molecular and Medical Virology, Ruhr University Bochum, Bochum, Germany*<sup>2</sup> *Institute of Virology, Hannover Medical School, Hannover, Germany***Corresponding Author:** pauline.wieczorek@rub.de

N6-methyladenosine (m6A) is the most prevalent cotranscriptional RNA modification in eukaryotes, regulated by m6A methyltransferases (writers), demethylases (erasers) and m6A-binding proteins (readers). Its role during hepatitis E virus (HEV) infection remains poorly understood. Therefore, we blocked METTL3 activity in inhibitor dose-response assays. METTL3 inhibitors STM2457, STM3006 and STC-15 reduced infection with EC50 values of 3.7, 1.2 and 5.4  $\mu$ M, respectively. These antiviral effects were confirmed in extrahepatic cells and primary human hepatocytes, where STM2457 demonstrated an 75% reduction at 25  $\mu$ M. Time-of-addition assays indicated that METTL3 primarily regulates the viral entry stage. Combining STM2457 with replication inhibitors Ribavirin or JNJ-9117 yielded additive antiviral effects. Interestingly, direct RNA Nanopore sequencing of HEV-transfected HepG2 cells treated either with STM2457 or DMSO detected no m6A sites on the HEV genome, suggesting that m6A instead regulates host-specific responses. Finally, co-treatment with the JAK/STAT inhibitor Baricitinib showed no differences compared to single treatment, indicating that METTL3 functions independently of the innate immune defense. In conclusion, our study identified m6A methylation as a component of HEV biology and suggests that it might be a promising target for antiviral interventions.

**Snacks & Poster Viewing I / 374****Post-vector-control Chagas disease as a One Health challenge in Chile****Author:** Franco Fernández Guardiola<sup>1</sup>**Co-authors:** Eduardo Undurraga<sup>1</sup>; Diego Sandoval Vargas<sup>2</sup>; Kasim Allel<sup>3</sup>; Mauricio Canals<sup>4</sup><sup>1</sup> *Escuela de Gobierno, Pontificia Universidad Católica de Chile*<sup>2</sup> *Universidad de Chile*<sup>3</sup> *Nuffield Department of Primary Care Health Sciences. Oxford University*<sup>4</sup> *Instituto de Salud Poblacional. Universidad de Chile***Corresponding Author:** [tecmed.f.fernandezguardiola@gmail.com](mailto:tecmed.f.fernandezguardiola@gmail.com)

Chagas disease is a neglected zoonosis linking vector ecology, reservoirs, congenital transmission, migration and long-term health-system outcomes. Although Chile has interrupted domestic vector-borne transmission, persistent sylvatic exposure, ageing cohorts, late diagnosis and underdetection still obscure transmission and care pathways across human, animal and environmental domains. We analysed notified cases in Chile (2007–2021) linked to mortality and hospital records. Chagas-specific death was assessed using competing-risks methods, while cause-specific Cox models included hospitalisation as a marker of clinical deterioration. Burden was estimated through years of life lost, years lived with disability and disability-adjusted life years. Among 17,508 individuals, 261 died from Chagas disease and 1,021 from other causes. Ten-year cumulative incidence of Chagas-specific death was highest among adults aged  $\geq 70$  years, men and chronic digestive or cardiac forms; recurrent hospitalisation was the strongest marker of death. The cohort accrued 9,869.5 DALYs, with disability contributing more than premature mortality. These findings describe a post-vector-control transition in which burden is sustained by non-vector transmission, chronic progression and delayed care. Chagas should therefore be reframed as a One Health challenge requiring ecological surveillance, congenital and migrant-focused strategies, linked administrative data, risk-stratified care and longitudinal follow-up.

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**Hepatitis E virus in shrews – a novel zoonotic risk?****Authors:** Calvin Mehl<sup>1</sup>; Mathias Schemmerer<sup>2</sup>**Co-authors:** Viola Haring<sup>1</sup>; Alexander Falkenhagen<sup>3</sup>; Anna Brueck<sup>1</sup>; Matthias Lenk<sup>4</sup>; Monika Erl<sup>2</sup>; Juergen Wenzel<sup>2</sup>; Florian Pfaff<sup>5</sup>; Reimar Johne<sup>3</sup>; Rainer G. Ulrich<sup>1</sup><sup>1</sup> Friedrich-Loeffler-Institut, Institute of Novel and Emerging Infectious Diseases, Germany<sup>2</sup> University Medical Center Regensburg, National Consultant Laboratory for HAV and HEV, Germany<sup>3</sup> German Federal Institute for Risk Assessment, Department of Biological Safety, Germany<sup>4</sup> Friedrich-Loeffler-Institut, Department of Experimental Animal Facilities and Biorisk Management, Germany<sup>5</sup> Friedrich-Loeffler-Institut, Institute of Diagnostic Virology, Germany**Corresponding Author:** calvin.mehl@fli.de

*Paslahepevirus balayani* (hepatitis E virus, HEV) is the most relevant human-pathogenic hepevirus, but zoonotic infections with ratHEV (species *Rocahepevirus rattii*) have been reported recently. A novel hepevirus, provisionally termed shrewHEV, was identified in *Crocidura russula* (greater white-toothed shrews, GWTS) that is phylogenetically more closely related to HEV than ratHEV. We investigated its prevalence in Germany and its infectivity in various cell lines.

222 GWTS collected in Germany between 2002 and 2022 were screened for shrewHEV RNA by RT-qPCR. ShrewHEV RNA sequences were determined and phylogenetically analysed. Liver homogenates of ten positive shrews were inoculated onto shrew-derived fibroblast-like cells and three HEV- and ratHEV-permissive human liver cell lines. Cells and supernatants were characterized by immunofluorescence assay, sequencing and density gradient centrifugation. Finally, we assessed the antiviral activity of ribavirin (RBV) and sofosbuvir (SOF) against shrewHEV.

ShrewHEV RNA was detected in 16/222 GWTS. Five of 10 liver-derived strains replicated in human liver cell lines, but none in shrew cells. Density gradient centrifugation demonstrated quasi-enveloped particles. Both RBV and SOF showed antiviral activity against shrewHEV in vitro. ShrewHEV was detected in 7.2% of GWTS across its distribution range. The virus replicated efficiently in human-derived liver cells indicating the necessity of further studies on its zoonotic potential.

**Snacks & Poster Viewing I / 385****Brucella Vesicles: Tiny Packages with Major Impact****Author:** Dominique Scheffler<sup>1</sup>**Co-authors:** Sascha Al Dahouk<sup>1</sup>; Christoph-Martin Ufermann<sup>1</sup><sup>1</sup> *Department 1 – Infectious Diseases, Robert Koch Institute, Berlin, Germany***Corresponding Author:** schefflerd@rki.de

The evolution of *Brucella* spp. was directly shaped by livestock domestication. Zoonotic transmission occurs through contact with infected animals and consumption of unpasteurized milk and dairy products as well as raw meat. Membrane vesicles (MVs) are small, cell-derived particles that transport proteins, lipids, and nucleic acids between cellular compartments or between individual cells. For *Brucella*, MVs are potential vehicles for the delivery of effector proteins or bacterial RNAs that could be involved in host manipulation.

In this project, we focus on MV production and extraction from *B. microti* and *B. suis*, followed by MV characterization using microscopy and proteomic analyses. In axenic *Brucella* cultures, starvation stress led to increased MV production. Using nanoparticle tracking analysis, fluorescence and transmission electron microscopy, a gravity-column based extraction yielded MVs more consistent and reproducible than ultracentrifugation. The MV proteome was analyzed by LC-MS. In an initial experiment, a subset of proteins was identified that was significantly enriched in MVs compared to the cellular fraction.

Our current data indicate that MV production by *Brucella* is elevated under conditions found in phagosomes and that the protein composition of MVs differs from their mother cells. In the future, we will address the potential RNA cargo of MVs that could induce silencing of target host RNA and interfere with gene expression to promote *Brucella* survival.

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**Towards assessing the role of surface waters in the environmental dissemination of *Campylobacter* spp.****Author:** David Baum<sup>1</sup>**Co-authors:** Corinne Pippig<sup>2</sup>; Katrin Oehm<sup>2</sup>; Sarah Brüggemann-Schwarze<sup>3</sup>; Kerstin Stingl<sup>3</sup>; Astrid Bethe<sup>1</sup>; Annette Hummel<sup>4</sup>; Christina Förster<sup>4</sup>; Birgit Walther<sup>1</sup><sup>1</sup> German Environment Agency (Umweltbundesamt (UBA)), Microbiological Risks (II 1.4), Corrensplatz 1, 14195 Berlin<sup>2</sup> German Environment Agency (Umweltbundesamt (UBA)), Microbiology of Drinking Water and Swimming Pool Water (II 3.5), German Environment Agency (Umweltbundesamt (UBA)), Microbiology of Drinking Water and Swimming Pool Water (II 3.5), Heinrich-Heine-Straße 12, 08645 Bad Elster<sup>3</sup> German Federal Institute for Risk Assessment (BfR), National Reference Laboratory for *Campylobacter*, Diedersdorfer Weg 1, 12277 Berlin<sup>4</sup> German Environment Agency (Umweltbundesamt (UBA)), Microbiology of Drinking Water and Swimming Pool Water (II 3.5), Heinrich-Heine-Straße 12, 08645 Bad Elster**Corresponding Author:** david.baum@uba.de

*Campylobacter* spp. are the leading bacterial cause of gastroenteritis worldwide. While foodborne transmission pathways are well established, surface waters may act as an environmental source and potential reservoir. Although recent studies link heavy rainfall events to sporadic campylobacteriosis outbreaks, the specific role of surface waters in the environmental dissemination of *Campylobacter* spp. remains poorly understood and is, thus, focus of the One Health consortium NICE.

As part of this study, seven sampling sites were selected in the regions of Berlin-Brandenburg and Saxony, Germany for a two-year monitoring. The selected surface water bodies include locations both impacted and not impacted by wastewater discharges and rainfall-driven runoff. Membrane filtration followed by culture- and molecular techniques such as viable quantitative and species-specific PCR approaches are used to detect and characterize *Campylobacter* spp.. Isolates will be subjected to further characterization and comparative downstream analyses using genomics.

Preliminary monitoring results indicate the presence of *Campylobacter* spp. in several sampled water bodies including *Campylobacter jejuni* and *Campylobacter coli*. Throughout the remainder of the two-year monitoring period, seasonal trends and the influence of heavy rainfall events on *Campylobacter* occurrence and abundance will be investigated.

**Snacks & Poster Viewing I / 392****Beyond Surveillance: Human Macrophage Responses as a Tool for Functional Risk Assessment of Emerging Influenza Viruses****Author:** Nicolas Corrales<sup>1</sup>**Co-authors:** Jana Gutknecht<sup>1</sup>; Jamina Molsen<sup>1</sup>; Kevin Ciminski<sup>1</sup><sup>1</sup> *Institute of Virology, Medical Center-University of Freiburg***Corresponding Author:** nicolas.corrales@uniklinik-freiburg.de

Influenza A viruses continue to emerge from animal reservoirs and challenge preparedness efforts. Current risk assessment strategies rely largely on genetic and epidemiological data, providing limited information on how emerging viruses interact with the human immune system. Macrophages are among the first immune cells encountered during infection and play a key role in antiviral and inflammatory responses. Functional characterization of virus-macrophage interactions may therefore complement surveillance efforts and improve our understanding of the consequences of human infection.

In this study, human monocyte-derived macrophages from six healthy donors were used to compare the replication dynamics and immunomodulatory properties of influenza A viruses representing different pathogenic and ecological backgrounds. Viral replication was quantified by qRT-PCR and infectivity assays, while flow cytometry was used to determine infection rates and characterize changes in immune markers. Integrating virological and immunological readouts revealed distinct response profiles associated with different influenza viruses.

These findings highlight the value of human macrophage models as a complementary approach for functional risk assessment while providing insights into how emerging influenza viruses replicate, modulate innate immunity and contribute to disease development. Together, this work contributes to a broader One Health framework for the evaluation of emerging influenza threats.

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**Investigating Emerging Monoxenous Trypanosomatids in Leishmaniasis Reservoirs and Vectors: A One Health Perspective**

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Trypanosomatids are flagellated protozoa classified as monoxenous or dioxenous parasites. While dioxenous species comprise agents of neglected tropical diseases, monoxenous trypanosomatids have long been regarded as insect-restricted. However, increasing reports of natural infections in mammals, including humans and animal reservoirs, challenge this paradigm. To explore their relevance within a One Health perspective, we combined epidemiological and experimental approaches including reservoirs, vectors and a clinical isolate. Trypanosomatids kDNA DNA was detected in 34 skin and spleen biopsies from dogs with leishmaniasis, while ITS sequencing identified *Crithidia fasciculata*, *Herpetomonas muscarum* and *H. samuelpessoai* in 3 dogs. In parallel, we investigated the behaviour of a *C. fasciculata* isolate recovered from a Peruvian patient with cutaneous leishmaniasis. Although the monoxenous parasite tolerated 32°C and successfully colonized sandflies, it failed to establish persistent infections in macrophages *in vitro*, mice or hamsters *in vivo*, even during coinfection with *Leishmania braziliensis*. Through an integrative approach involving a human-derived isolate, canine reservoirs and insect vectors, this study highlights the importance of molecular surveillance of emerging trypanosomatids and supports a One Health approach to better understand their epidemiological significance and potential impact on leishmaniasis.

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**Migratory shorebirds as key drivers of North American avian influenza virus introduction, spread, and evolution in South America**

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Wild aquatic birds are reservoirs of avian influenza virus (AIV), yet genomic surveillance in South America remains limited. In Argentina, studies in wild ducks revealed high AIV subtype diversity with internal gene constellations exclusively from South American (SA) lineage, despite frequent HA and NA reassortment with North American (NA) lineages. Migratory shorebirds connect breeding and nonbreeding grounds across the Americas and may facilitate the introduction of NA AIV lineages, as recently seen with H5N1 HPAI incursion. To assess their role in AIV evolution, we sampled migratory shorebirds in central Argentina and obtained the first AIV genomes from these hosts: H1N8 and HxNx from *Calidris fuscicollis* and H11N2 from *C. himantopus*. H11N2 possessed all eight gene segments of NA lineage, representing the first such detection in Argentina. In contrast, H1N8 and HxNx were reassortant viruses with internal genes from both NA and SA lineages, revealing an undocumented mechanism of viral genetic exchange. The PB1 segment of H1N8 formed a sister clade to PB1 genes linked to the 2022 H5N1 HPAI incursion and clustered with viruses from shorebirds in Brazil, suggesting regional circulation. These findings show that migratory shorebirds contribute to the introduction, spread, and evolution of AIV in South America, highlighting their importance for genomic surveillance as an early warning system for novel AIV incursions with potential implications for animal and human health.

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**Delayed Detection and High-Risk Livestock Exposure Drove a Mixed Anthrax Outbreak in Lyantonde District, Uganda, February 2026****Author:** Nasif Matovu<sup>1</sup><sup>1</sup> *Uganda National Institute of Public health***Corresponding Author:** matovan5@uniph.go.ug

**Background:** Anthrax, caused by *Bacillus anthracis*, is endemic in Uganda's cattle corridor. In January 2026, an outbreak was reported in Lyantonde District following sudden livestock deaths. We investigated to determine magnitude, risk factors, timeliness, and control measures.

**Methods:** We reviewed medical records, conducted active case finding, and performed a 1:4 matched case-control study. Case definitions spanned cutaneous and gastrointestinal presentations, confirmed via PCR. Conditional logistic regression identified risk factors, a common-reference-group analysis assessed dose-response, and the 7-1-7 framework evaluated timeliness.

**Results:** We identified 64 cases (60 suspected, 4 confirmed; 7 deaths), including 31 cutaneous (48.4%) and 2 mixed cases (3.1%). Care was initially sought from traditional healers by 65% of patients. Infection risk increased with dead livestock fluid contact (aOR=124.3, 95%CI: 8.9-1736.2), meat consumption (aOR=20.1, 95%CI: 4.5-89.6), and slaughter/dissection involvement (aOR=57.8, 95%CI: 5.1-653.6). Detection occurred 22 days post-emergence, and response 17 days post-notification. Delays were tied to low community awareness and traditional healer care.

**Conclusion:** Carcass handling and meat consumption drove this outbreak. Risks can be reduced via livestock vaccination, safe disposal, meat inspection, and One Health surveillance. Improving community awareness and clinical recognition will accelerate detection.

**Snacks & Poster Viewing I / 419****Reported Human and Animal Brucellosis in Uganda, 2017–2024: A One Health Analysis of National Surveillance Data****Author:** Aminah Namwabira<sup>1</sup>**Co-authors:** Alfred Wejuli<sup>2</sup>; Anne Loy Alupo<sup>1</sup>; Benard Lukenku<sup>3</sup>; Justine Wobusobozi<sup>1</sup>; Martha Dorcas Nalweyiso<sup>1</sup>; Winfred Nakaweesi<sup>1</sup><sup>1</sup> *Uganda National Institute of Public Health*<sup>2</sup> *Ministry of Health*<sup>3</sup> *Ministry of Agriculture, Animal Industry and Fisheries***Corresponding Author:** anamwabira@uniph.go.ug

**Background:** Brucellosis is a zoonotic bacterial disease endemic in Uganda. We described temporal and spatial distribution of animal and human brucellosis in Uganda during 2017–2024 to inform coordinated control.

**Methods:** We analyzed clinically diagnosed human brucellosis reported in the District Health Information Software version 2 and clinically diagnosed animal cases reported in the national animal health surveillance database. Brucellosis incidence was calculated using Uganda Bureau of Statistics projected human populations and reported animal populations at risk. Temporal trends were assessed using the Mann-Kendall trend test.

**Findings:** A total of 1,542,564 human cases (90% reporting rate) and 14,054 animal cases (22% reporting rate) were reported. Brucellosis incidence increased by 6 cases per 100,000 annually in animals ( $p=0.04$ ) but remained stable in humans (median incidence: 115/100,000,  $p=0.10$ ). South-Central Region had the highest brucellosis incidence in animals (578/100,000); Karamoja had the highest incidence in humans (733/100,000). Spatial co-reporting of human and animal brucellosis was concentrated mostly in Ankole Region.

**Conclusion:** Reported brucellosis incidence increased statistically in animals but remained stable in humans. Low animal-sector reporting suggests that observed geographic discordance may reflect surveillance gaps. Institutionalizing routine joint analysis of human and animal data is essential for targeted One Health brucellosis control.

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**Replication assessment of chimeric HEV-3 subtypes demonstrates enhanced replication fitness of HEV-3f isolates****Authors:** Alina Kohl<sup>None</sup>; Rui Marques Da Costa<sup>1</sup>**Co-authors:** André Gömer<sup>1</sup>; Daniel Todt<sup>2</sup>; Eike Steinmann<sup>1</sup>; Michelle Jagst<sup>1</sup><sup>1</sup> 1 Department for Molecular und Medical Medicine, Ruhr University Bochum, Germany; 2 Hepatitis E Virus Research Hub (HepE-Hub), Bochum, Germany<sup>2</sup> 1 Department for Molecular und Medical Medicine, Ruhr University Bochum, Germany; 2 Hepatitis E Virus Research Hub (HepE-Hub), Bochum, Germany; 3 Department of Translational and Computational Infection Research, Ruhr University Bochum, Germany**Corresponding Author:** alina.kohl@rub.de

Hepatitis E virus (HEV) remains an underestimated global health concern, causing an estimated 20 million infections and 3450 - 70,000 deaths annually. In Europe, genotype 3 (HEV-3) is the prevalent genotype, comprising 15 subtypes organized in three clades: Clade 1 (3efg), Clade 2 (3abchijklmno) & Clade 3 (3ra). Infections with HEV 3 clade 1 have been associated with more severe disease outcomes, although the underlying mechanisms remain unclear.

We performed a phylogenetic analysis of HEV-3 subtypes and generated a library of 15 primary isolate-derived polymerase chimeras, each inserted into the backbone of the Kernow-C1 p6 subgenomic replicon. We evaluated replication kinetics and identified molecular determinants of HEV replication.

Phylogenetic analysis revealed considerable diversity among the HEV-3 polymerases, with up to 21 substitutions relative to p6. 13 of the 15 chimeras demonstrated replication comparable to the parental p6 construct. The HEV-3f subtype showed significantly enhanced replication kinetic, with up to a 5-fold increase after 24 h.

Our findings highlight the genomic flexibility of HEV-3, which allows for efficient replication of diverse chimeric constructs. This model provides a robust platform for assessing intra-genotypic variability in antiviral responses and advances our mechanistic understanding of replication fitness. Such insights are critical for optimising treatment strategies and understanding the burden of disease in HEV-infected patients.

**Snacks & Poster Viewing I / 429****Comparative analysis of two membrane-based methods for the differentiation of viable and dead cells****Author:** Kerstin Heymann-Schmidt<sup>1</sup>**Co-authors:** Anna-Delia Knipper; Katharina Schaufler; Samuel Hauf; Szilvia Neuhaus<sup>1</sup> *Bundesinstitut für Risikobewertung***Corresponding Author:** kerstin.heyman-schmidt@bfr.bund.de

*Listeria monocytogenes* (Lm) is a foodborne pathogen with high hospitalization and mortality rates. Common route of infection is ingestion of contaminated food. Its persistence in food-processing environments can be facilitated by the induction of the viable but non-culturable (VBNC) state. VBNC cells have lost their ability to grow on culture media, but maintain their metabolic activity.

Bacterial load in food-processing environments is monitored using culture-based analysis of surface samples. With VBNC cells present, viable cell numbers may be underestimated.

In this study, two culture-independent methods, namely LIVE/DEAD™BacLight™ staining with fluorescence microscopy and viability real-time PCR using propidium monoazide (PMA-qPCR), were compared for their power to discriminate between viable and dead Lm and their ability to detect VBNC cells after long- and short-term induction.

We were able to show that both methods are reliable tools for differentiating viable and dead Lm. The dual staining of BacLight™ detected viable cells at ratios up to 1:1000 within mixtures of dead cells. PMA-qPCR detected viable cells at ratios up to 1:10,000. As PMA did not completely inhibit amplification of DNA from dead cells, viable cell numbers were overestimated.

