Agenda & Abstracts

Food safety research conference Luxembourg 2025
9 December – CELO (Hesperange)

Dear Participants,

Welcome to the One Health research conference, organised by the Luxembourg Veterinary and Food Administration (ALVA) and supported by the European Food Safety Authority (EFSA). This event brings together researchers, policymakers, and professionals committed to protecting public health and ensure food safety through interdisciplinary collaboration.

The One Health approach – recognising the interconnectedness of human, animal, and environmental health – is more relevant than ever. As health challenges grow increasingly complex, integrated solutions are essential.

The research presented today spans diverse areas, all contributing to a deeper understanding of the factors shaping health in our shared ecosystems and highlight the growing need for strong collaboration between national authorities and research institutes.

I extend my sincere thanks to all contributors and participants. Your work and engagement are vital to building a safer, healthier future. May this conference inspire new ideas, strengthen networks, and reinforce the value of working together under the One Health vision.

Warm regards,

Dr. Félix Wildschutz, Director
Luxembourg Veterinary and
Food Administration (ALVA)

Conference Chairs:	Dr. Caroline Merten (ALVA) & Dr. Henry-Michel Cauchie (LIST)
Organiser:	Dr. Miriam Fougeras (ALVA)

Agenda

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15h30 **Surveillance of West Nile and Usutu virus in birds in Luxembourg for animal and public health** (page 8)
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17h15 **Strengthening One Health surveillance under rising temperatures** (page 12)
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17h40 **Using genetic tools to infer the colonisation histories of the raccoon and its Baylisascaris procyonis roundworm parasite in Western and Central Europe** (page 14)
Alain Frantz, D.Phil; National Museum of Natural History Luxembourg (MNHNL)

18h05 **Illuminating the cave: Uncovering oral virome of bats in Luxembourg using metagenomics sequencing** (page 16)
Patrick Reteng, PhD; *Luxembourg Institute of Health (LIH)*

18h30 Wrap up & Closing: Conference Chairs

18h45 Reception & Poster session (page 18 - 24)

VectorNet-Update on arthropod vectors of medical and veterinary importance in Luxembourg

Alexander Weigand[1]

[1] *National Museum of Natural History Luxembourg, 25 Rue Münster, L-2160 Luxembourg, Luxembourg*

VectorNet is a joint project of the European Center for Disease Control (ECDC) and the European Food Safety Authority (EFSA), aiming at increasing overall preparedness for vector-borne diseases. The National Museum of Natural History of Luxembourg (MNHNL) acts as the national contact point for VectorNet.

Here, updated information on arthropod vectors of medical and veterinary importance in Luxembourg is presented. More precisely, the diversity and currently known distribution of relevant ticks (Acari, Ixodida), mosquitoes (Diptera, Culicidae) and sand flies (Diptera, Psychodidae, Phlebotominae) will be presented. Also, preliminary data from field surveys conducted during 2025 for *Culicoides* midges (Diptera, Ceratopogonidae) will be presented. Due to changing environmental conditions and increased globalization, several new arthropod vectors of medical or veterinary importance have been detected, have arrived or have further spread in the country over the last years, notably *Hyalomma marginatum, Hyalomma rufipes, Dermacentor reticulatus, Rhipicephalus sanguineus* s.l., *Aedes albopictus*, and *Phlebotomus mascittii*.

To assess vector-related disease risks, surveillance of main entomological vector species is important to determine presence, spread, abundance, as well as other vectorial capacity traits. Since 2024, the European 'OneHealth4Surveillance' network has been established. Within this network, nationally coordinated by LIH and ALVA, surveillance of ticks and tick-borne diseases is assisted by several national institutions (e.g. MNHNL, natur&ëmwelt Centre de Soins) and citizens. Mosquito surveillance (in particular for invasive Aedes spp.) is led by the *Direction de la Santé* in cooperation with LIST. Additionally, sandflies and *Culicoides* midges are targeted by the MNHNL. Distribution data for entomological vectors is annually uploaded to the Global Biodiversity Information Facility (GBIF) platform.