Both methods detected VBNC cells after long- and short-term induction. While BacLight™ staining and PMA-qPCR detected similar cell numbers after short-term induction, long-term induced VBNC cells were underestimated by PMA-qPCR.

**Snacks & Poster Viewing I / 434****Automated wing shape analysis for accessible identification of mosquitoes and other pathogen-transmitting Diptera****Authors:** Kristopher Nolte<sup>None</sup>; Renke Lühken<sup>None</sup>**Co-author:** Felix Sauer**Corresponding Author:** luehken@bnitm.de

Accurate species identification of Diptera, including vectors of pathogens, remains a persistent bottleneck in surveillance. Knowing which species are present is the basis for risk assessment and control. Reliable identification, however, depends on scarce taxonomic specialists or expensive alternatives. Analysing the shape of insect wings is a faster and cheaper, but measuring wings manually is slow and subjective.

We developed ITHILDIN, a free, open-access system that automatically places anatomical reference points (landmarks), on Diptera wings using deep learning and identifies species from their geometric arrangement rather than an opaque AI algorithms.

ITHILDIN distinguish 34 mosquito taxa with 91% accuracy, matching conventional “black-box” neural networks while remaining fully interpretable. It reliably flags images it cannot process, providing built-in quality control.

The underlying reference database now exceeds 50,000 wing images of over 100 taxa, and the pipeline has already been transferred to two further Diptera families, i.e. Drosophilidae and Glossinidae, demonstrating that it is not limited to mosquitoes.

By removing the need for specialist expertise and costly equipment, ITHILDIN makes species identification for insect vectors accessible to a far wider range of users. Its transparent results and expanding species coverage make it a practical tool for vector monitoring and control, including in regions where identification capacity is currently limited.

**Snacks & Poster Viewing I / 435****Impact of Library Miniaturization on Influenza Whole-Genome Assembly Quality**

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Influenza viruses remain a major public health concern due to their rapid evolution, zoonotic potential, and capacity to cause seasonal epidemics. Several past influenza pandemics originated from animal-to-human transmission events, and recent outbreaks of avian influenza A(H5N1) in mammals have raised concerns about the emergence of novel strains with pandemic potential. Continuous genomic surveillance is therefore essential for monitoring viral evolution and supporting public health decision-making. As Germany's national public health institute, the Robert Koch Institute routinely performs whole-genome sequencing, genome reconstruction, and downstream analyses of seasonal influenza A and B viruses and makes the resulting data publicly available for surveillance and research purposes. Sustained genomic surveillance is critical for tracking viral evolution, informing vaccine strain selection, and supporting outbreak preparedness. However, despite declining costs of next-generation sequencing, library preparation remains a major cost driver, limiting sequencing throughput and scalability. We developed a miniaturized library preparation protocol that reduces reagent consumption ninefold compared with our standard workflow using the Mosquito HV Genomics liquid handling system. We evaluated its performance using 181 seasonal influenza samples by comparing sequencing run metrics, consensus genome sequences, and quality indicators generated during genome reconstruction.

**Snacks & Poster Viewing I / 436****Anthrax outbreak associated with handling animals that died suddenly in Kazo District, Uganda, December 2025–March 2026****Author:** WINFRED NAKAWEESI<sup>1</sup>**Co-authors:** Aminah Namwabira<sup>1</sup>; Patrick Kwizera<sup>1</sup>; Pauline Achom<sup>1</sup><sup>1</sup> *Uganda National Institute of Public Health***Corresponding Author:** [wnakaweesi@uniph.go.ug](mailto:wnakaweesi@uniph.go.ug)

Anthrax is endemic in Uganda. On January 22 2026, Ministry of Health was notified of confirmed human cases after sudden livestock deaths in Kazo District. We investigated exposures and response timeliness. We defined suspected cutaneous anthrax as acute-onset skin lesions with  $\geq 2$  of: itching, red-ening, swelling, fever or malaise, in Kazo District residents from Dec 1, 2025 to Mar 31, 2026; suspected gastrointestinal anthrax as acute-onset abdominal pain with  $\geq 2$  of: vomiting, diarrhea, fever, or loss of appetite; and confirmed cases were PCR-positive for *Bacillus anthracis*. We conducted active case finding, calculated attack rates (ARs), an unmatched case-control study (1:4) and assessed timeliness using 7-1-7 framework. We identified 135 cases (14 confirmed); overall AR was 65/100,000 with two (1.5%) deaths. 113 (84%) were cutaneous. Six (60%) of 10 animal samples tested PCR-positive. Environmental assessment found improper carcass disposal. Among 45 cases and 184 controls, risk factors (ref: no exposure) included butchering (aOR=11,95%CI=4.7–24), handling without (aOR=65,95%CI=20–213), or with consumption of meat from sick animals (aOR=72,95%CI=10–98). Detection took 35 days, notification <1 day, response completion 10 days, delayed by weak surveillance and low suspicion index. This outbreak was driven by contact with and consumption of meat from animals that died suddenly. Strengthening animal disease surveillance and enforcing safe carcass disposal could reduce spillover.

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**Evaluation of the exposure risk to Andes hantavirus through domestic animal ownership at the human-wildlife interface in Andean Patagonia****Author:** Andrea Szmec<sup>None</sup>**Co-authors:** Ernesto Juan<sup>1</sup>; Alexandre Dobly<sup>2</sup>; Valeria Susana Ojeda<sup>3</sup><sup>1</sup> *Departamento de Conservación y Educación Ambiental Parque Nacional Lago Puelo- Administración de Parques Nacionales-Argentina*<sup>2</sup> *Sciensano, 14 J. Wytsman street, 1050 Brussels, Belgium*<sup>3</sup> *Grupo de Biología y Ecología de Animales Patagónicos, INIBIOMA, Universidad Nacional del Comahue-CONICET, 8400 Bariloche, Argentina***Corresponding Author:** [aszmec@comahue-conicet.gob.ar](mailto:aszmec@comahue-conicet.gob.ar)

In the northern Patagonian region of Argentina and Chile (33°-46° S), Andes orthohantavirus (ANDV) is a major public health concern due to its unique person-to-person transmission and high case fatality rates (30-50%). The expansion of human settlements into forested areas increases infection risk through greater exposure to native rodent reservoirs. In this context, domestic animals may influence the transmission dynamics of zoonotic agents such as ANDV. We collected blood samples from dogs (n=67) and cats (n=146), and assessed ownership patterns (including confinement status and outdoor access) and animal behavior through structured surveys with pet owners during municipal neutering campaigns in different Argentine localities. Preliminary results show that 13 % of pets are strictly confined, whereas 87 % are semi-free; no fully free-ranging animals were recorded. Rodent-hunting behavior was reported in 74% (18% dogs, 56% cats) of domestic animals. Additionally, 82% of respondents frequently observed free-roaming animals, and 86% considered this a public health risk. Unrestricted outdoor access, rodent hunting behavior, and weak responsible ownership practices (e.g., low vaccination compliance) highlight potential contacts between domestic animals and wild ANDV reservoirs. In a region with a high-risk of human hantavirus infection, these findings underscore the need to strengthen responsible pet ownership and promote health education strategies within a One Health framework.

**Snacks & Poster Viewing I / 442****Urban microhabitats differentially affect West Nile and Usutu virus infection rates in mosquitoes****Authors:** Corinna Patzina-Mehling<sup>None</sup>; Sandra Junglen<sup>None</sup>**Co-authors:** Anne Kopp; Romy Schönberger; Jonas T. Westerteicher; Selina L. Graff**Corresponding Author:** corinna.patzinamehling@charite.de

West Nile (WNV) and Usutu (USUV) viruses are both transmitted by *Culex* mosquitoes and can cause disease with differing pathologies in humans and birds. We have shown that urban land cover shapes WNV infection rates in mosquitoes, most likely driven by avian host community composition. It is unknown which factors drive USUV abundance and how this is influenced by WNV.

Here, we comparatively analysed WNV and USUV infection rates in mosquitoes at different urban microhabitats in Berlin over three seasons.

In total, 41,526 mosquitoes were trapped at seven study sites: a residential courtyard, a park-like residential area (RA), three cemeteries (C), a sponge city site, and a nature conservation area (N). Mosquitoes were morphologically identified and tested for WNV and USUV infection by qPCR. Genome sequencing is ongoing.

Minimum infection rates for WNV were 5.72, 3.00 and 3.43 and for USUV 1.54, 5.14 and 1.18 in 2023 to 2025. Consistent with our previous study, WNV infection rates were unevenly distributed at the sampling sites, with the lowest detection rate at N (up to 0.4 %) and highest at RA (up to 1.5 %) and C (up to 2.1 %). This was not observed for USUV which showed a more even abundance across sites.

Our study demonstrated extensive endemic circulation of WNV and USUV in Berlin. Notably, the two viruses exhibited distinct spatial and temporal abundance patterns, suggesting that different avian species may contribute to their amplification in urban environments.

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**Recurrent Anthrax Outbreak associated with consumption of meat from livestock that died suddenly, Kanungu District, Uganda, 2025–2026****Author:** Vianney John Kigongo<sup>1</sup>**Co-authors:** Agaba Benson<sup>2</sup>; Alex Riolexus Ario<sup>1</sup>; Benon Kwesiga<sup>1</sup>; Deborah Aujo<sup>1</sup>; Justine Wobusobozi<sup>1</sup>; Katto Besisira<sup>2</sup>; Patricia Eyu<sup>1</sup>; Richard Migisha<sup>1</sup><sup>1</sup> *Uganda Public Health Fellowship Program, Uganda National Institute of Public health, Kampala, Uganda*<sup>2</sup> *Department of Health, Kanungu District Local Government, Kanungu, Uganda***Corresponding Author:** kigongojv@uniph.go.ug

**Background:** Following Kanungu District's first-ever anthrax outbreak in 2024, a resurgence of laboratory-confirmed cases was reported in late 2025 and early 2026. We investigated to determine the magnitude of the outbreak and identify risk factors for transmission.

**Methods:** A confirmed case was any suspected case with confirmed *Bacillus anthracis* by PCR. We identified cases through medical record reviews and community searches. We conducted hypothesis-generating interviews and used a 1:4 unmatched case-control study to identify factors associated with illness.

**Results:** Among 52 cases (42 suspected, 10 confirmed) from October 2025–March 2026, there was one death (CFR=2%). The overall attack rate (AR) was 17/100,000. Males (AR: 28/100,000), persons aged ≥15 years (AR: 24/100,000), and Nyamirama Sub county (AR: 86/100,000) were most affected. Three of 5 cattle samples and 10 of 12 human samples were PCR-positive for *Bacillus anthracis*. Eating meat from livestock that died suddenly (aOR=6.4, 95% CI: 2.3–17) and male sex (aOR=5.1, 95% CI: 1.4–19) were associated with anthrax. There was a 37-day delay in detection.

**Conclusion:** Kanungu District experienced a recurrent anthrax outbreak associated with consumption of meat from livestock that died suddenly; delayed detection enabled ongoing human exposure and transmission. We recommend community education against consuming meat from sudden-death animals and immediate reporting of animal deaths to improve detection.

## Snacks &amp; Poster Viewing I / 449

## From Silos to Systems: Stakeholder Perspectives on Building a One Health Cohort in Germany

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### Background

While One Health (OH) recognizes the link between human, animal and environmental health, studies often focus on single domains. This study explores the needs to support OH cohort studies.

### Methods

We recruited two groups of stakeholders: individuals a) working in research, and b) with OH-related experiences, referred to as experts and stakeholders. From 11/2025 to 03/2026, we conducted three expert group discussions (4-5 participants/group) and three interviews, and 17 stakeholder interviews. All interviews and discussions were recorded and transcribed. Data collection stopped when topic saturation was achieved. We are conducting qualitative content analysis.

### Results

The 34-person sample incl. 17 scientific experts and 17 non-academic stakeholders; 26 (77%) were women. All participants could have more than one expertise/background, therefore, categories are not mutually exclusive. Experts represented veterinary medicine (n=6), virology (n=3), environmental science (n=8), public health (n=2), epidemiology (n=5), human health surveillance (n=1) and nursing (n=1). Stakeholders represented healthcare/pharmacy (n=3), pet ownership (n=7), agriculture (n=3), hunting (n=2), outdoor activities (n=2) and climate engagement (n=2).

### Outlook

To our knowledge, this is the first study in Germany of this scope to explore transdisciplinary stakeholder perspectives on translating OH into epidemiological research practice. The findings will support future OH-oriented cohort studies.

**Snacks & Poster Viewing I / 450****Molecular evidence of canine parvovirus type 2 (Protoparvovirus carnivoran1) circulation before the 1978 panzootic****Author:** Annika Graaf-Rau<sup>1</sup>**Co-authors:** Anne Voß<sup>2</sup>; Ayumu Hyodo<sup>1</sup>; Jenny Lorke<sup>1</sup>; Ariane Dux<sup>3</sup>; Achim Gruber<sup>2</sup>; Sébastien Calvignac-Spencer<sup>1</sup><sup>1</sup> *Department of Pathogen Evolution, Helmholtz Institute for One Health, Greifswald, Germany*<sup>2</sup> *Institut für Tierpathologie, Freie Universität Berlin, Berlin, Germany*<sup>3</sup> *Department of Ecology and Emergence of Zoonotic Diseases, Helmholtz Institute for One Health, Greifswald, Germany***Corresponding Author:** annika.graafrau@helmholtz-hioh.de

Canine parvovirus type 2 (CPV-2) caused a global panzootic in dogs in 1978 after emerging from a feline panleukopenia virus (FPV)-like ancestor. Although serological studies have suggested earlier circulation, direct pathological and molecular evidence has been lacking.

To investigate the early history of CPV-2, we screened 10 archival canine pathology specimens collected in 1977 and 1978 in Berlin, Germany, using shotgun high-throughput sequencing. We recovered a near-complete CPV-2 genome (99% genome coverage) from a dog that died in 1977. Histopathological findings were consistent with classical parvoviral disease. In addition, the reconstructed viral genome differed from the previous most ancient genome of CPV-2 (derived from a dog sampled in the USA in 1978) at only 2 noncoding positions.

These findings therefore show that CPV-2 circulated in dogs before its first recognition and already cause a similar disease. They also demonstrate that CPV-2 did not evolve measurably at the amino acid level in the first months of the panzootic. Together, these results support earlier serological observations and highlight the value of archival pathology collections for reconstructing pathogen emergence and early spread.

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**Detection and genetic characterization of *Erysipelothrix rhusiopathiae* in wild birds and poultry****Author:** Anna Sawicka-Durkalec<sup>1</sup>**Co-authors:** Grzegorz Tomczyk<sup>1</sup>; Olimpia Kursa<sup>1</sup>; Agata Sieczkowska<sup>1</sup>; Sylwia Kozak<sup>1</sup><sup>1</sup> National Veterinary Research Institute, Poland**Corresponding Author:** anna.sawicka@piwet.pulawy.pl

*Erysipelothrix rhusiopathiae* is a zoonotic, environmentally persistent bacterium causing erysipelas in livestock, wildlife and humans. Although poultry and waterfowl outbreaks are increasingly reported, the role of wild birds at the wildlife–farm interface and fluoroquinolone-resistance markers remain poorly defined. Between 2016 and 2025, we screened liver samples from 553 wild birds representing 31 species, and 205 poultry flocks: 100 chicken, 26 turkey, 38 duck, and 41 goose. Samples were tested by 16S rRNA PCR, and species identification was confirmed by *gyrB* sequencing. In confirmed positives, quinolone-resistance regions of *gyrA* and *parC* were analysed. *E. rhusiopathiae* 16S rRNA was detected in 7/553 wild birds: white storks (4/33), mute swans (2/129) and a raven (1/6). In poultry, 3/41 goose flocks were positive, whereas chicken, turkey and duck flocks were negative. Sequence analysis revealed high genetic similarity to strains previously detected in livestock, poultry and humans. Mutations consistent with fluoroquinolone resistance were detected in both *gyrA* and *parC* in one positive goose flock, while the remaining positives lacked these markers. These results indicate the occurrence of *E. rhusiopathiae* at the interface of wild birds and farmed waterfowl, with geese representing the positive poultry group. Molecular surveillance integrating wildlife, poultry and AMR markers can support risk assessment for this under-monitored zoonosis.

**Snacks & Poster Viewing I / 458****Assessment of Timeliness of Detection, Notification, and Response to a Human Anthrax Outbreak in Kazo District, Uganda, December 2025–March 2026**

**Authors:** Pauline Achom<sup>1</sup>; Richard Migisha<sup>2</sup>; Riolexus Alex Ario<sup>1</sup>; Sharon Namasambi<sup>1</sup>

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**Background:** Anthrax is endemic in Uganda's cattle corridor. During December 2025–March 2026, Kazo District reported 135 human anthrax cases, including 14 PCR-confirmed cases and two deaths, following repeated sudden livestock deaths. We assessed the timeliness of outbreak detection, notification, and early response using the 7-1-7 framework.

**Methods:** We reviewed records and interviewed district health, veterinary, and surveillance officials. We assessed detection within 7 days of outbreak emergence, notification within 1 day of detection, and completion of key response actions within 7 days of notification.

**Results:** The first human case developed symptoms on 10 December 2025. Detection occurred 35 days later, missing the target. Notification occurred within 1 day, meeting the target. Key response actions were completed 10 days after notification. Delays were due to poor reporting of livestock deaths, delayed care-seeking, low anthrax suspicion among health workers, weak human-animal surveillance linkages, resource constraints, and slow coordination. Existing reporting systems enabled timely notification, while district response capacity and deployment of the national rapid response team supported outbreak control.

**Conclusion:** Delayed recognition of livestock and human health signals slowed detection and response. Strengthening integrated surveillance, community reporting, health-worker awareness, and access to response resources could reduce delays in future outbreaks.

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**The Rise of the Tiger? Competitive Interactions between *Aedes albopictus* and Native Species in a Changing Climate****Author:** Rebecca Busse<sup>1</sup>**Co-authors:** Fanny Hellhammer<sup>1</sup>; Leonie Ebert<sup>1</sup>; Marius Kropf<sup>1</sup>; Stefanie C. Becker<sup>1</sup><sup>1</sup> *TiHo Hannover***Corresponding Author:** rebecca.busse@tiho-hannover.de

The presence of *Aedes albopictus* in Germany raises concerns about its potential ecological impact on native mosquito species, particularly *Culex* spp. and *Culiseta* spp. This study investigates whether *Ae. albopictus* exhibits competitive superiority over native mosquito species under varying temperature regimes, food concentrations and habitat structure and size, and sublethal exposure to *Bacillus thuringiensis* (BTI), testing the hypothesis that *Ae. albopictus* dominates under environmental pressure due to greater stress resilience.

Preliminary competition experiments were conducted in 6-well plates at 18°C and 25°C, using L1 larvae under two food levels (4 and 6mg Tetra Pleco per well). Development time, emergence rate, and mortality were monitored across two temperature regimes (25°C-19°C) and the various stressors. In a second step the competition assays were also conducted across different container sizes to include larval habitat size as a stressor (6-well plates, urine cups, 300mL containers, 500mL flat and high containers, and 1L trays).

The main experiment used field-collected eggs from ovitraps across urban areas in Hannover. Eggs were reared in cold chambers at 18°C and subjected to competition assays. Species composition of ovitrap catches was assessed using emerged adults. Different stressors were tested at 19°C and 25°C.

These findings will help to identify which larval habitats support the presence of the tiger mosquito in the context of climate change.

**Snacks & Poster Viewing I / 473****Need Data on foodborne Zoonoses and Antimicrobial Resistance in animals and foods? Look No Further Than ZooNotify****Author:** Tasja Crease<sup>1</sup>**Co-authors:** Dominic Toelle<sup>2</sup>; Carolina Plaza-Rodriguez<sup>2</sup>; Mahtab Iltarabian<sup>1</sup>; Katja Alt<sup>3</sup>; Bernd-Alois Tenhagen<sup>1</sup><sup>1</sup> *German Federal Institute for Risk Assessment (BfR), Department 4: Biological Safety, Unit 43: Epidemiology, Zoonoses and Antimicrobial Resistance*<sup>2</sup> *(1) German Federal Institute for Risk Assessment (BfR), Department 4: Biological Safety, Unit 43: Epidemiology, Zoonoses and Antimicrobial Resistance*<sup>3</sup> *German Federal Ministry of Agriculture, Food and Regional Identity (BMLEH), Department 3: Food Safety and Animal Health, Division 314: Meat and food hygiene***Corresponding Author:** [tasja.crease@bfr.bund.de](mailto:tasja.crease@bfr.bund.de)

We previously presented ZooNotify, a web-based platform providing access to zoonoses monitoring data collected along food chains in Germany. Significant developments have been made to enhance the platform's interactivity and flexibility. The available graphs are now dynamic, and filter options for data and graphs have been expanded. These improvements enable users to explore and analyze the data more efficiently. Currently, ZooNotify contains antibiotic resistance and typing data for > 60.000 representative bacterial isolates and > 800 prevalence estimates for different zoonotic agents and foodborne bacteria. The majority of the data is related to livestock and foods of animal origin. However, data is also available on feed, wild animals and plant-based foods, thereby taking a more holistic One-Health approach and including rarely available data. Moreover, data on antimicrobial use have been included. The data on ZooNotify can be downloaded, and the graphs can be reused in presentations or reports, facilitating the dissemination of information and supporting informed decision-making. We will highlight the new features and demonstrate the potential of ZooNotify for risk assessment, research, and decision-making in the context of one health. Overall, ZooNotify has the potential to greatly facilitate research in the field of zoonoses and antimicrobial resistance, and to support the development of new strategies for preventing and controlling the spread of zoonotic diseases.

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**Zoonotic virus dynamics in megadiverse regions: insights from wildlife across land-use gradients in Colombia****Authors:** Erika Garcia<sup>1</sup>; Natalia Trujillo<sup>2</sup>**Co-authors:** Alex Greenwood<sup>3</sup>; Gabriela Aliaga Samanez<sup>4</sup>; Gábor Á. Czirják<sup>3</sup>; Lucy Keatts<sup>5</sup>; Luz Dary Acevedo-Cendales<sup>5</sup>; Maily González<sup>6</sup>; Maricruz Jaramillo<sup>5</sup>; Marina Reyne<sup>3</sup>; Mathieu Pruvot<sup>5</sup>; Sarah H. Olson<sup>5</sup>; Yuliana Castañeda<sup>7</sup><sup>1</sup> *Instituto de investigación en recursos biológicos Alexander von Humboldt, Colombia*<sup>2</sup> *Instituto de Investigación en Recursos Biológicos Alexander von Humboldt*<sup>3</sup> *Leibniz Institute for Zoo and Wildlife Research*<sup>4</sup> *Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany*<sup>5</sup> *Wildlife Conservation Society*<sup>6</sup> *Instituto de investigación en recursos biológicos Alexander von Humboldt*<sup>7</sup> *Instituto de investigación en recursos biológicos Alexander von Humboldt,***Corresponding Author:** samanez@izw-berlin.de

Land-use (LU) change in highly biodiverse regions is increasingly recognized as a key driver of zoonotic disease emergence. Such transformations reshape wildlife communities, alter vector dynamics, and create new interfaces among wildlife, domestic animals, and humans. The SIMPEL project aims to evaluate pathogen diversity and prevalence across a land-use gradient in the Colombian Amazon (Objective 4). Fieldwork was conducted at two sites (Calamar and San José) representing different disturbance levels. Bats and rodents were sampled in dry and wet seasons using swabs and blood samples. Screening targeted coronaviruses and arenaviruses using pan-PCR, complemented by viral enrichment and high-throughput sequencing. Preliminary results show widespread circulation of both viral families, with patterns varying by site and taxon. Coronavirus prevalence in bats showed contrasting trends, decreasing with disturbance in Calamar but increasing in San José, without significant differences across LU categories. In rodents, prevalence remained high (85–100%) regardless of LU. Arenavirus showed site specific dynamics, remaining low in Calamar bats but increasing in transformed areas in San José ( $p < 0.05$ ), while remaining low in rodents ( $<10\%$ ). These results suggest that pathogen responses to LU change vary across host virus systems and local contexts, and highlights the need to integrate ecological and epidemiological data to better anticipate zoonotic spillover risk.

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## Persistent Microbial Signatures Connect Latin America's Largest Environmental Disaster to the South Atlantic's Largest Coral Reef Complex

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The Fundão tailings dam collapse released about 55 million m<sup>3</sup> of mining waste and is seen as Brazil's largest environmental disaster and a major event in global mining. Its impacts reached rivers, lagoons, coastal waters, and distant reefs such as Abrolhos Archipelago, the largest coral reef complex in the South Atlantic. However, its long-term biological effects, especially on environmental and coral microbiomes, remain poorly understood. Here, we analyzed sediment, water, and two coral species, *Millepora alcicornis* and *Mussismilia harttii*, via 16S rRNA gene sequencing. We assessed metals and biochemical markers of metal stress. From September 2018 to July 2024, with two campaigns per year, 4,391 samples were analyzed. Bacterial and archaeal groups associated with heavy metals and tailings were abundant in nearly all sample types, including Abrolhos corals. Although Abrolhos is 1,103 km from Fundão and 250 km from the Doce River mouth, coral microbiomes were more similar to Doce River sediments than to local Abrolhos sediment and water. During rainy seasons, metal- and tailings-associated taxa increased in the Doce River and were enriched in corals, sometimes dominating their microbiome. Coral communities also showed more microorganisms linked to environmental stress, suggesting dysbiosis. These results indicate that the Doce River plume may still influence riverine, coastal, and coral microbiomes, supporting a persistent “microbial bridge” between the disaster and Abrolhos.

**Snacks & Poster Viewing I / 486****Transcriptomic Profiling of Borna Disease Virus 1 Infection in Adult Rat Organotypic Hippocampal Slice Cultures****Author:** Maximilien Lépine<sup>1</sup>**Co-author:** Christiane Herden<sup>1</sup><sup>1</sup> *Institute of Veterinary Pathology, Justus-Liebig-University Gießen***Corresponding Author:** maximilien.lepine@vetmed.uni-giessen.de

Borna Disease Virus 1 (BoDV1) is a neurotropic zoonotic pathogen that causes fatal non-suppurative encephalitis in humans and various livestock. While the white-toothed shrew (*Crocidura leucodon*) acts as a natural reservoir hosting persistent, asymptomatic infections, the adult rat serves as a well-established model for studying the inflammatory response.

In this study, we utilized established organotypic hippocampal slice cultures (OHCs) from adult rats to investigate the transcriptomic landscape during acute BoDV1 infection. Building on previous findings that BoDV1 shows distinct intracellular distribution and viral loads between 3 and 7 days post-infection, we employed nCounter technology to identify differentially expressed genes.

Our results reveal significant regulation in pathways related to apoptosis, tissue/cellular growth and maturation, and inflammatory modulation indicating multifaceted modulation of cellular function of brain cells. Whether comparable regulatory effects in brain cells are also evident during acute infection of reservoirs such as shrews needs to be further investigated as well as effects of invading immune cells. This can be analyzed by hippocampal tissue from in vivo infection studies of rat and shrew models.

Ultimately, this study demonstrates that OHCs are a powerful tool for analyzing and modeling viral neuroinflammation, offering a high-throughput approach to refine experimental directions and reduce the reliance on live animal models.

**Snacks & Poster Viewing I / 488****Retention in paediatric and adolescent HIV care among the successive 2020–2023 ART quarterly initiation cohorts in Uganda****Author:** Kyomugisha Denise Aman<sup>1</sup>**Co-authors:** Benon Kwesiga<sup>1</sup>; Ivan Lukabwe<sup>1</sup>; Alex Ario<sup>1</sup>; Eleanor Magongo<sup>2</sup><sup>1</sup> *Uganda Public Health Fellowship Program, Uganda National Institute of Public Health, Ministry of Health*<sup>2</sup> *AIDS Control Program, Ministry of Health***Corresponding Author:** [akyomugisha@uniph.go.ug](mailto:akyomugisha@uniph.go.ug)

Retention in HIV care is critical for achieving viral suppression and the second UNAIDS 95 target. We described variation in paediatric and adolescent retention among 2020–2023 ART initiation cohorts in Uganda.

We analyzed aggregated paediatric (0–9 years) and adolescent (10–19 years) ART cohort data from the District Health Information Software. Sixteen quarterly ART initiation cohorts per age group (Q1 2020–Q4 2023) were assessed at 6, 12, and 24 months post-initiation. Retention was the proportion alive and on ART among the net current cohort (original cohort plus transfer-ins minus transfer-outs). It was described nationally and regionally, and compared with the 95% target.

National paediatric retention was 75–95% at 6 months, 60–100% at 12 months, and 70–80% at 24 months, except Q3 2023 (40%). Only Q4 2022 met the 6-month target and Q2 2020 the 12-month target; none met the 24-month target. West Nile region sustained the 6- and 12-month paediatric target.

National adolescent retention ranged from 70–85% at 6 months, 75–85% at 12 months, and 60–70% at 24 months, except Q4 2023 (30%). No adolescent cohorts met the target. Karamoja region had high target achievement in paediatric and adolescent cohorts.

Most paediatric and adolescent cohorts in Uganda failed to meet the 95% retention target, with the largest gaps among adolescents and at 24 months, varying by region. Strengthening follow-up, early tracing, and adolescent-centred support could improve engagement in HIV care.

**Snacks & Poster Viewing I / 495****Isolation of infectious Hepatitis E virus from wastewater treatment plants and its methodological challenges****Author:** Nele Gremmel<sup>1</sup>**Co-author:** Paul Becher<sup>1</sup><sup>1</sup> *University of Veterinary Medicine Hannover, Institute of Virology***Corresponding Author:** nele.gremmel@tiho-hannover.de

Hepatitis E virus (HEV) is a One Health pathogen causing acute hepatitis, severe disease in vulnerable patients, and chronic infection in immunocompromised individuals. While zoonotic transmission is established, environmental HEV spread remains poorly understood. We investigated urban wastewater treatment plants to recover infectious HEV and address methodological barriers of this sample matrix. Wastewater was sampled at sedimentation, after approximately 50% and 100% of biological treatment, and from the effluent. After ultracentrifugation-based pelleting, HEV RNA was detected by qPCR in one of four sampling events. Despite low viral loads in pellets (Ct 36–38), infectious virus was isolated on PLC/PRF/5 cells. Infectivity persisted after storage at 4°C for 5 weeks. Sequencing and phylogenetic analysis identified HEV subtype 3e.

These results demonstrate the sensitivity of the cell culture system, but also highlight critical challenges: large sample volumes, dilution, PCR inhibitors, microbial contamination, preservation of infectivity, and pellet-recovery controls. Detecting infectious HEV in wastewater is highly relevant, as it provides direct evidence for environmental persistence beyond RNA detection and supports risk assessment and surveillance at the human-animal-environment interface.

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**Wildlife Health Surveillance – Preventing Pandemics at Source: Findings from the Interdisciplinary Project ‘Bat Health in Central Germany – From Pathology to Protection’****Author:** Amelie Lisa Arnecke<sup>1</sup>**Co-authors:** Marcus Fritze<sup>2</sup>; Maxim Ludwig<sup>3</sup>; Juliane Hintzen<sup>4</sup>; Cora Delling<sup>4</sup>; Kristin Heenemann<sup>5</sup>; Kristin Mühldorfer<sup>6</sup>; Nicole Rudolph<sup>7</sup>; Michael Hardt<sup>7</sup>; Andrea Konrath<sup>7</sup>; Thomas Müller<sup>8</sup>; Conrad Freuling<sup>8</sup>; Susanne Ress<sup>9</sup>; Reiner Ulrich<sup>1</sup><sup>1</sup> *Institute of Veterinary Pathology, Faculty of Veterinary Medicine, Leipzig University*<sup>2</sup> *Competence Center for Bat Conservation in Saxony-Anhalt, Karst Landscape Biosphere Reserve, South Harz, Germany; Applied Zoology and Nature Conservation, Greifswald University, Greifswald, Germany; German Bat Observatory*<sup>3</sup> *Office for Environmental Protection, City of Leipzig*<sup>4</sup> *Institute of Parasitology, Faculty of Veterinary Medicine, Leipzig University*<sup>5</sup> *Institute of Virology, Faculty of Veterinary Medicine, Leipzig University*<sup>6</sup> *, Department of Wildlife Diseases, Leibniz Institute for Zoo and Wildlife Research*<sup>7</sup> *Saxon State Laboratory of Health and Veterinary Affairs, Leipzig*<sup>8</sup> *Institute of Molecular Virology and Cell Biology, Friedrich-Loeffler-Institut (FLI); WHO, WOA, FAO and National Reference Laboratory for Rabies*<sup>9</sup> *Education in a Digitalized World / Digital Education, Institute of Education, Technische Universität Berlin,***Corresponding Author:** amelie.arnecke@vetmed.uni-leipzig.de

Bats are keystone species and indicators of ecosystem health. Additionally, surveillance offers insights into zoonotic risks and anthropogenic impacts. Thus, understanding diseases and mortality in local bats enables assessing potential threats to animals, humans and the environment.

This interdisciplinary project combines macroscopic and histopathological examination, pathogen detection as well as analyses of the immune system. Additionally, a tissue biobank has been established to support future research. To date, 30 bats representing 11 species have been examined. Causes of mortality were classified according to the WHO ICD-11 system. Findings are integrated into science communication and educational activities.

Trauma was the leading cause of mortality (40%; n = 12), mainly blunt force trauma consistent with collisions, and sharp trauma consistent with predation. Combined infection and trauma (comorbidity; order unclear) represented the second most common cause (20%; n = 6), followed by infection alone (17%; n = 5), including one Daubenton's bat with polioencephalitis associated with European bat lyssavirus 2 infection. Furthermore, 63% (n = 19) of examined bats revealed predominantly subclinical endoparasitic infections, mainly trematodes.

Continued health surveillance of endemic bats will improve our understanding of host-pathogen interactions and support the One Health approach. A key challenge remains balancing public awareness of health risks with bat conservation.

**Snacks & Poster Viewing I / 503****Shiga toxin-encoding *Escherichia coli* from South American Camelids in Germany – prevalence, stx gene subtype distribution and strain characterization****Author:** Christian Berens<sup>1</sup>**Co-authors:** Michael Weber<sup>1</sup>; Christian Menge<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut***Corresponding Author:** christian.berens@fli.de

South American camelids (SAC) are popular in Europe, frequently kept with other livestock species and in close contact with humans. They, thus, represent a potential reservoir for transmission of epizootic and zoonotic bacteria to livestock and humans. To investigate the presence of Shiga toxin-encoding *Escherichia coli* (STEC) in SAC, 20 animals each were sampled four times in ten or nine herds. The overall prevalence of stx-positive samples was 32%. This resolved into 6.4%, 18% and 7.5% prevalence for stx1-, stx2- and stx1/stx2-positive samples, respectively. There was no difference in prevalence between alpacas (43%) and llamas (41%). The herd prevalence diverged widely from 0%-95% stx-positive animals. The stx-subtypes determined were primarily stx1c (78%) and stx2b (77%), while a few animals were PCR-positive for stx1a, stx2c, stx2d, stx2e and stx2f. Multiple stx2 subtype signals were detected in multiple samples (13%). In 27 stx2-positive samples, a subtype could not be assigned. So far, 13 isolates were obtained and sequenced. They feature the genoserotypes O5:H19, O55:H12, O76:H19, O87:H16, O128:H2, O151:O118:H16, and O187:H28. The prevalences determined are similar to prevalence ranges published for cattle, small ruminants and camelids. Colonization with STEC differed widely between individual farms and showed no seasonality. More isolates will be required to assess the STEC public health risk. Those identified so far would classify as having low pathogenic potential.

**Snacks & Poster Viewing I / 504****FoodChain-Lab Web: A One Health platform for integrated food-borne outbreak investigation and supply chain tracing****Author:** Marion Gottschald<sup>1</sup>**Co-authors:** Alexander Falenski<sup>2</sup>; Marco Rügen<sup>2</sup>; Bernd-Alois Tenhagen<sup>2</sup><sup>1</sup> *German Federal Institute for Risk Assessment*<sup>2</sup> *German Federal Institute for Risk Assessment***Corresponding Author:** marion.gottschald@bfr.bund.de

FoodChain-Lab Web (FCL Web, <https://fcl-portal.bfr.berlin/>) is a free, open-source software platform that supports food safety authorities in tracing food and feed through complex global supply chains during foodborne outbreaks. Developed by the German Federal Institute for Risk Assessment (BfR), FCL Web has evolved through collaborations including the EFSA–BfR cooperation, One Health EJP COHE-SIVE, and FoodSafeR into a modular, interoperable platform used by authorities such as AGES (Austria) and the U.S. FDA. Built on the One Health concept, it enables epidemiologists, veterinarians, and food safety professionals to jointly investigate outbreaks or other foodborne incidents by integrating tracing data collection with automated visualization, analysis, anonymization and reporting of the collected data within a single web-based application. Supply chains are displayed as interactive networks, allowing users to explore product flows, filter complex datasets, and test hypotheses such as cross-contamination events or geographic clustering using scoring algorithms. Through harmonized data formats and interfaces, FCL Web can be connected to national and European tracing systems, supporting cross-sectoral collaboration and rapid outbreak investigations. Beyond food supply chains, FoodChain-Lab has also been applied to animal movement tracing and hospital outbreak investigations, demonstrating its versatility as a One Health software solution for managing biological threats.

**Snacks & Poster Viewing I / 505****Health-related quality of life after tick-borne encephalitis in southern Germany in 2018-2020: a matched case-control study****Author:** Maurus Hagemeister<sup>None</sup>**Co-authors:** Antonia Pilic; Christiane Wagner-Wiening; Frank Sandmann; Merle M. Böhmer; Teresa Nygren; Thomas Harder; Wiebke Hellenbrand**Corresponding Author:** hagemeisterm@rki.de**Background**

Tick-borne encephalitis (TBE) is a vaccine-preventable neurological disease endemic in parts of Germany (~600 cases/year), yet evidence on its impact on health-related quality of life (HRQoL) is limited.

**Methods**

Adults and children with laboratory-confirmed TBE (2018–2020, Bavaria/Baden-Württemberg) were surveyed initially (t1, median 126 days after onset) and ~1.5 years later (t2); frequency-matched controls (age, sex, region) once at t1. We assessed eight Neuro-QoL domains spanning physical, cognitive, and psychosocial function. Impairment (>0.5 SD from norm) was compared by time point and age group using conditional logistic regression adjusted for age, sex, and region.

**Results**

The analysis comprised 542 cases and 481 controls at t1, and 499 cases at t2. At t1, adult cases showed higher impairment than controls across all domains, most markedly for cognitive function (38% vs. 8%) and social roles (34% vs. 11%); impairment remained elevated at t2 (cognitive function 30%). Regression confirmed significantly elevated odds of impairment in adult cases in every domain at both time points (all  $p < 0.001$ ), peaking at t1 for cognitive function (OR 2.93). At t2, ORs ranged from 1.79 (depression) to 2.71 (upper extremity function). In children, impairment was lower.

**Conclusions**

TBE imposes a substantial, persistent burden on HRQoL across functional and psychosocial domains, underscoring the importance of prevention and informing immunisation recommendations.

**Snacks & Poster Viewing I / 509****Comparative Characterization of Borna Disease Virus 1 Field and Laboratory Isolates in the Rat Model****Author:** Lorenz Ulrich<sup>None</sup>**Co-authors:** Donata Hoffmann; Martin Beer; Dennis Rubbenstroth; Kore Schlottau<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut Bundesforschungsinstitut für Tiergesundheit***Corresponding Author:** kore.schlottau@fli.de

The Borna disease virus 1 (BoDV-1) causes fatal encephalitis in animals and humans. Currently, five phylogenetic clusters (Clusters 1–5) are distinguished for BoDV-1. A characteristic feature is their distinct geographic distribution, as the individual clusters are closely associated with specific endemic areas in Germany as well as neighboring regions of Austria, Switzerland, and Liechtenstein. For some of these clusters, there are corresponding isolates that have been passaged multiple times in the past, both in cell culture and in various animal species. These are referred to as laboratory strains.

To identify differences between laboratory strains and relatively recently isolated field strains, and to uncover any differences that might exist between the individual clusters, a total of twelve different strains/isolates were characterized in the rat model. For this purpose, six neonatal or adult rats per isolate were inoculated intracerebrally, and the animals were monitored over a study period of up to eight weeks.

Two isolates, which differed most significantly in terms of their clinical presentation, were also characterized in greater detail using additional routes of infection and over a longer period of time.

The comparative characterization of field and laboratory isolates of BoDV-1 helps identify differences in virulence and pathogenesis. It thereby improves the validity of experimental animal models and the usability of the knowledge gained for natural infections.

**Snacks & Poster Viewing I / 511****Temporal Comparison of Malaria Incidence between Urban and Rural Areas in Uganda, 2020–2024****Authors:** Maria Nakabuye<sup>1</sup>; Michael Mutegeki<sup>1</sup><sup>1</sup> *Uganda National Institute of Public Health***Corresponding Author:** nakabuyemaria.mn@uniph.go.ug

**Background:** Malaria has traditionally affected rural populations, but transmission is increasing in rapidly-growing urban areas of sub-Saharan Africa. We compared malaria incidence trends in urban and rural Uganda to inform targeted interventions.

**Methods:** We conducted an ecological analysis of monthly District Health Information Software-2 malaria data (2020–2024) for 10 cities and their districts, using confirmed outpatient malaria cases as the numerator and Uganda Bureau of Statistics population estimates as the denominator. We conducted linear regression analysis to assess differences between urban and rural settings using an interaction term between setting and time. The model included year, setting, and their interaction term.

**Results:** Malaria incidence declined over time in both settings, with a greater reduction in rural areas. Rural incidence decreased significantly from 318 to 254 per 1,000 population ( $p=0.02$ ) while the decline in urban incidence from 249 to 198 per 1,000 population ( $p=0.34$ ) was not significant. The difference in trends between urban and rural settings was statistically significant (interaction  $p=0.047$ ).

**Conclusion:** Malaria incidence in Uganda declined over the study period, with a more significant decline in rural areas than urban areas. Uganda should sustain vector control and case management in rural areas while implementing targeted surveillance-driven interventions in urban hotspots such as improved housing and drainage of breeding sites.

**Snacks & Poster Viewing I / 519****Évaluation of the effets of wastewater on the prolifération of waterborne bacterial diseases in the Olezoa stream.****Author:** Raphaël Dieudonné Laurent FOUDA NGONO BELIBI<sup>1</sup>**Co-author:** Serge ZEBAZE<sup>2</sup><sup>1</sup> *University of Yaounde 1*<sup>2</sup> *University of Yaoundé 1***Corresponding Author:** rfoudabelibi@gmail.com

A study aimed at evaluating the impact of black water in the aquatic environment and on the proliferation of water-borne diseases was carried out in the Olézoa stream, during the period from April to September 2020. In this context, One Health approach emerges as a relevant conceptual framework for understanding the resurgence of these disease and the interactions between the different compartments (aquatic environment and human population) in order to assess the overall infectious risk. The survey carried out among the local population showed that the use of water ressources of Olezoa watercourse is responsible in humans for amoebic and bacillary dysentery, typhoid and paratyphoid fevers requiring expensive treatment, ranging from 7,500 to 18,500 FCFA per month. These waters harbor BHAMs; Fecal Coliforms; Fecal Streptococci whose abundances have varied between 6 to 4.56; 0 to 3.42 and from 0 to 4.39 units log CFU/100 ml respectively; the monthly abundances of these bacteria undergo spatio-temporal fluctuations. In addition, they harbor pathogenic bacteria such as *V. Cholerae* and *Salmonella Typhi* among others whose abundances vary between 0 to 4.03 and from 0 to 2.88 units log CFU / 100ml respectively.

The black water discharged without prior treatment increases the proliferation of water-borne diseases and makes the rivers unfit for all consumption.