Bio sketch

After graduating in biology from the Technical University of Darmstadt in 2009, Mr. Weigand completed his doctorate in evolutionary biology and biodiversity research at the Goethe University Frankfurt from 2010-2012. He then worked in various places (Frankfurt, Düsseldorf, Bochum, Essen) as a researcher and science coordinator as well as an eLearning manager and trainer of natural scientists.

Since 2019, he is Curator of Zoology at the National Museum of Natural History Luxembourg (Naturmusée), where he leads various studies in applied and basic research as well as in the field of invertebrate collection management. Using a combination of classical and DNA-based methods, he studies the diversity and distribution of different groups of organisms, including pollinators, parasites and the cave and groundwater fauna of Luxembourg and the Greater Region.

Since 2020, he has been appointed VectorNet representative of Luxembourg, a European network for medical and veterinary entomology. In his activities, he is always interested in acting at the interface between science and politics in order to raise stakeholder preparedness.

Surveillance of ticks and tick-borne pathogens in Luxembourg

Krawczyk A. I.[1], Gamio C. [1], Reteng P. [1], Aurélie Sausy[1], Alexander M. Weigand[2], Lena De Baets[3], Guillaume Fournier[3], Manon Bourg[3], Louis Kox[4], Jill Gaasch[4], Caroline Merten[3], Hübschen, J. M.[1]

[1] Clinical and Applied Virology Group, Department of Infection and Immunity, Luxembourg Institute of Health
[2] Musée National d'Histoire Naturelle de Luxembourg, Luxembourg, Luxembourg
[3] Luxembourg Veterinary and Food Administration (ALVA)
[4] Centre de Soins pour la Faune Sauvage, Natur&Emwelt

Tick-borne diseases of humans and animals are on the rise due to the geographical expansion of their tick vectors and higher frequencies of infected ticks. The distribution and density of ticks, as well as the prevalence of tick-borne pathogens, are currently under-characterized in Luxembourg. Therefore, surveillance activities have been implemented in the country in the context of the EU co-funded OneHealth4Surveillance project (2024-2026).

Since April 2024, ticks have been collected monthly via blanket dragging in 41 sites across Luxembourg. These sampling sites are primarily green spaces frequently visited by the public, such as parks, forests, and hiking trails. In addition, ticks collected from living and dead animals are investigated. Tick species are identified morphologically and if required by barcoding. DNA and RNA is extracted from all collected ticks and screened for tick-borne pathogens, including tick-borne encephalitis virus and *Borrelia burgdorferi* sensu lato.

Tick collection and analyses for tick-borne pathogens are ongoing. Preliminary findings on the spatiotemporal distribution of ticks and the prevalence of selected tick-borne pathogens in Luxembourg will be shared during the conference.

This surveillance will provide critical insights into our understanding of tick-borne disease risk in Luxembourg, particularly in green spaces with high public usage. The data generated will support One Health initiatives and contribute to European efforts to monitor and mitigate the emergence of tick-borne diseases.

Bio sketch

Aleksandra Krawczyk obtained her PhD in 2021 from Wageningen University and Research, where she studied the microbiome of ticks and its effect on tick-borne disease risk. She is currently a postdoctoral researcher at the Luxembourg Institute of Health, working on the surveillance of ticks and tick-borne pathogens in Luxembourg. Her research interests span from symbiotic associations between microbes and vectors to the ecology and epidemiology of infectious diseases.

Acknowledgements

We wish to thank all the people involved in sample collection and testing. Tick and tick-borne pathogens surveillance activities are supported by co-funding from the European Union's EU4Health programme under Grant Agreement No. 101132473 OH4Surveillance.

One Health Approach to Virus Surveillance in Luxembourg Surface Waters

Manon Chassaing[1], Cécile Walczak[1], Aurélie Sausy[2], Delphine Collard[1], Gwenaëlle Le Coroller[2], Manon Bourg[3], Judith M. Hübschen[2], Henry-Michel Cauchie[1], Leslie Ogorzaly[1],** and Chantal J. Snoeck[2]**

[1] LIST – Luxembourg Institute of Science and Technology*
[2] LIH – Luxembourg Institute of Health*
[3] ALVA – Luxembourg Veterinary and Food Administration*
* These authors contributed equally to this work and share the last authorship*
** Presenting author*

Although wastewater-based surveillance has proven effective in monitoring viral circulation in humans, this approach is incomplete as many emerging viral threats originate in animal reservoirs. To address this issue, we adopted a One Health approach, using surface water as a surveillance tool to monitor viral circulation among humans, animals and vectors within interconnected ecosystems.