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**Prevalence and genetic diversity of Puumala virus (*Orthohantavirus puumalaense*) in bank voles (*Clethrionomys glareolus*) from northern boreal forest Sweden****Author:** Alina Anton<sup>None</sup>**Co-authors:** Arne Hegemann<sup>1</sup>; Frauke Ecke<sup>2</sup>; Hannes Bergmann<sup>1</sup>; Lutz Breuer<sup>3</sup>; Rainer Ulrich; Sascha Knauf<sup>1</sup>; Valerie Allendorf<sup>1</sup>; Yonas Meheretu<sup>4</sup>; Zihan Dai<sup>5</sup><sup>1</sup> *FLI*<sup>2</sup> *University of Helsinki*<sup>3</sup> *JLU*<sup>4</sup> *SLU*<sup>5</sup> *Jülich Institut***Corresponding Author:** alina.anton@fli.de

Puumala virus (PUUV, *Orthohantavirus puumalaense*), the causative agent of human nephropathia epidemica, is an important zoonotic pathogen in Europe. Our study investigated PUUV RNA occurrence, genetic diversity, and environmental associations in bank voles (*Clethrionomys glareolus*) from two boreal forest areas in northern Sweden across a vole population cycle from 2020–2023. Lung-derived RNA from 519 bank voles was screened for a partial PUUV S-segment by RT-PCR and Sanger sequencing, and infection probability was analysed using logistic regression. Overall, 83/519 voles tested PUUV RNA-positive. Seasonality was the main factor influencing PUUV RNA occurrence, with study-area differences most evident in spring and body weight positively associated with infection probability particularly in autumn. Predicted prevalences were higher in males than females, 23.7% (95% CI: 17.0–32.0) vs. 8.3% (95% CI: 4.6–14.8), and increased from 8.6% in 2020 (95% CI: 3.6–19.2) to 25.6% in 2022 (95% CI: 17.6–35.6). All detected PUUV RNA sequences belong to the North-Scandinavian lineage, with limited spatial or temporal structuring. Land-use analyses at multiple spatial scales identified no significant habitat predictors. Overall, PUUV dynamics appeared to be shaped mainly by seasonality, reservoir demography, and vole population cycles rather than broad-scale landscape composition, emphasizing the importance of these factors for predicting periods of elevated human infection risk.

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**From landscape to liver: exploring trace element exposure in wild boar from Brandenburg, Germany****Author:** Maciej Durkalec<sup>1</sup>**Co-authors:** Rafael Hernán Mateus-Vargas<sup>2</sup>; Roman Schmidt<sup>1</sup>; Stephanie Panitz<sup>1</sup>; Jana Rupp<sup>1</sup>; Melanie Gimpel<sup>1</sup>; Alexander Roloff<sup>1</sup>; Carsten Fahl-Hassek<sup>1</sup>; Julia Steinhoff-Wagner<sup>3</sup>; Robert Pieper<sup>1</sup>; Anneluise Mader<sup>1</sup><sup>1</sup> Bundesinstitut für Risikobewertung<sup>2</sup> University of Göttingen<sup>3</sup> University of Munich**Corresponding Author:** maciej.durkalec@bfr.bund.de

Wild boar (*Sus scrofa*) can serve as a bioindicator of environmental exposure to trace elements because of its close contact with soil, omnivorous diet, and use of diverse habitats. Because wild boar meat and organs are consumed by humans, element accumulation in this species is relevant to food safety. This study explored factors associated with element accumulation in wild boar liver.

Liver samples from 81 wild boars from 12 hunting districts in Brandenburg were analyzed for 20 trace elements by ICP-MS. Linear mixed-effects models assessed associations between liver element concentrations and individual traits (age, sex), dietary and habitat-related indicators ( $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$ ), and landscape context (urban land cover, agriculture–forest gradient), with hunting district as a random effect.

Element-specific patterns were observed.  $\delta^{13}\text{C}$  showed the strongest and most consistent associations, suggesting that foraging ecology may influence exposure. Age was associated with selected elements, including higher Cd and lower As, Pb, Zn, and Tl. Landscape effects included higher As in forested areas and higher Cd in urbanized surroundings. Hunting district explained substantial variation for several elements.

Overall, these preliminary findings indicate that biological traits, isotope signatures, and landscape context contribute to trace element accumulation in wild boar liver. Further work will investigate element-specific sources and refine interpretation of contamination pathways.

**Snacks & Poster Viewing I / 528****Cryptosporidium spp. in HIV-Positive Patients with Diarrhea in Ecuador: Diagnostic Concordance and Risk Factors****Authors:** Fiorella Rodríguez<sup>1</sup>; Luis Solórzano<sup>None</sup>; Sunny Sánchez<sup>None</sup><sup>1</sup> *INSPI - National Institute for Public Health Research / Instituto Nacional de Investigación en Salud Pública***Corresponding Author:** fiorellarodrigueze@gmail.com

*Cryptosporidium* spp. is an opportunistic enteric pathogen in people living with HIV, yet data from Latin America are limited. We conducted a cross-sectional, record-level analysis of 150 stool-sample records from patients with HIV and diarrheal syndrome at a referral hospital in Guayaquil, Ecuador, in 2015. Modified Ziehl–Neelsen microscopy and real-time PCR were compared, and clinical and epidemiological correlates were explored.

*Cryptosporidium* was identified by microscopy in 6/150 records (4.0%; 95% CI, 1.9–8.5%); two were also PCR-positive. Methods agreed in 146/150 records (97.3% raw agreement): 144 double-negative and two double-positive. Four records were microscopy-positive/PCR-negative; none were PCR-positive/microscopy-negative. All positive records had CD4 counts <200 cells/μL (range, 4–196).

In exploratory analyses, positivity was higher among records reporting well or tanker-truck water than among those reporting potable or bottled water (25.0% vs 2.9%; Fisher's exact  $p=0.035$ ). Two records with unmapped water codes were excluded; this association should therefore be interpreted cautiously. Stool frequency, animal contact, boiling water, and recorded gastrointestinal symptoms were not significantly associated with positivity (all  $p>0.05$ ).

The small number of positive records, unresolved water coding, and microscopy–PCR discordance limit causal inference. Larger patient-linked studies with complete exposure coding and assay quality control are needed.

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## Pathogen Detection Through Wildlife Mortality Surveillance in Taï National Park, Côte d'Ivoire

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Global health and biodiversity conservation face increasing threats, with the emergence of infectious diseases posing a critical challenge. Especially regions of high biodiversity are thought to harbour numerous known and novel pathogens. Carcass monitoring of wildlife populations in these regions, combined with advanced diagnostic techniques, provide an opportunity to gain deeper insights into the pathogens present, their impact on wildlife mortality, and the broader implications for ecosystem and global health.

As one of West Africa's last major biodiversity hotspots, the tropical rainforest of Taï National Park, Côte d'Ivoire, provides a unique setting for long-term wildlife health surveillance and pathogen detection. Since 2002, veterinarians at the Taï Chimpanzee Project (TCP) have performed necropsies on all carcasses found within the study area. On site veterinary staff conduct comprehensive pathological assessments and collect biological samples from each reported case. To date, more than 450 necropsies and 14,000 biological samples have been added to the TCP necropsy collection. Here, we present the RNASeq workflow used for pathogen detection and highlight infections of rainforest anthrax (caused by *Bacillus cereus* biovar *anthracis*) and monkeypox virus in wildlife of Taï National Park.

**Snacks & Poster Viewing I / 533****Lassa fever disease risk: a socioecological study of the human-rodent-virus interface****Author:** Ellie Kirke<sup>None</sup>**Co-authors:** Emmanuel Sahr Kamanda<sup>1</sup>; Emmanuel Saidu<sup>1</sup>; Helen Esser<sup>2</sup>; Kevin Matson<sup>2</sup>; Maarten Voors<sup>2</sup><sup>1</sup> *Njala University*<sup>2</sup> *Wageningen University***Corresponding Author:** [ellie.kirke@wur.nl](mailto:ellie.kirke@wur.nl)

Lassa fever is a potentially fatal haemorrhagic disease caused by the zoonotic virus, Lassa mammarenavirus (LASV). It is endemic to West Africa, where an estimated 900,000 infections and 18,000 deaths occur each year. LASV is transmitted mainly by *Mastomys natalensis*; a rodent reservoir that thrives in human-dominated landscapes across sub-Saharan Africa. Reducing disease risk relies on limiting human exposure to rodents, yet human-rodent interaction dynamics and their drivers are poorly understood. We investigated the socioecological drivers of LASV exposure risk in Sierra Leone, combining concurrent rodent trapping, human mobility tracking, and surveys to understand human-rodent shared space-use and transmission risk. Fieldwork spanned four villages across the dry and wet seasons in 2025. Rodents were trapped in and around each village and tested for LASV RNA and antibodies. We simultaneously recorded the movement patterns of 240 participants and conducted interviews to understand demographic and behavioural drivers of disease. In 2026, we collected blood samples from these participants to test for LASV-specific IgG and IgM antibodies – providing the missing link between shared space-use and actual exposure risk. Serological work is currently underway in Sierra Leone. Here we present preliminary results, with the aim of identifying who is most at risk, when and where exposure occurs within the local landscape, and the socioecological factors driving these patterns.

**Snacks & Poster Viewing I / 534****Improving biosafety measures in high containment laboratories and patient care: a systematic analysis of Orthoebolavirus and Henipavirus stability****Author:** Denise-Carina Kranz<sup>None</sup>**Co-authors:** Joo-Hee Wälzlein; Katharina Kimmerl; Andreas Kurth; Susann Kummer**Corresponding Author:** kummers@rki.de

Emerging and re-emerging high-risk pathogens demand strong biosafety protocols for both patient care and laboratory practices. This study aimed to produce experimental data to support evidence-based guidelines for improving safety measures related to Orthoebolavirus and Henipavirus. Viruses in solution were applied to materials commonly found in hospital and lab settings—stainless steel, glass, plastics, cotton, nitrile and rubber gloves, and protective suits. Stability and infectivity were monitored over time under two conditions: (1) a typical indoor lab/hospital environment and (2) warmer, humid conditions resembling a European summer. While laboratory and clinical environments are typically climate-controlled, inclusion of the higher temperature and humidity condition provides comparative data relevant for situations where environmental controls may be less consistent, such as in public or outdoor settings. Results show that virus stability depends on both the suspension medium and the surface texture. Personal protective materials generally retained the virus for shorter durations. No viable virus was found after 112 days, with most becoming undetectable by day 28. Routine chemical disinfection protocols remain the primary biosafety measures, and our findings offer key insights for refining disinfection strategies and enhancing biosafety in high-containment settings and clinical care environments.

**Coffee & Poster Viewing II / 353****Green Extraction of Bioactive Compounds from Amazonian Biodiversity for Sustainable Food Systems: A One Health Perspective****Author:** Lucas Cantão Freitas<sup>1</sup>**Co-authors:** Marcos Lucio Corazza<sup>2</sup>; Maria Lucia Masson<sup>2</sup><sup>1</sup> *Instituto Federal do Paraná*<sup>2</sup> *Universidade Federal do Paraná***Corresponding Author:** lucas.freitas@ifpr.edu.br

The Amazon rainforest represents one of the world's richest reservoirs of biodiversity, offering unique opportunities for the development of sustainable food ingredients and bioactive compounds. This work synthesizes findings generated by our research group on the valorization of Amazonian fruits, seeds, and agro-industrial by-products through green extraction technologies. Experimental studies conducted with species including tucumã, bacuri, umari, and uxi employed compressed propane, supercritical carbon dioxide, and integrated extraction approaches to recover high-value bioactive compounds.

The developed processes efficiently recovered carotenoids, phenolics, tocopherols, and health-promoting fatty acids with lower environmental impacts. Furthermore, these technologies support bioeconomy and circular economy strategies by promoting the sustainable use of underutilized resources and adding value to regional production chains.

From a One Health perspective, the sustainable recovery of bioactive compounds from Amazonian biodiversity establishes a connection between environmental conservation, human well-being, and socio-economic development. Green extraction technologies promote the production of functional ingredients, reduce waste generation, and strengthen sustainable food systems. These findings highlight the importance of integrating technological innovation, biodiversity conservation, and sustainable food systems to address global health and environmental challenges.

**Coffee & Poster Viewing II / 354****Linking Landscape Structure to Mosquito Communities: Habitat Characteristics and Vector Risk in a Changing Climate****Author:** Cara Leonie Ebert<sup>1</sup>**Co-authors:** Annika Emlinger<sup>2</sup>; Björn Maronga<sup>3</sup>; Nadja Kabisch<sup>2</sup>; Stefanie C. Becker<sup>1</sup><sup>1</sup> *Working Group for Vector-associated Biodiversity and Infection (VABI) and Research Center for Emerging Infections and Zoonoses (RIZ), University of Veterinary Medicine Hannover*<sup>2</sup> *Leibniz University Hannover, Institute of Earth System Sciences, Physical Geography and Landscape Ecology, Faculty of Natural Sciences, Hanover, Germany*<sup>3</sup> *Leibniz University Hannover, Institute of Meteorology and Climatology, Hanover, Germany***Corresponding Author:** cara.leonie.ebert@tiho-hannover.de

Landscape structure plays a key role in shaping mosquito distribution and associated health risks in changing climates. As part of the UMEX-HOPE project at the Lower Saxony Centre for Climate Research (ZKfN), we investigate how different landscape structures influence mosquito community abundance across urban–rural gradients in and around the city of Hanover. Using high-resolution remote sensing data, we classify the study area into distinct structural types based on land cover and spatial patterns. Mosquitoes are sampled systematically within these types using CO<sub>2</sub>-baited traps and ovitraps to assess species presence and abundance. This approach enables a direct comparison of mosquito community abundance across landscape settings and helps identify structural features linked to vector activity. By integrating spatial landscape patterns with field monitoring, we evaluate how habitat characteristics influence mosquito abundance. The findings support the development of targeted, evidence-based strategies for vector surveillance and risk reduction. This work advances adaptive public health planning by linking landscape patterns to potential disease transmission hotspots in the context of climate change.

**Coffee & Poster Viewing II / 359****Proteomic Profiling Reveals Distinct Molecular Response to West Nile Virus Infection Across Host Species****Author:** Marie Luise Eweleit<sup>None</sup>**Co-authors:** Axel Karger<sup>1</sup>; Birke Andrea Tews<sup>2</sup>; Kati Franzke<sup>2</sup><sup>1</sup> *Friedrich-Loeffler-Institute, Institute of Molecular Virology and Cell Biology, Greifswald, Germany*<sup>2</sup> *Friedrich-Loeffler-Institute, Institute of Infectiology, Greifswald, Germany***Corresponding Author:** marieluise.eweleit@fli.de

West Nile virus (WNV) is a mosquito-borne Orthoflavivirus, naturally circulating between its vector mosquitoes and its reservoir, birds. Mammals, like horses and humans, can be infected but are considered as dead-end hosts. Avian WNV symptoms can differ from asymptomatic to multiple organ failure. Most infected mammals show no symptoms, but in rare cases neurological diseases can occur, which can be fatal. This project aims to identify the molecular mechanisms for these diverse host responses during WNV infection. Kidney cell lines (Vero, human HEK-293, horse PFN, goose GN-R) were analyzed as possible targets of WNV infection. At 24 hours post infection, WNV titers were high in Vero, HEK-293 and GN-R, while PFN cells showed a tenfold lower titer, suggesting less efficient virus replication in equine cells. These observations were supported by immunofluorescence and transmission electron microscopy where virus particles were detected in endoplasmic reticulum, Golgi apparatus and transport vesicles. In proteome analyses, genes related to viral immune response were upregulated only in Vero cells while response in the other cells was weak. However, HEK-293 and PFN showed markers for viral infection which were absent in GN-R. In this study, we examined the replication of and host response to WNV in kidney cell lines from four different host organisms of WNV for the first time, providing insights into potentially distinct regulatory mechanisms against the virus.

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**Antimicrobial Resistance in Food-Borne Enteric Bacterial Pathogen at the Human–Animal–Environment Interface in Addis Ababa, Ethiopia: A One Health Approach****Author:** Jirata Abosse<sup>1</sup>**Co-authors:** Bekele Megersa<sup>1</sup>; Fasil Eregno<sup>2</sup>; Feleke Zewge<sup>3</sup>; Stalle Haaland<sup>4</sup><sup>1</sup> *Department of Veterinary Epidemiology and Public Health, College of Veterinary Medicine and Agriculture, Addis Ababa University, Bishoftu, Ethiopia*<sup>2</sup> *Department of Building, Energy and Material Technology, Faculty of Engineering Science and Technology, UiT The Arctic University of Norway.*<sup>3</sup> *Addis Ababa University, College of Natural and Computational Science, Africa Centre of Excellence for Water Management, Addis Ababa, Ethiopia*<sup>4</sup> *Norwegian University of Life Sciences, NMBU, Faculty of Environmental Sciences and Natural Resource Management, Norway***Corresponding Author:** jirata.shiferaw@aau.edu.et

This study employed a One Health approach to investigate the prevalence and AMR patterns of enteric bacterial pathogens circulating among humans, animals, and environmental sources in Addis Ababa, Ethiopia. A total of 512 samples, including human stool, animal feces, water, grass, and vegetables, were collected and analyzed using standard microbiological techniques, MALDI-TOF MS identification, and antimicrobial susceptibility testing in accordance with CLSI guidelines. Overall, 72 samples (14.1%) tested positive for enteric bacterial pathogens. The most frequently isolated organisms were *Escherichia coli* (3.3%), *Salmonella* spp. (4.1%), *Proteus* spp. (3.1%), and *Klebsiella* spp. (1.2%). Environmental samples exhibited the highest prevalence of bacterial contamination (22.1%), followed by human (16.3%) and animal samples (5.6%). High levels of antimicrobial resistance were observed against ampicillin, chloramphenicol, cefotaxime, and cefepime, whereas lower resistance rates were detected for ceftriaxone, ceftazidime, kanamycin, and ciprofloxacin. Resistance levels were highest among environmental isolates, suggesting that environmental sources may serve as important reservoirs and transmission pathways for resistant bacteria. The detection of AMR enteric pathogens highlight the interconnected nature of AMR for integrated surveillance, evidence-based intervention, and antimicrobial stewardship programs within a One Health framework to limit the burden of enteric diseases and AMR.

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**Genomic analysis of *Staphylococcus aureus* in the Zambian dairy value chain reveals a pandemic clone with high virulence potential****Author:** Ângelo J.F. Mendes<sup>1</sup>**Co-authors:** Bruno S.J. Phiri<sup>2</sup>; Michael Biggel<sup>3</sup>; Bernard M. Hang'ombe<sup>2</sup>; Sara Schaarschmidt<sup>4</sup>; Alexandra Fetsch<sup>5</sup><sup>1</sup> *University of Glasgow*<sup>2</sup> *University of Zambia*<sup>3</sup> *University of Zurich*<sup>4</sup> *German Federal Institute for Risk Assessment*<sup>5</sup> *LMU Munich***Corresponding Author:** alexandra.fetsch@lmu.de

Raw milk is a key exposure route for zoonotic pathogens including *Staphylococcus* (S.) *aureus* in low- and middle-income countries. *S. aureus* causes food intoxication and severe infections; pandemic clones circulate across human and animal reservoirs, raising One Health concerns. We characterised genomic diversity, AMR, and virulence potential of *S. aureus* from the Zambian dairy value chain and assessed global phylogenetic context.

Whole-genome sequencing (Illumina) data from 94 isolates collected across farms, collection centres, processors, traders, and markets (Lusaka, Southern, Western Provinces) were analysed. Analyses comprised MLST, cgMLST, AMR/virulence gene detection, and maximum-likelihood phylogenetics using 7,054 global assemblies of bovine and human origin.

Predominant local sequence types were ST97 (23.4%), ST152 (16.0%), and ST7344 (13.8%). AMR genes were detected in 69.1% of isolates. All ST152 carried PVL genes; local ST152 were closely related to human blood culture isolates from Malawi. The *tsst-1* gene was present in all ST7344 and four ST152 isolates. cgMLST revealed identical or near-identical isolates spanning multiple supply chain levels and provinces, indicating active transmission.

Circulation of the pandemic clone ST152, carrying PVL genes and *tsst-1*, across the Zambian dairy supply chain poses a direct One Health risk. Targeted control measures are needed.

**Coffee & Poster Viewing II / 377****Benchmarking cgMLST: The Impact of Allele Calling & ORF-based Post-Processing on Profile Similarity****Author:** Clara Daßio<sup>1</sup>**Co-authors:** Caroline Roschek; Martin Fischer<sup>1</sup>; Maximilian Driller Povill; Silver Wolf<sup>1</sup>; Torsten Houwaart<sup>1</sup><sup>1</sup> *Robert Koch-Institut***Corresponding Author:** dassioc@rki.de

Core genome multilocus sequence typing (cgMLST) is a modern computational method widely used for bacterial genotyping and commonly utilized in bacterial outbreak investigations. By comparing allelic profiles, closely related isolates can be identified and infection chains reconstructed. As data is exchanged between laboratories, consistent allele assignments are essential for reliable cluster detection and epidemiological interpretation. However, different allele-calling tools produce slightly differing allele assignments from identical sequence data, affecting distance calculation and cluster definition.

For several integrated genomic surveillance (IGS) relevant pathogens we analyzed 100 samples each using multiple cgMLST allele-calling tools and investigated the impact of open reading frame validation. For each tool, three profile versions were generated and compared against the profile produced by MBioSEQ Ridom Typer with respect to missingness patterns and similarity: (1) consisted of the original allele calls, (2) only novel alleles reported by the tools were validated and filtered, and (3) both novel and known alleles were excluded based on additional validation of schema alleles.

Comparison of these profiles revealed differences in missingness patterns and concordance with SeqSphere across all versions. This demonstrates that allele-calling and post-processing strategies influence cgMLST profile comparability and affect downstream analyses strongly.

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**Effects of sugar and blood diets on the proteome of female *Lutzomyia longipalpis*****Author:** Juliana Welbert<sup>1</sup>**Co-authors:** Fernando Genta<sup>1</sup>; Jeniffer Fonseca<sup>1</sup>; Redouane Ouali<sup>2</sup>; Sabrina Bousbata<sup>2</sup><sup>1</sup> Fiocruz<sup>2</sup> Université Libre de Bruxelles**Corresponding Author:** juliana.welbert@hotmail.com**Introduction**

Leishmaniasis is a vector-borne disease caused by protozoa of the genus *Leishmania* and remains a significant public health concern in tropical regions. In its vectors, blood feeding provides a suitable environment for parasite establishment in the female gut. Understanding the proteome associated with blood digestion may contribute to studies on vector competence and insect biology. Here, we compared the proteomes of different tissues from uninfected female *Lutzomyia longipalpis*, the main vector of visceral leishmaniasis in the Americas, subjected to blood and sugar feeding.

**Methods**

Blood-fed and sugar-fed *L. longipalpis* females were dissected, and their proteins were analyzed by LC-MS/MS using a bottom-up discovery proteomics approach. Proteins with differential metabolic functions in gut and body samples were identified using Perseus and UniProt annotations, and analyzed through orthology inference, multiple sequence alignment, and phylogenetic reconstruction using OrthoFinder, MAFFT, IQ-TREE, VectorBase, and NCBI Blast.

**Results**

Approximately 9,000 proteins were identified and grouped into four categories: blood-induced gut proteins, sugar-induced gut proteins, blood-induced body proteins, and sugar-induced body proteins. Comparative analyses revealed protein sets exclusive to sand flies as well as orthologs shared among hematophagous insects. Blood-induced gut proteins exclusive to sand flies emerged as promising markers of the digestive process.

**Coffee & Poster Viewing II / 381****Beyond antibiotics: The impact of reduced use and alternative interventions on livestock welfare****Author:** Melanie Westermann<sup>1</sup>**Co-authors:** Philipp Gírl<sup>2</sup>; Sophie Ramsauer<sup>3</sup>; Sonja Hartnack<sup>3</sup>; Carola Sauter-Louis<sup>4</sup>; Sophia Johler<sup>1</sup>; Alexandra Fetsch<sup>1</sup><sup>1</sup> *Competence Center for Food Safety, Chair of Food Microbiology, Faculty of Veterinary Medicine, LMU Munich, Schönleutnerstr. 8, 85764 Oberschleißheim, Germany*<sup>2</sup> *Chair of Bacteriology and Mycology, Institute for Infectious Diseases and Zoonoses, Department of Veterinary Sciences, Faculty of Veterinary Medicine, LMU Munich, 80539 Munich, Germany*<sup>3</sup> *Centre for Veterinary Public Health & One Health, Vetmeduni Vienna, Veterinärplatz 1, 1210 Vienna, Austria*<sup>4</sup> *Institute of Epidemiology, Friedrich Loeffler Institute, Südufer 10, 17493 Greifswald, Germany***Corresponding Author:** melanie.westermann@lmu.de

The global rise of antimicrobial resistance (AMR) poses a major One Health challenge, threatening animals, humans, and the environment. Antimicrobial use (AMU) is a key driver of AMR, particularly in high-density livestock production systems. However, evidence on the animal welfare implications of AMU reduction strategies and non-antibiotic interventions remains fragmented.

This scoping review aimed to map the extent and characteristics of available literature on reduced antibiotic use and non-antibiotic interventions in global livestock production, focusing on reported animal welfare outcomes and their implications across the human-animal-environment interface.

Following the Joanna Briggs Institute (JBI) methodology, systematic searches were conducted in MEDLINE, Scopus, and Web of Science Core Collection, complemented by regulatory grey literature, including evidence published from 2015 onwards. Two-stage screening by independent reviewers applied a Population-Concept-Context framework; data were extracted using DistillerSR, and results were reported in accordance with PRISMA-ScR.

This review provides a synthesized evidence base on the effects of reduced antibiotic use and non-antibiotic interventions on animal welfare in food-producing livestock, identifies key knowledge gaps at the human-animal-environment interface, and supports researchers, veterinarians, and policymakers in designing sustainable evidence-informed AMR mitigation strategies within a One Health framework.

**Coffee & Poster Viewing II / 382****Early-Life Environmental Exposures, Microbiome, and Immune Development: A One Health Perspective on Viral Infections in Children (EMVIC)****Authors:** Carolina Klett-Tammen<sup>1</sup>; Vanessa Melhorn<sup>1</sup>; Marius Vital<sup>2</sup>; Corinna Pietsch<sup>3</sup>; Gunda Herberth<sup>4</sup><sup>1</sup> *Department of Epidemiology, Helmholtz Centre for Infection Research GmbH (HZI), Braunschweig*<sup>2</sup> *Institute for Medical Microbiology and Hospital Epidemiology, Hannover Medical School, Hannover*<sup>3</sup> *Institute of Medical Microbiology and Virology, Medical Faculty, Leipzig University, Leipzig*<sup>4</sup> *Helmholtz Centre for Environmental Research - UFZ, Leipzig***Corresponding Author:** gunda.herberth@ufz.de

The EMVIC network project investigates how early environmental exposures from pregnancy onwards – including chemical exposures, psychosocial stressors and lifestyle factors – shape immune development, virus-related immune and vaccine responses, the microbiome, and long-term health in children and adolescents.

EMVIC builds on a well-characterised birth cohort with longitudinal data and biosamples from pregnancy to adolescence. Existing information on environmental exposures, immunological parameters, health outcomes, vaccination status and infections is complemented by new analyses of viral infections, immune responses, microbiome structure and function, and vaccine effectiveness. This enables an integrated assessment of complex exposure patterns and their relevance for immune resilience and viral disease risk across the life course.

Four interlinked sub-projects address environmentally associated effects on acute (measles, SARS-CoV-2) and persistent viral infections (Epstein-Barr virus), cellular immune mechanisms, microbiome-mediated immune modulation and vaccine responses. Harmonised data management and interdisciplinary analyses will strengthen the One Health Platform's methodological and infrastructural foundations. EMVIC thus provides a basis for disease prevention, vaccination strategies, and the identification of health-relevant environmental pollutants, thereby supporting evidence-based decision-making in the field of public health.

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**Inter-laboratory proficiency on antimicrobial susceptibility testing across six Sub-Saharan African countries**

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Surveillance of antimicrobial resistance (AMR) in humans, livestock, and the environment is important for early detection and understanding AMR spread across sectors. Although surveillance is mostly carried out in the human health sector, an effective AMR surveillance requires a One Health approach, supported by standardized methods for antimicrobial susceptibility testing (AST) and ring trials for quality assurance.

Seven laboratories across six Sub-Saharan African countries participated in an AST ring trial using disc diffusion, focusing on the detection of ESBL and carbapenem-resistance. The BfR provided the laboratories with ten *E. coli* strains with different resistance profiles. A panel of 14 cephalosporin and carbapenem antibiotics and antibiotic-inhibitor combinations were recommended and data interpretation according to CLSI and EUCAST guidelines were accepted.

Five laboratories performed AST according to CLSI, while two laboratories followed EUCAST guidelines. 3/7 laboratories reported at least 90% of the zone diameter and corresponding interpretation category correctly, when compared to reference values. 3/7 laboratories reported at least 80% correctly, while one laboratory reported 75% correctly.

The majority of laboratories performed properly in the ring trial. Nevertheless, the ring trial highlighted the importance of continuous inter-laboratory quality assessment and identified specific challenges that affect AST results e.g., material quality and availability.

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**Carbapenemase-producing *Klebsiella pneumoniae*: Method development for a reliable AMR monitoring in wastewater****Author:** Katharina Werner<sup>None</sup>**Co-authors:** Vladimir Bajić; Christian Blumenscheit; David Baum; Daniel Desirò; Somayyeh Sedaghatjoo; Jeanette Barthelmes; Anne-Kathrin Liebschner; Christina Förster; Stephan Fuchs; Silver Wolf; Astrid Bethe; Martin Hölzer; Birgit Walther**Corresponding Author:**

Infectious diseases caused by multidrug-resistant pathogens present a growing global public health threat causing millions of deaths each year. The surveillance of antimicrobial resistance (AMR) in wastewater will become mandatory as regulated by the revised European urban wastewater treatment directive (2024). We therefore aimed at developing reliable detection methods to monitor influent wastewater. Carbapenemase-producing *Klebsiella pneumoniae* (CP-KP) were chosen as the primary target due to their Public Health relevance. A filtration-based workflow was employed, involving colony enumeration on selective media, species verification and susceptibility testing, followed by PCR screening for key resistance genes and whole genome sequencing (WGS) of selected isolates. CP-KP concentrations ranged from 102 to 104 colony-forming units (cfu)/100 ml. All samples were positive for CP-KP, and 93 % of the subcultures were confirmed as *K. pneumoniae* (n= 297), including 79 % verified CP-KP (n= 253). PCR screening identified blaOXA-48 as the most common carbapenemase gene across the isolate collection, followed by blaNDM-1, blaKPC, and blaVIM. WGS revealed a broad range of sequence types with clinical relevance among CP-KP isolates, i.e. ST15, ST35, ST37, ST147, ST258, ST273, ST307, and ST485. Overall, the combination of culture-based methods and molecular analysis demonstrates a promising framework for monitoring and characterizing AMR in influent wastewater.

**Coffee & Poster Viewing II / 390****Combating WNV through an integrated One Health approach (WN-Vcomat) – TP 4 One Health & Climate modelling****Author:** Alina Domdey<sup>None</sup>**Co-authors:** Oliver Mbaoma<sup>1</sup>; Carl Beierkuhnlein<sup>2</sup>; Stephanie Thomas<sup>3</sup><sup>1</sup> *University Bayreuth*<sup>2</sup> *University Bayreuth, Bayreuth Center of Ecology and Environmental Research BayCEER*<sup>3</sup> *University Bayreuth, Bayreuth Center of Ecology and Environmental Research BayCEER, Geographical Institute Bayreuth GIB***Corresponding Authors:** [alina.domdey@uni-bayreuth.de](mailto:alina.domdey@uni-bayreuth.de);

West Nile virus (WNV) is a mosquito-borne virus that poses a public health risk, causing febrile illness and neuroinvasive infections in humans. WNV spreads increasingly in Europe and the intensity of outbreaks is being exacerbated by climate change.

This project seeks to understand the interactions between WNV vectors, avian hosts, human infection rates, land cover, and climate change at fine temporal and spatial scales and is coordinated by the Charité, Berlin, encompassing 6 sub-projects. Sub-project 4 One Health and Climate modelling is developing a multi-host eco-epidemiological model to understand host-vector networks and pathogen epidemiology in the metropolitan area of Berlin in light of climate change. Data from mosquito and bird sampling, and human and environmental factors will serve as input. High resolution temperature data is derived from remote sensing products with a machine learning approach. We will also develop and feed a mosquito-population model into the eco-epidemiological model. A first risk map for the area of Berlin will be presented. The approach serves as a model for other at-risk cities in Germany and beyond.

Key research questions include the spatial distribution and temporal variation of WNV transmission risk, and the impact of changes in bird diversity, mosquito abundance, and urban heat island effects. The outcomes aim to provide an online platform depicting monthly and local WNV risks in a high spatial resolution and inform the public health.

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**Is This a Gene? The Impact of ORF Filtering on cgMLST-Based Clustering and Distance Thresholds for Genomic Surveillance****Author:** Caroline Roschek<sup>1</sup>**Co-authors:** Clara Daßio<sup>1</sup>; Maximilian Driller Povill<sup>1</sup>; Silver Wolf<sup>1</sup>; Torsten Houwaart<sup>1</sup><sup>1</sup> Genome Competence Centre (MF1), Robert Koch Institute**Corresponding Author:** roschekc@rki.de

Core genome multilocus sequence typing (cgMLST) is a widely applied method for bacterial pathogen surveillance and outbreak investigations, in which pairwise genetic distances are commonly used to calculate relatedness between samples through single-linkage clustering. However, cluster definitions heavily depend on the underlying typing scheme and allele calling strategy.

Using datasets of *Mycobacterium tuberculosis* and *Listeria monocytogenes*, we evaluated the impact of open reading frame (ORF) filtering on cgMLST-based clustering. We directly compared clustering results calculated from complete and ORF-filtered cgMLST profiles generated by multiple established allele calling tools. For this, an element-centric similarity score was utilized.

We determined allelic distance thresholds required to obtain comparable clustering results across different allele calling methods. In summary, ORF-filtering reduced pairwise allelic distances between isolates by increasing cgMLST missingness. Consequently, complete profiles produced clusters with potentially increased genomic resolution compared to ORF-filtered profiles at fixed distance thresholds.

We observed that ORF-filtering substantially affects cgMLST-based distances and outbreak cluster definitions. Re-evaluating clustering thresholds based on each method enables a more consistent, meaningful intersectoral exchange regarding outbreak analyses and routine genomic surveillance.

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**Identification and impact of macrolide hemi-resistance in the food-borne pathogen *Campylobacter* spp.**

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Thermotolerant *Campylobacter* spp. are the leading cause of foodborne infections in the European Union, with macrolides being the antibiotics of choice. The point mutation A2075G in the 23S rRNA gene is the most common resistance determinant conferring high-level erythromycin resistance.

We observed that prediction of phenotypic resistance from short-read sequence assemblies failed for some isolates carrying one or two of the three copies of the 23S rRNA gene with the resistant point mutation A2075G. This hemi-resistant genotype conferred only intermediate resistance to macrolides. However, it facilitated the acquisition of a complete set of mutated 23S rRNA gene copies upon erythromycin selection, in turn conferring high-level resistance. Transition states from one to three 23S rRNA A2075G gene copies were resolved at single 23S rRNA gene loci by Oxford Nanopore sequencing.

Without antibiotic selection and upon nutrient depletion and cold stress in the water environment, the hemi-resistant genotype was stable, even upon entry into and exit from the viable but non-culturable state. It may represent a memory of macrolide resistance in *Campylobacter* from antibiotic selection in the animal (and human) host, relevant in the One Health context and currently eluding and/or perturbing detection in routine diagnostics.

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**Genetic Diversity and Molecular Epidemiology of *Giardia duodenalis* in Humans and Wildlife from the Brazilian Amazon: A One Health Perspective****Author:** Lisiane Lappe dos Reis<sup>None</sup>**Co-authors:** Lirna Salvioni Silva de Souza; Geovani Ribeiro; Maria Gabriela Rodrigues Antunes; Alessandra Ferreira Dales Nava; Sérgio Mascarenhas Morgado; Ana Carolina Paulo Vicente**Corresponding Author:** lisiane.reis@fiocruz.br

*Giardia duodenalis* infects humans and a wide range of animal hosts; however, information on its genetic diversity in wildlife from the Brazilian Amazon remains scarce. This study investigated the genetic diversity and molecular epidemiology of *G. duodenalis* in humans and wild animals from the Amazon region using multilocus sequence typing (MLST). Assemblages A and B were identified in different host species. Genetic analyses revealed, for the first time, the occurrence of assemblage A in sloths and five bat species from the Amazon region. Assemblage A was also detected in non-human primates, an anteater (*Tamandua tetradactyla*), and humans. Sub-assemblage AII was identified exclusively in humans, whereas AI, a sub-assemblage with recognized zoonotic potential, was detected in sloths, bats, and an anteater. A novel genotype, designated AIV, was identified in non-human primates and formed a distinct lineage in multilocus phylogenetic analyses. Assemblage B exhibited higher genetic diversity than assemblage A and displayed a reticulated phylogenetic pattern. High-resolution MLST schemes based on six loci for assemblage A and three hypervariable loci for assemblage B provided lineage resolution comparable to genome-based analyses. These findings expand current knowledge of *G. duodenalis* diversity in the Brazilian Amazon and provide molecular data for epidemiological investigations at the human–wildlife interface within a One Health perspective.

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**Sex-dependent impairment of antibody responses to tick-borne encephalitis virus vaccination and infection in obese mice****Author:** Jiri Salat<sup>1</sup>**Co-authors:** Andrea Fortova<sup>1</sup>; David Pajuelo Roguera<sup>2</sup>; Dominik Arbon<sup>2</sup>; Jan Prochazka<sup>2</sup>; Jana Balounova<sup>2</sup>; Jiri Holoubek<sup>3</sup>; Michal Dvorak<sup>3</sup>; Radislav Sedlacek<sup>2</sup>; Tereza Frckova<sup>1</sup>; Daniel Ruzek<sup>3</sup><sup>1</sup> *Veterinary Research Institute, Brno, Czechia*<sup>2</sup> *Czech Centre for Phenogenomics, Institute of Molecular Genetics of the Czech Academy of Sciences, Vestec, Czechia*<sup>3</sup> *Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czechia***Corresponding Author:** jiri.salat@vri.cz

Obesity is a growing global health concern with profound effects on immune function and vaccine efficacy. This study investigated the impact of obesity on immune responses to tick-borne encephalitis virus (TBEV) vaccination and infection using a mouse model. Mice fed a high-fat diet (HFD) developed increased body weight, fat mass and pre-diabetic features compared to standard chow diet (SCD) controls. Following vaccination with the TBEV vaccine (Encepur), HFD mice showed reduced TBEV-specific IgG titres and lower neutralizing antibody levels relative to SCD mice. Splenocyte counts normalized to organ mass were higher in vaccinated SCD mice, consistent with their stronger humoral response. After TBEV infection, HFD mice did not exhibit greater disease severity or higher viral titres in serum, spleen or brain, indicating that obesity did not enhance viral replication. A sex-dependent effect emerged: male HFD mice mounted antibody responses comparable to SCD males, whereas female HFD mice displayed markedly impaired IgG and neutralizing antibody production compared to female SCD mice and both male groups. These findings highlight a complex interplay between obesity, sex and immune function, with obesity disproportionately impairing the immune response after TBEV vaccination and infection.

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**Atacama Trench Microbiomes as Genome-Guided Antifungal Resources for Low-Residue Postharvest Crop Protection****Author:** Diego Sandoval Vargas<sup>1</sup>**Co-authors:** Nick Allenby<sup>2</sup>; Weijie Zhou<sup>2</sup>; Franco Fernández-Guardiola<sup>3</sup>; Juan Asenjo<sup>1</sup>; Barbara Andrews<sup>1</sup><sup>1</sup> *Universidad de Chile*<sup>2</sup> *University of Sunderland*<sup>3</sup> *Pontificia Universidad Católica de Chile***Corresponding Author:** diego.esv@gmail.com

Reliance on synthetic fungicides in postharvest systems creates a One Health challenge by linking crop losses, chemical residues, environmental pressure, and resistant fungal pathogens across agri-food, ecosystem, and food-safety interfaces. We explored whether microorganisms from the Atacama Trench, a hadal ecosystem off Chile, could provide antifungal resources against *Botrytis cinerea*, a major crop pathogen. Five metagenomes spanning 2,560–7,995 m were analysed by shotgun sequencing and genome mining to identify biosynthetic potential. To connect this potential with function, 64 trench isolates were screened in vitro against *B. cinerea* using plug- and supernatant-based assays. Fourteen isolates inhibited fungal growth by  $\geq 30\%$  in at least one condition. Activity was strongest in direct-contact assays, and three isolates were consistently active; isolate 63 reached 90.5% inhibition after 24 h pre-establishment. No visible inhibition was detected against the natural fruit-colonising fungus *Aureobasidium* sp., suggesting preliminary target selectivity. Molecular identification placed two active isolates within *Aspergillus* spp. and isolate 63 within *Bacillus* spp.; genome mining of isolate 63 revealed secondary-metabolite biosynthetic gene clusters. These findings position Atacama Trench microbiomes as an underexplored reservoir of genome-guided antifungal candidates for low-residue, microbiome-conscious and environmentally safer crop protection within a One Health framework.

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## Exploratory Profiling of Resistome Dynamics Along a Freshwater Gradient Influenced by Aquaculture Effluents

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Aquaculture is expanding globally, yet antibiotic use raises concerns about antimicrobial resistance, posing risks to environmental, animal and human health. This study investigates the impact of a freshwater aquaculture farm in Brazil on microbial communities and ARG dissemination in water, sediment and algae-associated microbiomes. Samples were collected along a spatial gradient - from an upstream control site to locations up to 6 km downstream - and analyzed using shotgun metagenomics. Water and algae samples revealed distinct shifts in microbial community composition at pond effluent outlets and downstream sites, characterized by increased abundances of potential pathogens (e.g. *Flavobacteriaceae*) and elevated loads of antimicrobial resistance genes (ARGs). Algae represented an overlooked ARG hotspot and showed the highest ARG diversity. Detected ARGs included resistance to multiple antibiotic classes and were associated with diverse microbial taxa (e.g. members of Pseudomonadota). ARG mobilization potential was highest in water samples, where co-localization analysis identified linkage between a vancomycin resistance gene and phage-associated mobile genetic element. The findings demonstrate downstream effects of aquaculture on microbial communities and ARG dissemination in adjacent freshwater environments, emphasizing potential risks to environmental, animal and human health and the need to evaluate and manage veterinary antibiotic use through a One Health approach.

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## Mapping AMR Research Investments Against the One Health Priority Research Agenda for AMR: A Global AMR R&D Hub–WHO Quadripartite Organizations Portfolio Analysis

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**Background:** AMR burden is greatest in LMICs and requires a One Health approach. The Global AMR R&D Hub and WHO Quadripartite AMR technical core team assessed how AMR investments align with the One Health Priority Research Agenda for AMR (OHPRAA) and identified gaps.

**Methods:** Cross-sector AMR projects were identified by the Hub/WHO Quadripartite working group. A Dimensions search retrieved 1,420 grant records. Using an OHPRAA-based codebook, abstracts were coded by pillar, subpillar, and cross-cutting theme. Pilot intercoder reliability was high (Cohen's kappa 0.8); disagreements were resolved by review. After excluding 477 out-of-scope records, 943 projects were analyzed for counts, funding, award size, annual disbursement, 2020–2025 cohorts, funder concentration, and theme coverage.

**Results:** Transmission dominated (489 projects; 51.9%), followed by integrated surveillance (185; 19.6%), intervention (149; 15.8%), economics and policy (62; 6.5%), and behavioural insights and change (58; 6.2%). Sustainability appeared in 396 projects (42%), vulnerability in 253 (26.8%), and gender in only 8 (0.8%). Transmission and integrated surveillance attracted similar funding (USD 237.4M and USD 235.8M). Top five funders supplied 54.3% of funding. Annual disbursement peaked at USD 107M in 2020; awards shifted toward intervention in 2024 and behavioural work in 2025.