Between August 2022 and August 2024, ten freshwater sites across Luxembourg were sampled bi-monthly. Sites were selected based on proximity to wildlife and livestock faecal contamination sources and potential mosquito breeding areas. Viruses were concentrated by ultrafiltration and detected by RT-qPCR. Noroviruses (NoV GI-III), human/bovine enteroviruses (h/bEntV), influenza A virus (IAV), porcine respiratory coronavirus (PRCV), bovine respiratory syncytial virus (bRSV), bovine coronavirus (bCoV) and Usutu virus (UsuV) were targeted.

Of the 4,790 analyses conducted, 557 (11.6%) returned positive results. Only enteric viruses (NoV and EntV) were detected, with no evidence of IAV, PRCV, bCoV, bRSV or UsuV. In rivers near livestock production areas, NoV GI, GII, GIII, hEntV and bEntV were detected in 70.8%, 41.1%, 45.3%, 5.2% and 84.4% of samples, respectively, with RNA concentrations ranging from 9.10^2 to 3.10^6 copies/L. In contrast, the same viruses were mostly detected below quantification limits at sites impacted by wildlife or mosquitoes.

These results highlight that the proximity of livestock had a strong influence on the detection of enteric viruses in surface water. Our innovative study showed that monitoring surface water has the potential to provide valuable complementary surveillance, paving the way for additional technological improvements that will enable comprehensive viral risk assessment at the human-animal-environment interface.

Bio sketch

Dr. Leslie Ogorzaly is a Senior Lead R&D scientist in the Environmental Microbiology and Biotechnology research group at LIST. She is a virologist with a PhD in the environment and health domain.

Dr Ogorzaly initiates and participates in R&D projects in the field of water microbiology at LIST. Her primary research focus is on detecting viral particles in water and characterising the infectious state of viruses in a One Health perspective. She develops advanced technological tools for monitoring viruses in water, combining novel molecular tools such as aptamers, real-time detection and next-generation sequencing with classical culture-based approaches and biosensing.

She also emphasises the relationship between viral contamination and the water cycle, collaborating closely with hydrologists at LIST. This enables a more accurate characterisation of microbial risk in water resources by providing a more comprehensive understanding of the environmental behaviour of viral particles from faecal sources to water resources. This dual expertise has enabled Dr Ogorzaly to establish a new and original area of research at the LIST, opening up new avenues and perspectives in environmental virology.

Acknowledgement: This study was supported by the Luxembourg National Research Fund (C21/BM/15793340/VIRALERT).

Surveillance of West Nile and Usutu virus in birds in Luxembourg for animal and public health

Chantal J. Snoeck[1,], Aurélie Sausy[1], Lena de Baets[2], Louis Kox[3], Jill Gaasch[3], Guillaume Fournier[2], Manon Bourg[2], Caroline Merten[2], Judith M. Hübschen[1]*

[1] Clinical and Applied Virology Group, Department of Infection and Immunity, Luxembourg Institute of Health
[2] Luxembourg Veterinary and Food Administration (ALVA)
[3] Centre de Soins pour la Faune Sauvage, Natur&Emwelt
** Presenting author*

Although the burden of mosquito-borne diseases has traditionally been high in (sub-)tropical regions, it is expected to also increase in Europe in the future. West Nile (WNV) and Usutu (USUV) viruses are already enzootic in certain European regions, with widening geographic repartition. The two viruses share similar epidemiological characteristics such as bird-to-bird transmission through mosquito (mainly *Culex pipiens*) bites. Both viruses may also be transmitted to mammals, including humans, leading to a wide range of symptoms. Therefore, WNV and USUV surveillance in birds – shown to be cost-effective and timely to provide early warning signal for increased risk of transmission to human - was initiated in Luxembourg in 2018. The first USUV case was detected in 2020 in the capital [1]. Starting in 2024, the surveillance activities were intensified in the framework of the EU project "OneHealth4Surveillance" by screening systematically a wider range of bird species. While WNV has not yet been detected in Luxembourg, USUV was detected again in several birds during the summer and fall of 2024 and in the summer of 2025. Phylogenetic analyses based on whole genomes suggest that the 2024-2025 strains do not originate from a new virus introduction but that USUV was rather maintained in the region since 2020. This finding, together with the overlapping host and vector range of WNV and USUV, suggests that local conditions would likely also allow the maintenance of WNV in the area once introduced, with wider consequences for public and animal health.