**Conclusion:** AMR investments support transmission and surveillance research, but gender-responsive research remains a gap.

**Coffee & Poster Viewing II / 407****Cellular Agriculture and Genome Editing for Sustainable Production of High-Protein Soybean Biomass****Author:** Danna Melissa Susunaga Gómez<sup>1</sup><sup>1</sup> *Universidad EAFIT***Corresponding Author:** dmsusunagg@eafit.edu.co

Global population growth, environmental degradation, and rising demand for high-quality proteins are increasing pressure on food production systems. Cellular agriculture has emerged as a promising approach to produce nutritious biomass under controlled conditions while reducing dependence on conventional agriculture. Soybean (*Glycine max* L.), one of the world's leading protein crops, offers a valuable platform for sustainable protein production. This research aims to develop a soybean cellular agriculture platform integrated with genome editing technologies to enhance the yield and nutritional quality of protein-rich biomass for human and animal nutrition. The project combines plant tissue culture, cell suspension cultures, molecular biotechnology, and CRISPR-based genome engineering. Soybean cell cultures are being optimized to maximize biomass and protein accumulation. Targeted modulation of storage proteins, particularly glycinin (11S) and  $\beta$ -conglycinin (7S), is proposed to improve protein quality and increase sulfur-containing essential amino acids. The integration of cellular agriculture and precision genome editing is expected to generate a scalable platform for sustainable production of high-value nutritional biomass, contributing to food security, resilient food systems, and reduced environmental impacts associated with conventional protein production.

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**Ticks and Their Pathogens in Northern Germany: A Seasonal Investigation of Questing Activity and Pathogen Prevalence in Putzar.****Author:** Rabina Prajapati<sup>1</sup>**Co-author:** Susanne Fischer<sup>1</sup><sup>1</sup> Institute of Infectology , Friedrich-Loeffler-Institut- Federal Research institute for Animal health Greifswald-Riems, Germany**Corresponding Author:** vetrabinaprajapati7@gmail.com

Tick-borne pathogens pose risks to both human and animal health across the globe. These risks are worsening due to climate-related shifts in tick distribution and activity, yet local field data remain limited. This study investigated how temperature and relative humidity influence tick questing and pathogen prevalence in rural northern Germany. Ticks were collected biweekly from February to May 2025 in Putzar by flagging while recording climate data. Molecular screening used conventional PCR for *Borrelia* spp. and *Rickettsia* spp. nested PCR for *Anaplasma phagocytophilum*, and *Babesia* spp., followed by sequencing. Spearman correlation and negative binomial regression assessed the environmental effect on tick abundance. Of 85 ticks collected, *Dermacentor reticulatus* dominated (71.76 %). Peak questing occurred in March for *D. reticulatus* and April for *Ixodes ricinus*. Air temperature and humidity positively influenced questing activity, while ground temperature had a negative effect. All samples were negative for *Babesia* spp. and *A. phagocytophilum*. *Rickettsia* spp. was detected in 68.85% of *D. reticulatus* and *Borrelia* spp. in 60% of *I. ricinus*. Coinfection was observed in 5.12 %. Microclimate was the primary driver of tick questing in Putzar. High prevalence of *Rickettsia* spp. and *Borrelia* spp. poses a considerable threat to public and veterinary health. These findings support continued tick surveillance and awareness in northern Germany.

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**Estimating *Toxoplasma gondii* exposure in Swedish wolverines (*Gulo gulo*) – a retrospective study****Authors:** Gábor Árpád Czirják<sup>1</sup>; Peter Segerström<sup>2</sup>; Jens Persson<sup>2</sup>; Jon M. Arnemo<sup>3</sup><sup>1</sup> Leibniz Institute for Zoo and Wildlife Research<sup>2</sup> Swedish University of Agricultural Sciences<sup>3</sup> University of Inland Norway**Corresponding Author:** czirjak@izw-berlin.de

The wolverine (*Gulo gulo*), the largest member of the family Mustelidae, is a top predator and scavenger found in circumpolar regions of North America and Eurasia. Due to its trophic position and large home range sizes, the species could serve as a sentinel for the health of northern ecosystems. The species is listed as Vulnerable by the IUCN; still, limited information exists on the potential importance of diseases in regulating and/or threatening the species, especially in the recovering Scandinavian population. *Toxoplasma gondii* is a zoonotic foodborne parasite that has been reported in mortality events of various Mustelids. Exposure to the parasite has been found in Canadian wolverines, but there is no information from Scandinavia, where felids, the parasite's final host, are less common than in North America. Using a commercial multi-species ELISA kit, we tested samples (n=108) collected between 1994 and 2003 from Swedish wolverines for the presence of antibodies to *T.gondii*. A seroprevalence of 24% was found, which is lower than previously reported from Canada (Northwest Territories 62%, Nunavut 41%, but British Columbia 0%). Surprisingly, there was no significant difference in exposure between sex (18% male vs. 28% female) and age (33% adult vs. 19% juvenile) groups. With climate change, the northward expansion of parasites is expected; thus, monitoring the population health of Swedish wolverine populations is relevant to both One Health and conservation biology.

**Coffee & Poster Viewing II / 423****TBEV in dogs – human behavior leading to an increased infection risk?**

**Authors:** Rebecca Vogt<sup>1</sup>; Alexander Lindau<sup>2</sup>; Katrin Facht-Lehmann<sup>2</sup>; Ute Mackenstedt<sup>2</sup>

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Tick-borne encephalitis virus (TBEV) is a zoonotic flavivirus of growing concern within the One Health framework, as its transmission cycle intricately links wildlife, domestic animals, vectors, and human populations. Its circulation is highly focal, depending on competent tick vectors and reservoir hosts in defined natural foci that can remain stable over decades.

In this study, residual serum samples from routine diagnostics were used to investigate TBEV exposure in two canine populations: dogs from an animal shelter located near a well-known TBEV focus active for over 30 years, and a control group from a veterinary clinic without known TBEV exposure. Shelter dogs are regularly walked along routes intersecting the endemic focus, implying increased exposure risk.

A total of 167 samples, comprising 67 from shelter dogs and 104 from the veterinary clinic, were screened using ELISA and virus neutralization tests. A higher proportion of individuals in the shelter population than in the control group showed neutralizing antibodies against TBEV. Additionally, ticks collected along the shelter's walking routes tested positive for TBEV-RNA, confirming local virus circulation.

These results demonstrate that dogs can serve as valuable sentinels for detecting active TBEV circulation and past exposure. The integration of animal surveillance, vector monitoring, and environmental context illustrates the necessity of a One Health approach to mitigating arboviral risks.

**Coffee & Poster Viewing II / 438****Unlocking natural Antarctic and Arctic archives of thousand-year-old RNA viruses****Author:** Lilli Gralla<sup>1</sup>**Co-authors:** Benjamin Guinet<sup>2</sup>; Sébastien Calvignac-Spencer<sup>2</sup>; Annika Graaf-Rau<sup>2</sup>; Tjorven Hinzke<sup>2</sup>; Steve Emslie<sup>3</sup><sup>1</sup> *Helmholtz Institut for One Health*<sup>2</sup> *Helmholtz Institute for One Health*<sup>3</sup> *University of North Carolina Wilmington***Corresponding Author:** [lilli.gralla@helmholtz-hioh.de](mailto:lilli.gralla@helmholtz-hioh.de)

Historical samples provide unique insights into pathogen evolution and help to uncover mechanisms underlying pathogen emergence, adaptation, and spread. While DNA pathogens can be retrieved from millennia-old environmental samples, less stable RNA viruses are usually limited to pathology collections from the last centuries.

To expand the temporal reach of RNA virus research, we targeted naturally dry and cold environments that may facilitate long-term viral RNA preservation.

Recently, our group detected two rotavirus sequences in Adélie penguin (*Pygoscelis adeliae*) remains from the Ross Sea area of Antarctica, one remain dated to ~ 1,900 years before present. We analyzed 12 additional specimens from the same region and identified further rotavirus-related sequences as well as a partial genome of the Penguin circovirus (PenCV). Ongoing work aims to complete the PenCV genome, further investigate the detected rotavirus, and obtain radiocarbon dates for the newly analyzed samples to inform downstream phylogenetic analyses under clock models.

In parallel, we collected soil in dense bird colonies in Svalbard, Norway, another naturally cold region. Here too, we focus on the detection of historical viral RNA from bird-infecting agents. Analyses of this material are still ongoing.

Overall, these results highlight the potential of naturally frozen specimens as archives of ancient viral

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**Prevalence of *Brucella suis* biovar 2 in Wild Boars from Brandenburg and the Harz, Germany****Author:** Doreen Muth<sup>None</sup>**Co-authors:** Dirk Hofreuter; Szilvia Neuhaus**Corresponding Author:** doreen.muth@bfr.bund.de

*Brucella suis* biovar 2 is widely distributed among wildlife populations in Europe, where wild boars are an important reservoir host. The pathogen occasionally transmits to domestic pigs, especially in regions with extensive outdoor pig farming. Given its low pathogenicity for humans and the rarity of reported human cases, surveillance primarily focuses on understanding infection dynamics at the wildlife–livestock interface.

Here, we describe the prevalence of *B. suis* bv. 2 in wild boars from Brandenburg and the Harz region in Eastern Germany. More than 100 spleens, collected between November 2025 and January 2026, were analyzed by qPCR targeting the *Brucella*-specific *bcsp31* gene and used for the isolation of bacteria. *Brucella* DNA was detected in approx. 8% of the investigated animals, whereas successful bacterial isolation was achieved less frequently. These findings are consistent with recent reports on the occurrence of *B. suis* bv. 2 in wild boar populations from Southeastern Germany, indicating its continued circulation in German wildlife.

The detection of *Brucella suis* bv. 2 in wild boars from different regions of Germany is consistent with its established occurrence in European wildlife. Continued surveillance of wild boar populations can improve understanding of the pathogen's distribution and temporal trends in Germany and support animal-health monitoring and evidence-based assessment of its epidemiological relevance at the wildlife–livestock interface.

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**Effects of Climate Change-Induced Reforestation on Mammal Communities and Potential Implications for Zoonotic Pathogen Reservoirs****Author:** Kyra Jacoblinnert<sup>1</sup>**Co-authors:** Sönke Holch<sup>2</sup>; Anke Benten<sup>2</sup>; Elisabeth Striese<sup>3</sup>; Birke A. Tews<sup>3</sup>; Anna Obiegala<sup>3</sup>; Rainer G. Ulrich<sup>4</sup>; Julia Tiede<sup>5</sup>; Martin Pfeffer<sup>6</sup>; Jens Jacob<sup>1</sup><sup>1</sup> *Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Rodent Research*<sup>2</sup> *Northwest German Forest Research Institute (NW-FVA)*<sup>3</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Infectology*<sup>4</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Novel and Emerging Infectious Diseases*<sup>5</sup> *University of Münster, Institute for Evolution and Biodiversity*<sup>6</sup> *University of Leipzig, Institute of Animal Hygiene and Veterinary Public Health***Corresponding Author:** kyra.jacoblinnert@julius-kuehn.de

Forest ecosystems are currently undergoing profound changes. Large-scale reforestation and climate adaptations are expected to drive substantial ecological change. The aim of the ANTIZOONS project is to investigate the effects of climate change-induced forest conversion on wildlife reservoirs and zoonotic pathogens in an interdisciplinary approach. It promotes a One Health perspective on the health of forest ecosystems, wildlife and humans.

In a subproject, wildlife is monitored by two camera traps installed at each of 21 reforestation sites of different (climate-adapted) tree composition in Hesse to investigate whether sites differing in tree species composition (conifer-/or broadleaf-dominated, and evenly mixed stands) affect mammal communities. In addition, the study examines, if observed changes are associated with the abundance of zoonotic pathogen reservoirs.

Results from camera trapping in autumn 2025 and spring 2026 as well as snap trapping rodents are presented. A total of 764 photographs of mammals were obtained during the first trapping period. They suggest that wild boar (*Sus scrofa*), roe deer (*Capreolus capreolus*) and red fox (*Vulpes vulpes*) are common. Wild boar seemed more active in conifer-dominated forests, whereas red foxes were less often detected in broadleaf-dominated stands and deer (*Capreolus capreolus*) were recorded at similar frequencies across tree compositions. Further results will be reported and their relevance for zoonotic pathogens discussed.

**Coffee & Poster Viewing II / 451****A psychometric tool to measure AMR related knowledge, attitudes, and behavior****Author:** Mattis Geiger<sup>1</sup>**Co-authors:** Franziska Rees; Robert Böhm; Oliver Wilhelm; Lars Korn; Khadija Noor Omar; Jabir Ayindo; Ayan Hussein; Simon Kühnert; Miroslav Sirota; Cornelia Betsch<sup>1</sup> *Bernhard Nocht Institut für Tropenmedizin***Corresponding Author:** mattis.geiger@bniitm.de

Antimicrobial resistance (AMR) is an escalating global health crisis, with particularly devastating impacts on developing countries in the Global South. AMR development is largely driven by human behavior. To mitigate current trajectories of global AMR development, it is vital to understand the psychology underlying this behavior. Therefore, we developed a new measurement toolbox to assess individuals' knowledge, attitudes, and behavior regarding AMR. Item development was based on a Delphi study. We administered the initial item pool to a general-population sample of N = 502 German participants, evaluated psychometric criteria, and used them to select the best items. Next, we used the best items to assess AMR-related knowledge, attitudes, and behavior in Zanzibar. Items were professionally translated to Swahili. N = 1218 Zanzibari participated in a large field study. Finally, knowledge and behavior were criterion validated in a third study with Slovakian GPs (N = 121). Based on this data, we establish cross-cultural validity of our tool and identify knowledge gaps and the prevalence of problematic behaviors in relevant target groups. The tool is open source, and this study can serve as a blueprint for cross-cultural adaptation. Considering the psychometric quality of the tool and the flexibility of the large item pool, we recommend it as a standard tool for behavioral studies on AMR.

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## Evolutionary Dynamics of Classical Swine Fever Virus in the First Half of the 20th Century

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Classical swine fever virus (CSFV) has been a major pathogen of domestic pigs for over a century. However, its early evolutionary history remains poorly understood due to the lack of historical genomic data, with current phylogenetic frameworks relying on sequences obtained since the 2000s. Archival tissue collections represent a valuable yet underexplored resource for investigating the historical diversity of economically important livestock viruses.

This project presents a paleogenomic study of CSFV based on 132 archival samples collected from seven European institutions and dating to the first half of the 20th century. Using optimized high-throughput sequencing protocols, we successfully recovered historical viral RNA genomes. Phylogenetic analyses revealed distinct lineages that are absent from contemporary datasets, indicating a greater level of viral diversity in the past. These results suggest that vaccination and eradication programs may have substantially reduced CSFV diversity over time.

Our findings provide direct genomic insights into the early evolutionary history of CSFV, contributing to a better understanding of long-term viral diversity and population dynamics. More broadly, this study demonstrates the potential of paleogenomic approaches to reconstruct the evolutionary trajectories of RNA viruses from archival material.

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**Leptospira spp. prevalence in bank voles (*Myodes glareolus*) from north-western Germany in 2023/2024****Author:** Elisabeth Striese<sup>1</sup>**Co-authors:** Birke A. Tews<sup>1</sup>; Alina J. Anton<sup>1</sup>; Sascha Knauf<sup>1</sup>; Marion Saathoff<sup>2</sup>; Lutz Fischer<sup>2</sup>; Rainer G. Ulrich<sup>1</sup>; Martin Pfeffer<sup>3</sup>; Anna Obiegala<sup>1</sup><sup>1</sup> Friedrich-Loeffler-Institut<sup>2</sup> Lower Saxony State Office for Consumer Protection and Food Safety<sup>3</sup> University of Leipzig**Corresponding Author:** elisabeth.striese@fli.de

Leptospirosis is among the most widespread zoonoses worldwide. Transmission is often via direct or indirect contact with infected rodents which serve as a reservoir. As *Leptospira* spp. can cause severe infections in humans, it is important to understand the transmission dynamics and identify risk factors for zoonotic infections.

A previous study conducted during 2018 - 2020 in northwestern Germany demonstrated that season, population density, and individual host characteristics significantly influenced *Leptospira* prevalence in bank voles. The current study aims to compare the prevalence of *Leptospira* spp. and their genomospecies and sequence types in bank voles from the same trapping sites in 2023 and 2024 with previously published data.

In total, 560 bank voles (*Myodes glareolus*) were caught in 2023 and 2024 at seven trapping sites at forest plots near Osnabrück. So far six of 161 kidney samples were positive for the *lipl32* gene of pathogenic *Leptospira* spp.. Multilocus sequence typing (*glmU*, *pntA*, *sucA*, *tpiA*, *pfkB*, *mreA* and *caiB* gene) resulted in the identification of sequence types 24 (*L. interrogans*), 110 (*L. kirschneri*) and 197 (*L. borgpetersenii*). The results of this first subset indicates that in addition to a similar prevalence (3.7% (95% CI: 1.4–7.9)), the occurrence of sequence types remains stable over longer time periods.

These findings underscore the importance of long-term monitoring and further research based on the One Health approach.

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**Communicate! Increasing Vaccination Readiness through Targeted Risk Communication in Lambaréné, Gabon****Author:** Lars Korn<sup>1</sup>**Co-authors:** Paul Anthony Mboumessieyi Ngorouma<sup>2</sup>; Mattis Geiger<sup>1</sup>; Pamela Minsoko<sup>2</sup>; Elisabeth Sievert<sup>1</sup>; Gaylord Lucien Ondoumbé<sup>2</sup>; Cornelia Betsch<sup>1</sup>; Selidji Todagbe Agnandji<sup>2</sup><sup>1</sup> *Bernhard Nocht Institute for Tropical Medicine*<sup>2</sup> *CERMEL***Corresponding Author:** lars.korn@bnitm.de

Effective health communication is essential for addressing One Health challenges, including infectious disease outbreaks. However, psychological research underlying communication interventions predominantly originates from the Global North, raising questions about cross-cultural generalizability, particularly given the ongoing replication crisis in psychology.

This randomized controlled trial conceptually replicated a health communication intervention (Horne et al., 2015) in Lambaréné, Gabon, a distinct cultural context from original research context with high disease burden (i.e., Malaria). Using a 2 (Disease: COVID-19 vs. Malaria) x 2 (Type: Risk communication vs. Myth debunking) + 1 (Control) factorial design, 720 adults received video interventions on vaccination risks/benefits or myth debunking, followed by assessment of vaccination readiness.

Both risk communication and myth debunking significantly increased vaccination readiness for COVID-19 and Malaria versus control (COVID-19:  $F(2,276) = 11.70$ ,  $p < .001$ ; Malaria:  $F(2,295) = 5.51$ ,  $p = .004$ ). Notably, myth debunking, which was ineffective in the original US study, proved effective in Gabon.

These findings underscore the need for context-specific replication studies and caution against transferring Global North evidence to other settings. Adapting health communication to local contexts is crucial for effective One Health interventions globally.

**Coffee & Poster Viewing II / 462****Hybridization capture optimization for monkeypox virus genomics****Author:** Yvonne Ukamaka Ajamma<sup>1</sup>**Co-authors:** Christian Noël Malaka<sup>2</sup>; Livia Victoria Patrono<sup>1</sup>; Annika Graaf-Rau<sup>1</sup>; Sébastien Calvignac-Spencer<sup>3</sup><sup>1</sup> *Helmholtz Institute for One Health (HIOH), Helmholtz Centre for Infection Research (HZI)*<sup>2</sup> *Institut Pasteur de Bangui*<sup>3</sup> *Helmholtz Institute for One Health (HIOH), Helmholtz Centre for Infection Research (HZI) and University of Greifswald***Corresponding Author:** yvonne.ajamma@helmholtz-hioh.de

Mpox is a zoonotic disease endemic in West and Central Africa. It is caused by spillovers of monkeypox virus (MPXV) from its rodent reservoir(s) into humans and animals, where it often generates self-limiting outbreaks. MPXV spillovers became more common over the last decades, increasing the risk of longer human to human (h-t-h) transmission chains, such as those recently caused by MPXV clades 1b and 2b. MPXV genomes from such long h-t-h transmission chains exhibit distinct APOBEC3G mutational profiles that can readily be identified through sequencing. So, genomic surveillance can directly aid MPXV control by rationalizing resource distribution via the prioritization of events involving sustained h-to-h transmission. MPXV genome is sequenced using hybridization capture (HC) coupled to high-throughput sequencing, that is very effective but also very expensive, which hinders its routine use in developing countries. Here, we aimed to reduce HC cost through the very simple means of bait dilution. We compared the effects of diluting baits (down to a dilution 1/64) on capture efficiency performed on libraries derived from clinical samples with different virus concentrations. Our results suggest that high-quality, assignable genomes can still be recovered from majority of the samples using baits diluted to 1/32. We conclude that combined with half-reactions during library preparation and pooled library HC, bait dilution can significantly lower the costs of MPXV genomic surveillance.

**Coffee & Poster Viewing II / 463****A quantile viability frontier for characterising basis risk in crop index insurance for climate-vulnerable food systems****Author:** YEIME LEANDRO MUNOZ SERNA<sup>1</sup>**Co-authors:** JUAN DAVID MARTÍNEZ VARGAS<sup>1</sup>; LINA MARÍA SEPÚLVEDA CANO<sup>1</sup><sup>1</sup> EAFIT UNIVERSITY**Corresponding Author:** ylmunozs@eafit.edu.co

Smallholder farmers produce nearly half of the world's food, yet 80% lack formal insurance. In Colombia, the highest disaster-risk country in the Americas, less than 3% of cultivated hectares are insured against climate risks. Crop index insurance is a scalable instrument for climate risk transfer, but its effectiveness is limited by basis risk: the mismatch between index-triggered payouts and actual farm-level losses. Loss thresholds are conventionally estimated through mean-based methods that systematically underestimate the asymmetric, tail-concentrated behaviour of agricultural losses.

This research proposes a viability frontier that delimits the empirical loss domain of insurable risk through quantile regression on field-level yield distributions. By estimating conditional quantiles without distributional assumptions, the approach captures the tail risk that conventional methods overlook. Optical and radar satellite covariates (Sentinel-2 vegetation indices, Sentinel-1 backscatter, and the SPEI as a proxy for soil water deficit) are explored as conditioning variables to reflect plot-level agronomic conditions.

This contributes to the One Health framework by operationalising the Soil-Plant-Atmosphere continuum as the interface where climate stress, agroecosystem health, and human food security converge. Strengthening climate risk-transfer instruments protects the food systems on which the health of vulnerable rural communities depends.

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**ANTIZOONS - Cascading effects of climate-induced forest conversion on zoonotic pathogens in mammals****Author:** Julia Tiede<sup>1</sup>**Co-authors:** Anke Benten<sup>2</sup>; Sönke Holch<sup>2</sup>; Jens Jacob<sup>3</sup>; Kyra Jacoblinnert<sup>3</sup>; Anna Obiegala<sup>4</sup>; Martin Pfeffer<sup>5</sup>; Elisabeth Striese Striese<sup>4</sup>; Birke Tews Tews<sup>4</sup>; Rainer Ulrich<sup>6</sup><sup>1</sup> *Universität Münster, Institute for Evolution and Biodiversity*<sup>2</sup> *Northwest German Forest Research Institute, Department of Forest Protection*<sup>3</sup> *Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Epidemiology and Pathogen Diagnostics*<sup>4</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Infectology*<sup>5</sup> *University of Leipzig, Institute of Animal Hygiene and Veterinary Public Health*<sup>6</sup> *Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Institute of Novel and Emerging Infectious Diseases***Corresponding Author:** tiedej@uni-muenster.de

Forest ecosystems provide habitat for numerous wildlife reservoirs of zoonotic pathogens and are currently undergoing profound changes: The consequences of climate change—such as droughts, storms, and pest infestations—are causing widespread damage and require large-scale reforestation efforts using tree species that can withstand future climatic conditions. These habitat changes are likely to influence the interaction between environmental conditions, wildlife reservoirs, and zoonotic pathogens to an unprecedented extent.

The aim of the collaborative ANTIZOONS project is to investigate the cascading effects of climate change-induced forest conversion on wildlife reservoirs and zoonotic pathogens. At 21 forest restoration sites in Hesse, which differ in their tree species composition, the habitat characteristics, the diversity and composition of the mammal community, and their zoonotic pathogens are being studied using an interdisciplinary approach. Changes in the composition of diets and gut microbiomes will be addressed as possible mediating mechanisms between forest conversion, infection status of wildlife and infection risk of the human population. As some of the most important reservoirs for zoonotic pathogens are also major forest pests, the ANTIZOONS project also serves to optimize forest pest management and thus support plant protection efforts as part of the planned large-scale forest conversion measures.

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## Land-Use Change and Zoonotic Spillover Risk in the Amazon: An Integrative One Health Approach

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Rapid Land-Use Change (LUC) across the Amazon is transforming biodiverse forests into fragmented agricultural landscapes, creating novel interfaces among wildlife, livestock, and people. Despite recognition of LUC as a major driver of pandemic risk, the interacting ecological, physiological, and social mechanisms remain insufficiently understood. The SIMPEL project (IZW-WCS, Volkswagen Foundation) applies an integrative One Health approach in Bolivia and Colombia to support evidence-based interventions that protect both biodiversity and human health.

Using a space-for-time design, we investigate four components across a disturbance gradient: (1) human-nature relations and spillover risks with local and indigenous communities; (2) wildlife host community dynamics in bats, rodents, their ectoparasites and vectors; (3) physiological and immune responses of wildlife hosts to habitat degradation; and (4) pathogen diversity and dynamics.

Early results confirm that LUC restructures wildlife communities and modulates pathogen dynamics in taxon- and site-specific ways. People living in areas bordering deforestation become vulnerable due to the degradation of their environment, their livelihoods, and their health. By integrating ecological, molecular, immunological, and social data, the project aims to generate actionable evidence to inform surveillance, land-use planning, and risk reduction in a biodiverse region where deforestation is outpacing our understanding of its consequences.

**Coffee & Poster Viewing II / 479****Screening of overwintering female Culicidae for mosquito-borne viruses****Author:** Nihal Telli<sup>1</sup>**Co-authors:** Doreen Werner<sup>2</sup>; Helge Kampen<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut*<sup>2</sup> *Leibniz-Centre for Agricultural Landscape Research***Corresponding Author:** helge.kampen@fli.de

Mosquitoes can transmit numerous pathogens that are dangerous to human and animal health. In temperate climates, the major mode of arbovirus overwintering is in their infected vectors. Thus, hibernating female *Culex* mosquitoes play an important role in the winter persistence of West Nile virus (WNV) and Usutu virus (USUV) in Europe. To investigate overwintering mosquito populations in northeastern Germany for mosquito-borne viruses, female mosquitoes were manually collected from more than 190 caves, bunkers and cellars during the winters of 2024/2025 and 2025/2026. In total, more than 52,900 mosquitoes representing seven taxa were collected, including approximately 46,500 individuals of the *Culex pipiens* complex. Additional taxa detected were *Culiseta annulata* (n = 4,872), *Cx. territans* (n = 384), *Cx. hortensis* (n = 19), *Uranotaenia unguiculata* (n = 2), *Aedes cinereus/geminus* group (n = 1), and *Anopheles maculipennis* complex, including *An. daciae* (n = 713), *An. messeae* (n = 320) and *An. maculipennis* (n = 99). RT-qPCR analyses of individual mosquitoes and mosquito pools ( $\leq 10$  specimens) yielded only a single virus detection (USUV) in one pool of the *Cx. pipiens* complex, consisting of ten individuals of the biotype *pipiens*, collected during the winter of 2024/2025. The low detection rate likely reflects a temperature-dependent lack of viral replication during mosquito hibernation, resulting in viral RNA levels below the detection limit.

**Coffee & Poster Viewing II / 483****Ornithogenic colony soils as an AMR baseline: an ancestral, non-mobile resistome that converges across three penguin species in Antarctica****Author:** Jaime Alarcon<sup>1</sup>**Co-authors:** Claudio Valenzuela<sup>1</sup>; Julieta Orlando<sup>1</sup>; Katerin Almendras<sup>1</sup><sup>1</sup> *Millennium Institute Biodiversity of Antarctic and Subantarctic Ecosystems (BASE)***Corresponding Author:** jalarcon@institutobase.cl

Wildlife is increasingly seen as a reservoir of environmental AMR, yet a pristine baseline to interpret it is missing. We characterized the resistome, metallome, biocidome and mobilome of 84 soil metagenomes from 24 sites and three sympatric *Pygoscelis* species on the Antarctic Peninsula, for multi-species comparison of ornithogenic soils. The resistome is dominated by a ubiquitous core (45 genes in >90% of samples; 92.8% of abundance) of intrinsic mechanisms (efflux, target alteration) in environmental psychrophilic genera with no recognized pathogens. Five independent lines show no mobility signatures: 99.3% chromosomal location, decoupling of insertion sequences, fragmented MGE candidates, marginal lysogeny, and no clinical plasmids or resistance-bearing integrons. Antibiotic, metal and biocide resistance co-vary with community phylogeny while mobile elements remain decoupled: resistance is inherited with genomes, not between them. The resistome converges across all three species: community explains ~30% of variance and guano ~3%, while the core assembles deterministically, the periphery stochastically (NST 0.05 vs 0.69). No local anthropogenic signal appeared: the resistome was unstructured by distance to stations. Resistance is a vertically inherited, ecologically integrated trait carried chromosomally, not on mobile elements, positioning Antarctica as a sentinel baseline of pre-antibiotic resistance for tracking anthropogenic and climate-driven change.

**Coffee & Poster Viewing II / 484****Surveillance of Invasive Arthropods in Tropical Plant Imports at Frankfurt International Airport, Germany****Author:** Alix Drobinia<sup>1</sup>**Co-authors:** Martin Beer<sup>1</sup>; Doreen Werner<sup>2</sup>; Helge Kampen<sup>1</sup><sup>1</sup> *Friedrich-Loeffler-Institut*<sup>2</sup> *Leibniz Centre for Agricultural Landscape Research***Corresponding Author:** alix.drobinia@fli.de

The import of goods from tropical and exotic regions into Germany is increasing, alongside with the emergence of pest and vector species. To check the role of air cargo in these introductions, we started a systematic arthropod monitoring at Frankfurt International Airport, Germany's main hub for imported perishable goods, of incoming containers carrying fruits, vegetables and ornamental plants in March 2025.

Five times a year for periods of two to three weeks, randomly selected containers and cargo are sampled using a handheld vacuum device. Additionally, five insect traps are operated in strategic locations throughout the facility and checked daily. Collected arthropods are pre-sorted morphologically, with potential pest and vector species being separated. Potential vectors will later be screened for pathogens using next-generation sequencing, while all remaining specimens are promptly identified by COI barcoding.

So far, 2,979 arthropods have been collected, including mosquitoes, *Culicoides* biting midges and numerous Thysanoptera and Hemiptera. Although high-quality DNA sequences were obtained, COI barcoding often failed to identify robust similarities to database entries.

Surveillance at entry points offers an opportunity to better characterise pathways of pest and vector introduction. The data obtained can help prepare risk assessments for public health, livestock and agricultural systems, and adjust measures to reduce accidental introductions.

**Coffee & Poster Viewing II / 491****In-silico genomic characterization of *Vibrio alginolyticus* on a global scale: lineages, resistome, and virulome****Author:** Sergio Morgado<sup>1</sup>**Co-authors:** Ana Carolina Vicente<sup>1</sup>; Erica Fonseca<sup>1</sup>; Fernanda Freitas<sup>1</sup><sup>1</sup> Oswaldo Cruz Institute**Corresponding Author:** sergiomm0509@gmail.com

*Vibrio alginolyticus* is a halophilic marine bacterium and an opportunistic pathogen for humans and marine organisms. Recently, it has been increasingly associated with outbreaks in aquaculture, impacting fish, shrimp, and shellfish production, particularly in Asia and Europe, while also posing zoonotic risks through contaminated seafood. Rising seawater temperatures and intensive farming practices may favor its persistence and dissemination worldwide. Here, we performed a genomic characterization of 1,250 *V. alginolyticus* genomes, including isolates recovered from sharks (n=5) and coastal upwelling events (n=9) in Rio de Janeiro/Brazil, together with publicly available genomes from GenBank. An SNP-based phylogenomic tree revealed the existence of spatiotemporally distributed lineages spanning the three One Health axes. Importantly, several lineages circulating among clinical, environmental, and animal sources harbored a complete Type III Secretion System, its effectors, and genes related to adhesion/colonization, indicating a potentially pathogenic profile. Moreover, we identified an integrative conjugative element carrying multiple antibiotic resistance genes (*ant*, *aph*, *veb-1*, *vim-71*, *arr-2*, *floR*, and *sul2*) in a genome belonging to a lineage detected in China, Canada, and Brazil (2014-2024) from different sources. Our findings show that this opportunistic pathogen has the potential to emerge with virulence and antibiotic resistance traits across One Health axes worldwide.

**Coffee & Poster Viewing II / 493****Systematic assessment of cell-penetrating peptides for antisense oligomer delivery in *Bacteroides*****Author:** Taís Franco de Carvalho<sup>1</sup>**Co-authors:** Ann-Sophie Rüttiger<sup>1</sup>; Lena Amend<sup>1</sup>; Thomas Guest<sup>1</sup>; Nandika Sahani<sup>2</sup>; Maria Sokolova<sup>2</sup>; Alexander Westermann<sup>1</sup><sup>1</sup> *Würzburg University*<sup>2</sup> *Max Planck Institute of Biochemistry***Corresponding Author:** tais.franco-de-carvalho@uni-wuerzburg.de

Cell-penetrating peptides (CPPs) can be harnessed to deliver antisense oligomers (ASOs) into bacterial cells. However, CPPs that are efficiently taken up by *Bacteroides*—an abundant species of the human gut microbiota—are not currently known. Here, we perform a global screen for CPP uptake by *Bacteroides thetaiotaomicron*. We perform a global screen for bacterial cell-penetrating peptides (CPPs), identifying MK2i (mitogen-activated protein kinase-activated protein kinase 2 inhibitory peptide) as a suitable carrier peptide with high uptake efficiency and specificity. Our data further propose a TonB-dependent import mechanism and reveal influences of media composition, growth phase, and cell surface structure on CPP uptake efficiency. Building on these results, we design an MK2i-coupled to an ASO peptide nucleic acid (PNA) against *fabG*, an essential *Bacteroides* gene involved in envelope fatty acid synthesis. Low micromolar concentrations of this CPP-PNA conjugate evoke a dose-dependent growth inhibition and bactericidal effects. Leveraging a fluorescent *B. thetaiotaomicron* reporter strain, we monitor the effect of PNA-targeting on GFP transcript, protein, and fluorescence levels. These findings lay the groundwork for delivering ASOs into and leveraging ASO technology in a microbiota keystone species.

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**Integrated fungal surveillance in poultry litter matrices: profiling yeast and filamentous mold diversity, diagnostic gaps, and multidrug resistance boundaries at the One Health interface****Author:** Dario Corrêa-Junior<sup>1</sup>**Co-authors:** Igor Avellar-Moura<sup>1</sup>; Flora Bohner<sup>2</sup>; Vinicius Alves<sup>1</sup>; Marcos de Abreu Almeida<sup>3</sup>; Alessandro F. Valdez<sup>1</sup>; Daniel Zamith Miranda<sup>2</sup>; Rodrigo Almeida-Paes<sup>4</sup>; Leonardo Nimrichter<sup>1</sup>; Joshua D. Nosanchuk<sup>2</sup>; Allan Jefferson Guimarães<sup>3</sup>; Cláudio Ernesto Taveira Parente<sup>1</sup>; Susana Frases<sup>1</sup><sup>1</sup> UFRJ<sup>2</sup> Albert Einstein College of Medicine<sup>3</sup> UFF<sup>4</sup> FIOCRUZ**Corresponding Author:** correajuniordario@gmail.com

Poultry litter can select and disperse opportunistic fungi. We characterized yeast and mold diversity in commercial broiler farms in Rio de Janeiro, evaluating diagnostic gaps and functional persistence traits. Isolates were screened via MALDI-TOF and verified by ITS sequencing. Yeasts were tested for microstructural adaptations, biofilms (25–40°C), and CLSI/BrCAST-EUCAST susceptibility. Filamentous mold monitoring identified high-confidence *Aspergillus fumigatus* (scores 2.01–2.26) and *Aspergillus niger* (1.86–1.94), alongside *Scedosporium* sp. (2.05), *Penicillium* sp., and *Lichtheimia corymbifera* (2.24). Concurrently, 29 yeasts were recovered; standard proteomics missed 31% of them (low scores/"no peak found"). ITS sequencing resolved these gaps, revealing *Blastobotrys chiropterorum*, *B. allociferi*, and *Debaryomyces hansenii* complex. Non-conventional yeasts showed advanced fitness: dense cell wall chitin, massive lipid reservoirs, absolute halotolerance (2.0M NaCl), and robust biofilms. Pharmacological screening unveiled high azole tolerance: *C. palmiophila* had 100% resistance to fluconazole (MICs 32 to >128 µg/mL) and elevated amphotericin B MICs (up to 2 µg/mL) without fitness costs, while *B. chiropterorum* reached fluconazole MICs of 64 µg/mL and micafungin tolerance of 8 µg/mL. Poultry litter is a dynamic reservoir of high-consequence molds and multidrug-resistant yeasts, highlighting the urgency integrating agricultural waste into One Health surveillance.

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**Prevalence and parasite burdens in coyote (*Canis latrans*) feces from the Médanos de Samalayuca Flora and Fauna Protection Area, Mexico****Author:** Jose Petters Cabrera<sup>1</sup>**Co-authors:** Ana Gatica<sup>2</sup>; Angelica Escarcega<sup>3</sup>; Cuauhcihuatl Vital<sup>3</sup>; Jesus Martinez-Calderas<sup>3</sup>; Lilian Batista<sup>4</sup><sup>1</sup> Servicio Nacional de Calidad y Salud Animal - SENACSA; Itaipu Binacional, Paraguay<sup>2</sup> Universidad Autonoma de Ciudad Juarez, Mexico)<sup>3</sup> Universidad Autonoma de Ciudad Juarez, Mexico<sup>4</sup> Centro de Ensino Superior de Valença, CESVA, UNIFAA. Rio de Janeiro/ Brasil.**Corresponding Author:** gasparpy@hotmail.com

This study evaluated gastrointestinal parasite prevalence and infection intensity in coyotes (*Canis latrans*) from two sectors of the Médanos de Samalayuca Flora and Fauna Protection Area (Chihuahua, Mexico) differing in anthropogenic disturbance.

**Methods:** A total of 180 fecal samples were collected from a disturbed (n = 110) and a less disturbed sector (n = 70). Scats were identified as coyote feces using published criteria, including size, tapered ends, deposition along trails, associated tracks, and hair and bone remains. Samples were examined by centrifugal flotation, Hoffman sedimentation, and McMaster techniques.

**Results:** Overall, 97 samples (54%) were positive for at least one parasite taxon. 15 taxa, mostly identified to genus level, were detected microscopically. The most prevalent taxa were *Toxocara* (29%), *Ancylostoma* (28%), *Strongyloides* (16%), *Balantidium* (8%), and *Cystoisospora* (7%). Prevalence was similar between sectors (52% and 57%), but the disturbed sector exhibited higher infection intensities, particularly for *Ancylostoma* (1,890 EPG), *Strongyloides* (800 EPG), and *Toxocara* (600 EPG). Samples collected during the cold season were 2.17 times more likely to contain parasitic forms.

**Conclusions:** Similar prevalence but higher infection intensity in the disturbed sector suggests that parasite burden may better indicate ecosystem alteration. Zoonotic taxa highlight the importance of wildlife parasite surveillance within a One Health framework.

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**Integrated entomological and virological surveillance of mosquito-borne arboviruses across an urban–rural gradient in Moyen-Ogooué province, Gabon****Author:** Gédéon Prince MANOUANA<sup>1</sup>**Co-authors:** Fanny Hellhammer<sup>2</sup>; Ynous Djida<sup>3</sup>; Jessica Mariam Koumba<sup>1</sup>; Maminirina Fidélis Ambinintsoa<sup>4</sup>; Moustapha Nzamba Maloum<sup>4</sup>; Steffen Borrmann<sup>5</sup>; Stefanie C Becker<sup>2</sup>; Ayola Akim Adegnika<sup>4</sup><sup>1</sup> *Centre de Recherches Médicales de Lambaréné (CERMEL)*<sup>2</sup> *Working group for vector associated biodiversity and infection, University of Veterinary Medicine Hanover, Hanover, Germany*<sup>3</sup> *Centre de Recherches Médicales de Lambaréné, Lambaréné, Gabon,*<sup>4</sup> *Centre de Recherches Médicales de Lambaréné, Lambaréné, Gabon*<sup>5</sup> *Institute for Tropical Medicine, University of Tübingen, Tübingen, Germany***Corresponding Author:** manouanacermel@gmail.com

**Background:** Mosquito-borne arboviruses are an increasing public health concern in sub-Saharan Africa, but data on vector ecology and virus circulation remain scarce in Gabon, particularly outside urban areas.

**Methods:** Entomological and virological surveys were conducted between March 2023 and January 2025 across urban, peri-urban, and rural sites in Moyen-Ogooué Province. Mosquitoes were collected using WHO ovitraps, CDC light traps, and Prokopack aspirators. Female mosquitoes were pooled and screened for flaviviruses, alphaviruses, and phleboviruses by conventional RT-PCR, with positive samples confirmed by Sanger sequencing.

**Results:** A total of 22,216 mosquitoes (21 species, 8 genera) were collected. *Aedes* (57.2%), *Culex* (23.3%), and *Mansonia* (16.3%) predominated, with *Aedes albopictus* the most abundant species. Six species were recorded for the first time in Gabon, and rural sites showed the greatest species richness. Among 9,690 mosquitoes screened in 245 pools, 53 (21.6%) tested positive for arboviruses: flaviviruses (13.1%) and alphaviruses (8.2%), while no phleboviruses were detected. Quang Binh virus was identified in 12 pools, mainly from *Mansonia uniformis*, representing its first detection in Gabon.

**Conclusions:** Mosquito communities and arbovirus circulation varied across the urban–rural gradient. These findings highlight the value of integrated entomological and virological surveillance to strengthen arbovirus preparedness and vector control in Gabon.

**Coffee & Poster Viewing II / 502****Elucidating the mechanisms of constitutive interferon (IFN) expression in Egyptian Roussette bats****Author:** Gang Pei<sup>1</sup>**Co-authors:** Axel Karger<sup>2</sup>; Jonathan Börnicke<sup>3</sup>; Anca Dorhoi<sup>3</sup><sup>1</sup> *Friedrich-Loeffler-Institut*<sup>2</sup> *Institute of Molecular Virology and Cell Biology, Friedrich-Loeffler-Institut*<sup>3</sup> *Institute of Immunology, Friedrich-Loeffler-Institut***Corresponding Author:** gang.pei@fli.de

Interferons (IFN) are a crucial family of cytokines that rapidly trigger antiviral responses upon infection by inducing the expression of IFN-stimulated genes (ISGs). Contradictory findings regarding constitutive IFN expression have been reported for Egyptian Roussette bats (ERB). To address this discrepancy, we established qPCR to quantify IFN transcripts in human and ERB cells. We observed significantly higher bat IFN transcript numbers in both primary and immortalized cells. To determine the presence of functional IFN proteins, we evaluated the basal expression of downstream ISGs by Western blotting. Consistently, we observed higher levels of ISG proteins in ERB cells under resting conditions. This strongly suggests that their expression is driven by constitutive IFN signaling. To confirm the secretion of IFN proteins, we tested various protocols to detect IFN in the supernatants by mass spectrometry (MS). A total of around 500 proteins were identified, most of which were extracellular, demonstrating the efficiency of our enrichment protocol. Unfortunately, no IFN peptides were detected. To validate IFN secretion, we are currently establishing an IFN ELISA and generating IFN reporter cell lines as complementary approaches. Finally, to elucidate which IRF contributes to constitutive IFN expression, ERB cells deficient of individual IRF were generated. We are currently evaluating the roles of different IRFs in IFN expression under both basal conditions and upon infection.