[1] Snoeck CJ, Sausy A, Losch S, Wildschutz F, Bourg M, Hübschen JM (2022). Usutu Virus Africa 3 Lineage, Luxembourg, 2020. Emerg Infect Dis 28(5):1076-1079

Bio sketch

Dr Chantal Snoeck is a scientist within the Clinical and Applied Virology group at the Luxembourg Institute of Health (LIH). She graduated as bio-engineer and obtained a PhD in life and health sciences.

Building on her PhD work, Dr Snoeck further developed her research axis on zoonoses under a One Health approach at LIH, by investigating pathogens in domestic animals and wildlife, human and the environment. Her work focuses on monitoring pathogen circulation and characterizing their diversity to elucidate seasonal trends, geographic spread, pathogenicity markers, inter-species transmission events and identifying protective or risk factors for spillover to humans.

Her work contributes to the development or consolidation of new surveillance schemes to support public and animal health authorities, such as waste- and surface-water surveillance. She is also invested in capacity building projects with partners from low- and middle income countries to increase global resilience to infectious diseases.

Acknowledgements

We wish to thank all the people involved in animal care, sample collection and testing. Flavivirus surveillance activities are a collaborative effort between LIH, ALVA, Administration de la Nature et des Forêts and the Centre de Soins pour la Faune Sauvage. These activities are supported by co-funding from the European Union's EU4Health programme under Grant Agreement No. 101132473 OH4Surveillance, the Ministry of Agriculture, Food and Viticulture of Luxembourg and LIH.

Key note – One Health: The edge of integrated approaches to health and sustainable natural resources management

Jakob Zinsstag, Professor, PhD, DVM; Head of Unit Human and Animal Health & Group Leader One Health, Swiss Tropical and Public Health Institute

While clinical medicine essentially concentrates on the human body and its parts, public health focuses on the health of human populations and their social and environmental determinants. Integrated approaches to health extend the focus of attention to humans in their socio-cultural and ecological environment and their mutual interdependencies, paying attention to inter-species interdependencies. Since the beginning of the 21st century, ecosystem approaches to health (EcoHealth), One Health and Planetary Health have emerged as integrated approaches that relate to and expand public health and related fields. In this article, we aim at clarifying their respective definitions, philosophical foundations and methodological positions. This clarification is important because the way we define integrated approaches to health shapes research, teaching methods and their translation into policy and practice. Key methods and case studies are summarized and compared. Among the three integrated approaches, EcoHealth and Planetary Health operate largely in academic networks and non-governmental organizations (NGOs). One Health is currently operationalized at the level of international organizations, regional organizations and national governments. Integrated approaches to health require urgent adoption and implementation, as they are pivotal for complex problem-solving regarding challenges such as pandemic prevention, climate change, biodiversity loss and antimicrobial resistance.

Bio sketch

Prof. Dr. Jakob Zinsstag is a veterinarian with a PhD in tropical animal health. He spent eight years in West Africa at the International Trypanotolerance Centre in The Gambia and four years as the director of the Centre Suisse de Recherches Scientifiques in Côte d'Ivoire. Since 1998 he heads a research group on human and animal health at the Swiss Tropical and Public Health Institute. Since 2011 his is deputy head and since 2025 head of department of Epidemiology and Public Health at Swiss TPH. He focuses on the control of zoonoses in developing countries and the provision of health care to mobile pastoralists using a One Health approach.

He is past president of the International Association for Ecology and Health and former president of the scientific board of the Transdisciplinary network of the Swiss Academies. He teaches One Health and Trandisciplinary theory and methods and is lead educator of massive open access online courses. He is editor-in-chief of CABI One Health resources. He received the Meritorious Award by the World Organization of Animal Health (WOAH) in 2023. He is a member of the One Health High Level Expert Panel (OHHLEP).