**Coffee & Poster Viewing II / 507****Linking bat ecophysiology and viral dynamics****Author:** Jonathan Börnicke<sup>1</sup>**Co-authors:** Gang Pei<sup>1</sup>; Marike Geldenhuys<sup>2</sup>; Rochelle Rademan<sup>2</sup>; Marinda de Vries<sup>2</sup>; Wanda Markotter<sup>2</sup>; Anca Dorhoi<sup>1</sup><sup>1</sup> *Institute of Immunology, Friedrich Loeffler Institute, Greifswald – Insel Riems, Germany*<sup>2</sup> *Center for Viral Zoonoses, University of Pretoria, Pretoria, South Africa***Corresponding Author:** jonathan.boernicke@fli.de

In recent years, bats have attracted significant attention due to their ability to harbor a variety of high-impact viruses like Marburg, Ebola and SARS-related coronaviruses. However, factors that influence viral transmission within bat populations and potential spillover to humans are largely unknown. Integrating environmental, ecological, virological and immunological data could generate a multi-factorial model of viral shedding from bats. In this study, we are sampling Egyptian fruit bats (*Rousettus aegyptiacus*) from a wild maternity colony in South Africa and analyze their health, physiology, stress, and levels of viral shedding. Current infections are probed by PCR on rectal swabs, and blood samples are taken for the detection of previous infections by a multiplex immunoassay as well as for the determination of systemic immune fingerprints based on RNA sequencing and mass spectrometry with prior enrichment of low-abundance serum proteins. In these analyses, particular focus will be on establishing the effect of pregnancy on antiviral defense and virus shedding. Finally, environmental data will be integrated to generate a model that correlates the bat viral status and shedding with climate and vegetation factors, along with bat health and immune profile, as well as reproductive state. Thus, we hope to derive predictors of viral shedding to help prevent transmission of viral pathogens from animal reservoir hosts to humans.

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**The PERMA project - Introduction and persistence of zoonotic pathogens from domestic and wild animals into farmland and transfer into the flour production chain, using the example of Shiga toxin-producing and antibiotic-resistant \*Escherichia coli\*****Author:** Michaela Projahn<sup>1</sup>**Co-authors:** Angelika Fruth<sup>2</sup>; Christian Berens<sup>3</sup>; Christian Menge<sup>3</sup>; Christina Böhnlein<sup>4</sup>; Christina Lang<sup>2</sup>; Elisabeth Schuh<sup>1</sup>; Gregor Fiedler<sup>4</sup>; Jan Kabisch<sup>4</sup>; Sylvia Schnell<sup>5</sup><sup>1</sup> *German Federal Institute for Risk Assessment*<sup>2</sup> *Robert Koch-Institute*<sup>3</sup> *Friederich-Loeffler-Institute*<sup>4</sup> *Max-Rubner-Institute*<sup>5</sup> *Justus Liebig University Giessen***Corresponding Author:** michaela.projahn@bfr.bund.de

Shiga toxin-producing *Escherichia coli* (STEC) are important food-borne pathogens and a serious threat to human health. They naturally colonize ruminants, like cattle, but are also increasingly found in plant-based foods, like flour, which has been linked to several international outbreaks. The source(s) contaminating the flour is still unclear; however, an indirect contamination via manure or animal feces, or from the grain field environment is speculated.

The PERMA project will investigate possible transmission routes for STEC into and along the flour production chain as well as STEC persistence in the environment on two German research farms. Due to their (veterinary) clinical significance, antimicrobial-resistant *E. coli* will be included into the investigation. Furthermore, possible contamination of the grain and during the milling process will be examined and the impact of the soil microbiota and the varying soil characteristics regarding environmental persistence of STEC will be assessed. The genetic and metabolic traits of flour-associated STEC strains are still poorly understood and might play a role in persistence and transmission. Therefore, these strains will be further characterized and compared to other STEC isolates from cattle, wildlife, food, and human sources. PERMA is a joint One Health project aimed at a better understanding of STEC in flour and flour products with regard to environmental persistence, transmission pathways and implications for human health.

**Coffee & Poster Viewing II / 512****Development of antibiotic treatment frequencies and consumption quantities in the German Antibiotics Minimization Concept's new animal populations, 2023 to 2025****Author:** Matthias Flor<sup>1</sup>**Co-author:** Bernd-Alois Tenhagen<sup>1</sup><sup>1</sup> *German Federal Institute for Risk Assessment***Corresponding Author:** matthias.flor@bfr.bund.de

The German Antibiotics Minimization Concept was established in 2014 for the fattening livestock sector and defines a benchmarking system based on farm-level treatment frequencies with antibiotic substances (measured in days treated per time period and average animal held). In 2023, several new animal populations were included: purchased calves ( $\leq 12$  months), dairy cows, breeding sows, suckling piglets, laying hens, and young hens intended for egg production. In addition, a weighting factor for AMEG B substances (3rd and 4th generation cephalosporins, fluoroquinolones, polymyxins) was introduced in order to de-incentivize their use. Here, we report on the development of population-wide treatment frequencies as well as antibiotic consumption quantities, stratified by antibiotic class, in the new animal populations.

Antibiotic treatment was most frequent in suckling piglets ( $>50$  days per year and average animal held in the total population), followed by purchased calves ( $\sim 20$  days) and breeding sows ( $\sim 7$  days). The largest total antibiotic quantities were used in treatments of purchased calves ( $>50$  t per year), breeding sows (35 to 40 t), and dairy cows (25 to 35 t). In comparison, treatment frequencies as well as antibiotic quantities for young and laying hens were low. In all new animal populations except young hens, use of AMEG B substances became less frequent over time.

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**Lyme borreliosis in Bavaria, Germany, 2013–2025: a pre-vaccination baseline****Author:** Eva Martschew<sup>1</sup>**Co-authors:** Merle M. Böhmer<sup>2</sup>; Volker Fingerle<sup>3</sup>

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**Corresponding Author:** [eva.martschew@lgl.bayern.de](mailto:eva.martschew@lgl.bayern.de)**Background**

Lyme borreliosis (LB) is endemic in Bavaria and a One Health challenge at the interface of human behavior, climate and tick vectors. Given ongoing climate change and a forthcoming vaccine, we describe long-term epidemiological patterns to identify target groups and establish a baseline for vaccine impact assessment.

**Methods**

We analyzed Bavarian LB surveillance data from 01.03.2013–31.12.2025, calculating incidence by time, place and person. We assessed seasonality using monthly aggregates, overall incidence trend using Mann–Kendall test and age-specific trends using Poisson regression.

**Results**

Of 55,990 confirmed cases (median age 54), average annual incidence was 33.1/100,000 (23.2–47.6), with no monotonic long-term trend ( $\tau=0.05$ ,  $p=0.855$ ). Seasonality was stable: 77.8% of cases occurred May–September, peaking in July. Incidence was highest in adults aged 60–69 years (54.6/100,000), followed by those aged 50–59 years (43.6) and children aged 5–9 years (40.5;  $p<0.001$ ). Incidence increased in children aged 0–4 years ( $IRR=1.047/\text{year}$ ; 95% CI:1.036–1.058), while slight decreases occurred in some older age groups. Females comprised 53.8% of cases, but males predominated in severe manifestations.

**Conclusions**

LB remains of high public health relevance in Bavaria. Our findings reveal important subgroup differences that support risk-based prevention and age-targeted vaccination strategies and warrant further study of underlying risk factors particularly in young children.

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**Intense *Wolbachia*-*Aedes aegypti* proteome crosstalk under adverse semi-field conditions in Rio de Janeiro, Brazil****Authors:** Lena Delen<sup>None</sup>; Milan Keirsebelik<sup>1</sup>**Co-authors:** Guillaume Nugue; Guy Caljon; Magno Junqueira; Rafael Maciel-de-Freitas<sup>1</sup> Oswaldo Cruz Institute/FIOCRUZ, Brazil**Corresponding Author:** milankeirsebelik96@gmail.com

Dengue and other *Aedes*-borne arboviruses are expanding in Latin America and globally, demanding novel vector-control strategies. *Wolbachia*-based replacement can reduce transmission, but field performance is context-dependent, shaped by the interplay between mosquito background, *Wolbachia* strain, arbovirus genotype, microbiota and local pressures. We used the ovary, responsible for *Wolbachia* maternal transmission and reproductive fitness, to evaluate how Rio de Janeiro summer semi-field conditions affect *Aedes aegypti*-wMel interactions. Ovaries from 3-5-day-old wMel-infected and uninfected females were analyzed by quantitative proteomics. Under these adverse conditions, *Wolbachia* infection remodeled ovarian translation, metabolism, mitochondrial maintenance, proteostasis, cytoskeletal organization and PIWI-mediated antiviral regulation, while *Wolbachia* proteins were enriched in translation, folding, DNA repair, oxidative stress response and cellular maintenance. These signatures indicate that local stress can alter molecular conditions supporting symbiont stability, maternal transmission and arbovirus blocking.

Framing *Wolbachia* as an ecological intervention rather than a fixed product that works equally in every setting, this study identifies candidate molecular readouts for future studies investigating how environmental stress may influence vector biology, symbiont performance and arbovirus-control outcomes.

**Coffee & Poster Viewing II / 527****Antibiotics and Occupational Health from a One Health perspective in animal husbandry****Author:** Dierk Pöther<sup>1</sup>**Co-authors:** Marion Berger<sup>2</sup>; Susann Meyer<sup>2</sup><sup>1</sup> *Bundesanstalt für Arbeitsschutz und Arbeitsmedizin*<sup>2</sup> *German Federal Institute for Occupational Safety and Health***Corresponding Author:** poether.dierk-christoph@baua.bund.de

Scenarios with overlaps between human health, animal health and environmental health can often be associated to workplaces, making occupational safety and health (OSH) an important aspect in the One Health approach. However, OSH and One Health are not specifically integrated with another, although they can both benefit from each other.

E.g. workplaces in animal husbandry can be characterized by a high exposure to bioaerosols but also antibiotics. Thus, occupational safety and health needs to broaden its horizon because health of employees can also be influenced by parameters that go beyond classical risk assessment of workplaces, e.g. transfer of antimicrobial resistance genes. In addition, findings in occupational safety and health may also be helpful in promoting health of animals and the environment.

We present workplace measurements ranging from classical methods like cultivation up to novel methodologies like metaproteogenomic approaches, biomonitoring and exposure to antibiotics in animal husbandry to support this hypothesis.

**Coffee & Poster Viewing II / 532****Land use shapes host–pathogen associations and disease hazard in small mammal communities****Author:** Laura Jaramillo Ortiz<sup>1</sup>**Co-authors:** Fred de Boer<sup>1</sup>; Hein Sprong<sup>2</sup>; Helen Esser<sup>1</sup>; Miriam Maas<sup>2</sup><sup>1</sup> *Wageningen University*<sup>2</sup> *RIVM***Corresponding Author:** laura.jaramilloortiz@wur.nl

Human-driven land-use change is recognized as a major driver of zoonotic disease emergence by altering interactions among hosts, vectors, and pathogens. In the Netherlands, landscapes are expected to undergo substantial transitions in response to population growth, biodiversity conservation, and societal well-being. To assess the potential impact of future landscape transitions, it is necessary to first understand how disease hazard is currently distributed across dominant land-use types.

We investigated host–pathogen associations and disease hazard across three Dutch land-use types representing different levels of anthropogenic disturbance: forests, farmlands, and urban areas. We characterized host communities and evaluated the contribution of individual host species to pathogen circulation. We also quantified variation in disease hazard and pathogen infection probability among land-use types at both the community level and within *Apodemus sylvaticus*, a widespread habitat-generalist rodent. We captured 1,621 small mammals belonging to 10 species. Although *A. sylvaticus* was associated with the greatest number of pathogens, *C. glareolus* was disproportionately important in maintaining pathogen communities in forests, while *Microtus arvalis* played a similar role in urban habitats. Disease hazard for tick-borne pathogens was highest in forests, whereas *Leptospira* spp. and *Toxoplasma gondii* were more prevalent in anthropogenic habitats.

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**Non-Digestible Carbohydrate Structure Modulates Resilience to ETEC F18: Towards Reduced Antimicrobial Reliance in Pig Production****Author:** Niloofar Razmgah<sup>1</sup>**Co-authors:** Knud Erik Bach Knudsen<sup>2</sup>; Mette Skou Hedemann<sup>2</sup>; Nuria Canibe<sup>2</sup><sup>1</sup> Postdoc Institute of Animal Nutrition School of Veterinary Medicine Freie Universität Berlin/ former PhD Department of Animal and Veterinary Sciences, Aarhus University, 8830 Tjele, Denmark<sup>2</sup> Department of Animal and Veterinary Sciences, Aarhus University**Corresponding Author:** niloofar.razmgah@fu-berlin.de

Post-weaning diarrhoea (PWD), commonly caused by enterotoxigenic *Escherichia coli* (ETEC) F18, is a major health challenge in pig production and a driver of antimicrobial use. Given concerns over antimicrobial resistance and restrictions on zinc oxide, nutritional strategies to enhance gut resilience are important. We evaluated 4% arabinoxylan (AX), xylo-oligosaccharides (XOS), or chito-oligosaccharides (COS) in an ETEC F18 challenge model.

Eighty piglets were allocated to a non-challenged Control and four ETEC-challenged groups (Control-ETEC, AX-ETEC, XOS-ETEC, COS-ETEC).

COS-ETEC showed faecal consistency and dry matter profiles closest to Control. During acute infection, diarrhoea probability remained below ~50% in COS-ETEC versus ~50–100% in other challenged groups, although differences were limited by variation. COS did not reduce ETEC shedding, suggesting resilience rather than pathogen suppression. AX-ETEC resembled Control-ETEC in diarrhoeal outcomes and showed numerically the highest ETEC shedding. Haptoglobin was lowest in XOS-ETEC on days 2 and 4 post-challenge ( $P<0.05$ ), intermediate in AX-ETEC and COS-ETEC, and highest in Control and Control-ETEC. Daily gain was lowest in supplemented challenged groups ( $P<0.05$ ), highest in Control, and intermediate in Control-ETEC.

NDC structure differentially modulated ETEC F18 responses, supporting nutritional strategies to enhance resilience and potentially reduce antimicrobial reliance.

**Coffee & Poster Viewing II / 536****Rethinking Livestock Nutrition: Regenerative Feed Systems for One Health****Author:** Birte Wulfes<sup>1</sup>**Co-authors:** Niloofar Razmgah<sup>1</sup>; Beatriz Martinez Vallespin<sup>1</sup>; Jürgen Zentek<sup>1</sup><sup>1</sup> *Institute for Animal Nutrition, School of Veterinary Medicine, Freie Universität Berlin, 14195 Berlin***Corresponding Author:** birte.wulfes@fu-berlin.de

Animal nutrition sits at the intersection of animal health, food security and ecosystem integrity, yet its role within One Health is often overlooked. The EU Horizon project Nutrifeds applies a One Health approach to livestock nutrition by connecting research innovation and field validation.

Nutrifeds combines targeted fermentation, insect upcycling and silvopasture and circular farm models. Targeted fermentation with consortia of non-GMO microorganisms can improve the nutritional value and the digestibility of feed ingredients. Fermented feed may promote a more eubiotic intestinal microbiota, thereby supporting gastrointestinal health. This can reduce disease susceptibility and the need for antimicrobial interventions, linking livestock nutrition to the broader challenge of antimicrobial resistance. Black soldier fly larvae can be employed to produce high quality protein out of low-value agri-food by-products, promoting circularity in the food system. After *in vitro* testing, these regenerative feed ingredients will be assessed in farm animals. The work also includes silvopasture systems, testing the effects on soil health, biodiversity and the social and economic viability.

The project will deliver practical guidelines, farmer-oriented tools and a European knowledge network to accelerate the uptake of One Health-based regenerative feed systems across Europe.

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| Kiju                | Pratik          |
| Kimari              | Martin Wainaina |
| Kippels             | Georg           |

|                |               |
|----------------|---------------|
| Kirke          | Ellie         |
| Kligman        | Michelle      |
| Klümper        | Uli           |
| Knauf          | Sascha        |
| Kohl           | Alina         |
| König          | Sarah         |
| Korn           | Lars          |
| Kramer         | Isabelle      |
| Kramer-Schadt  | Stephanie     |
| Kummer         | Susann        |
| kwiringira     | mugisha       |
| Landeck        | Astrid        |
| Lappe dos Reis | Lisiane       |
| Leendertz      | Julius        |
| Leendertz      | Fabian        |
| Lépine         | Maximilien    |
| Lindau         | Alexander     |
| Löber          | Ulrike        |
| Ludwig         | Stephan       |
| Lühken         | Renke         |
| Luttermann     | Christine     |
| Makarova       | Olga          |
| MANOUANA       | Gédéon Prince |
| Markotter      | Wanda         |
| Marques        | Christiane    |
| Martschew      | Eva           |
| Matar          | Katia         |
| Matovu         | Nasif         |
| Maurer         | Jakob         |
| Mehl           | Calvin        |
| Meier          | Fred          |
| Meinen         | Anika         |
| Melhorn        | Vanessa       |
| Merkureva      | Sofiia        |
| Meyer          | Folker        |
| Meyer          | Magdalena     |
| Meyerdierks    | Dörthe        |
| Miani          | Giovanna      |
| Militzer       | Nina          |
| Mohring        | Franziska     |
| Molsen         | Jamina        |
| Morgado        | Sergio        |
| Moss           | Andreas       |
| Moutinho       | Tomas         |
| MUNOZ SERNA    | YEIME LEANDRO |
| Münstermann    | Melina        |
| Munzel         | Hannah        |
| Muth           | Doreen        |
| Nalweyiso      | Martha Dorcas |

|                  |                   |
|------------------|-------------------|
| Namasambi        | Sharon            |
| Namwabira        | Aminah            |
| Neema Bora       | Brigitte Sarcelle |
| Ngene            | Chinedu Innocent  |
| Nitsche-Melkus   | Elisa             |
| Nsofor           | Chijioke          |
| Nuvey            | Francis Sena      |
| NYOMAKWA-OBIMPEH | James             |
| Olbrich          | Anne              |
| Pafčo            | Barbora           |
| Pahl             | Kira              |
| Pandey           | Santos            |
| Paraskevopoulou  | Sofia             |
| Patzina-Mehling  | Corinna           |
| Pei              | Gang              |
| Pen Nasser       | Gabriela          |
| Peters           | Christoph         |
| Pfeffer          | Martin            |
| Pfrommer         | Elisabeth         |
| Pietsch          | Corinna           |
| PIRES            | LUCIANA           |
| Port             | Julia Rebecca     |
| Pöther           | Dierk             |
| Potindji         | Malraux           |
| Prajapati        | Rabina            |
| Prescott         | Joseph            |
| Prinzenberg      | Eva-Maria         |
| Projahn          | Michaela          |
| Rabold           | Denise            |
| Rademan          | Rochelle          |
| Rademan          | Rochelle          |
| Rainer           | Felix             |
| Razmgah          | Niloofar          |
| Ress             | Susanne           |
| Reuß             | Friederike        |
| Rimondi          | Agustina          |
| Rodríguez        | Fiorella          |
| Rohde            | Maximilian        |
| Roschek          | Caroline          |
| Ruiz             | Patricia          |
| Rukh             | Lala              |
| Sababa           | Veronica Fatima   |
| Salat            | Jiri              |
| Salchow          | Frank             |
| Sambucci         | Kelly             |
| Sauer            | Felix             |
| Sawicka-Durkalec | Anna              |
| Schäfer          | Mandy             |
| Schaufler        | Katharina         |

|                   |                  |
|-------------------|------------------|
| Scheffler         | Dominique        |
| Scheuch           | Dorothee         |
| Schlottau         | Kore             |
| Schmidt           | Tammy            |
| Schmidt-Chanasit  | Jonas            |
| Schnettler        | Esther           |
| Schöneberg        | Hannah           |
| Schrötter         | Jakob            |
| Schweizer         | Paula            |
| Schwemmle         | Martin           |
| Sedaghatjoo       | Somayyeh         |
| Sehi              | Gaelle           |
| Semmler           | Torsten          |
| Sick              | Franziska        |
| Sieben            | Christian        |
| Simon             | Miriam           |
| Sittner           | Max              |
| Soeiro-Barbosa    | David            |
| Sogliani          | Davide           |
| Sommer            | Simone           |
| Somogyi           | Sybille          |
| Sprengel          | Sebastian        |
| Starke            | Robin            |
| Steinbrück        | Jenny            |
| Streb             | Lisa-Marie       |
| Streparola        | Gaia             |
| Striese           | Elisabeth        |
| Sydlik            | Ulrich           |
| Szmelc            | Andrea           |
| Tadege            | Tenaw Andualem   |
| Taylor            | Roz              |
| Temperton         | Nigel            |
| Temperton         | Vicky            |
| Tenhagen          | Bernd-Alois      |
| Tews              | Birke Andrea     |
| Thal              | Dana             |
| Thoma             | Dorothea         |
| Thomas            | Stephanie        |
| Tiede             | Julia            |
| Tomczyk           | Samuel           |
| Ufermann          | Christoph-Martin |
| Ulrich            | Rainer           |
| Vital             | Marius           |
| Vogt              | Rebecca          |
| von Creytz        | Isabel           |
| Wagemann          | Anett            |
| Wakimoto          | Mayumi           |
| Weber-Steinhilber | Paulina          |
| Webster           | Fay              |

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|-------------|-----------|
| Westermann  | Melanie   |
| Wickenhagen | Arthur    |
| Widdig      | Anja      |
| Wieczorek   | Pauline   |
| Wilking     | Hendrik   |
| Wimhöfer    | Philipp   |
| Wolf        | Silver    |
| Wolff       | Thorsten  |
| Woyde       | Jonas     |
| Wu          | Haorui    |
| Wulfes      | Birte     |
| Wurzbacher  | Christian |
| Yakubu      | Fuseini   |
| Zeihe       | Hannah    |
| Zeiske      | Sophie    |
| Zhang       | Yao       |
| Zwingmann   | Christian |