Strengthening One Health surveillance under rising temperatures

*R. Schober[1], Y. Pires-Afonso[1], C. Ernst[1], D. Bejko[1], X. Collette[1], T. Velez[1], E. Culetto[1], I. Kerrec[1], D. Gashi[1], P. Hoffmann[1], G. Urth[1], G. Scheiden[1], J. Mossong1, A. Vergison[1]**

[1] Luxembourg Directorate of Health, Health Inspection, Luxembourg
** Presenting author*

A One Health approach calls for integrated surveillance that unites human, animal, and environmental health, while monitoring drivers of disease emergence such as climate change. Here, we report two recent outbreaks in Luxembourg that coincided with a heat wave, requiring a coordinated One Health approach and response.

The first outbreak, involving Legionnaires' disease (LD), included ten confirmed cases linked to the commune of Steinfort, seven of whom were clustered in or near a local long-term care facility (LTCF). We investigated various potential sources including the water distribution system, the LTCF, two nearby cooling towers, a lake fountain and a cross-border wastewater treatment plant. Environmental sampling was undertaken in collaboration with LIST, LNS, ITM, AGE, and the Administration for the Environment, with typing support from the EU Reference Laboratory in Lyon.

The second outbreak, caused by *Yersinia enterocolitica* O:9, consisted of 30 genetically identical cases since May with a clear peak at the end of June 2025. *Yersinia enterocolitica* is primarily foodborne, with pork, vegetables, or unpasteurized dairy products being responsible. Case investigations suggested a Luxembourg-based food source distributed in canteens.

Investigations for both outbreaks are still ongoing, and we will present latest findings including collaborations with our cross-sectoral One Health partners. Climate change may influence both pathogens in the future, as rising temperatures and humidity could increase LD risk, while altered agricultural practices may affect foodborne pathogen dynamics. These outbreaks show the importance of One Health approach and cross sector collaborations when investigating environmental and food-borne infectious outbreaks.

Acknowledgements:
We would like to acknowledge contribution of our partners, Henry-Michel Cauchie, Leslie Ogorzaly, Delphine Collard, Cecile Walczak, Monique Perrin, Catherine Ragimbeau and Jainaba Roussel.

Bio sketch

Dr. Vergison is a pediatrician with a specialization in infectious diseases and infection control. Holding a master's degree in public health and a PhD in Medical Sciences, her research focused on the epidemiology of pediatric bacterial infections. She has an extensive background spanning 17 years as a Pediatric Infectious Diseases Consultant, Infection Control Epidemiologist, and Teaching Assistant at a university teaching hospital.

Dr. Vergison has served on the boards of the World Society for Pediatric Infectious Diseases and the European Society for Pediatric Infectious Diseases. She has contributed as a reviewer for numerous infectious disease journals and was an editorial board member for the Pediatric Infectious Disease Journal.

After transitioning to roles in social security and public health in Belgium for five years, Dr. Vergison joined the Health Directorate at the Ministry of Health in Luxembourg in 2018. Since the COVID-19 pandemic, she led the Sanitary Inspection division, overseeing infectious disease surveillance, outbreak investigation, crisis response, and public health protection. Her division also serves as the focal point for International Health Regulations (IHR), the Early Warning and Response System (EWRS), and various European Centre for Disease Prevention and Control (ECDC) working groups. She represents Luxembourg in multiple international boards and committees.

Dr. Vergison has authored or co-authored 60 papers in peer-reviewed journals and delivered numerous presentations at international congresses, contributing significantly to the field of pediatric infectious diseases and public health.

Using genetic tools to infer the colonisation histories of the raccoon and its *Baylisascaris procyonis* roundworm parasite in Western and Central Europe

A.C. Frantz, M. Heddergott*

[1] *Musée National d'Histoire Naturelle, 25 rue Muenster, L-2160 Luxembourg*
** Presenting author*

The raccoon roundworm (*Baylisascaris procyonis*), a gastrointestinal nematode of the raccoon (*Procyon lotor*), excretes eggs in its droppings that, if ingested, can cause severe disease in a range of vertebrates. In humans, this may result in a severe form of larval migrans, potentially leading to death or permanent neurological damage. Although roundworms were inadvertently introduced to Europe alongside their raccoon hosts, the parasite is not present in every raccoon population. It is important to understand the geographic distribution of *B. procyonis*, as early and rapid treatment can prevent severe pathologies in humans. In Western and Central Europe, raccoons are especially common in Germany. While the raccoon roundworm was known to occur in some German populations, its precise European distribution was unknown. However, both the raccoons and the roundworm are currently increasing their geographic distribution. We investigated the precise distribution of the roundworm in Western and Central Europe, as well as used genetic tools to infer colonisation histories and invasion pathways of both the raccoons and the roundworm. We show that raccoons were introduced multiple times, but that not all founder populations were infested with *B. procyonis*. We present evidence for the roundworm spreading into naïve raccoons population through natural dispersal of infected raccoons. We also present the first evidence for the presence of *B. procyonis* in Luxembourg, where up to 50% of adult raccoons are infested with the parasite. Persons likely to come into contact with raccoons, as well as health practitioners, should be made aware of the presence of the parasite.

Bio sketch

Alain Frantz is Curator of Zoology at the National Natural History Museum of Luxembourg. He is interested in applying genetic and genomic methods to address applied problems in conservation and wildlife management. His research spans a wide range of topics, including the study of invasive species, where he uses genetic data to reconstruct colonisation history and spread. His work provides valuable insights into the processes that shape biodiversity and has important applications for the management and control of wildlife populations.

Illuminating the cave: Uncovering oral virome of bats in Luxembourg using metagenomics sequencing

Patrick Reteng[1], Morten Rasmussen[2], Aleksander Ring[2], Christine Harbusch[3], Judith M. Hübschen[1]*

[1] Clinical and Applied Virology Group, Department of Infection and Immunity, Luxembourg Institute of Health, Esch-sur-Alzette, Luxembourg
[2] Virus Research and Development Laboratory, Statens Serum Institut, Copenhagen, Denmark
[3] ProChirop, Bureau of Bat Research and Conservation
** Presenting author*

Bats (order *Chiroptera*) are increasingly being recognized as a reservoir host for several viruses of zoonotic concern, notably those belonging to the families *Coronaviridae*, *Paramyxoviridae*, and *Astroviridae*. Given their geographical distribution and mobility, bats play a significant role in the ecology of emerging infectious diseases. Consequently, they represent a pivotal focal point for virus surveillance under the One Health approach. A previous study from Luxembourg provided initial evidence of circulation of paramyxovirus, alpha-, and betacoronaviruses in local bat populations.[1] However, the viruses were detected using a targeted approach and therefore, other viruses could have been missed. To expand on the initial findings, a comprehensive approach using metagenomics sequencing is being employed for samples collected from captured individuals across six different sites in Luxembourg. Oropharyngeal swabs are subjected to a next-generation sequencing workflow. To enhance the sensitivity and specificity of virus detection, sequencing libraries are enriched using a commercially available probe-based target capture system designed to detect a broad range of known vertebrate viruses. This study aims to characterize the virome of local bat populations, as well as to assess the utility of metagenomics sequencing in proactive virus surveillance. The results will contribute valuable insights for regional pathogen monitoring efforts and inform future risk assessments regarding emerging bat-related viruses.

[1] Pauly M, Pir JB, Loesch C, Sausy A, Snoeck CJ, Hübschen JM, Muller CP. 2017. Novel Alphacoronaviruses and Paramyxoviruses Cocirculate with Type 1 and Severe Acute Respiratory System (SARS)-Related Betacoronaviruses in Synanthropic Bats of Luxembourg. Appl Environ Microbiol 83:e01326-17.

Bio sketch

Current and past position

- *2023 – present: Post-doctoral fellow at Clinical and applied virology group, department of infection and immunology, Luxembourg Institute of Health*
- *2017 – 2018: General practicioner, Rumah Sakit Tentara R.W. Mongisidi, Manado, Indonesia*

Education

- *2019 – 2023: Doctor of infectious diseases – Graduate School of Infectious Diseases, Faculty of Veterinary Medicine, Hokkaido University, Japan*
- *2022-2023: Research student – Graduate School of Frontier Sciences, The University of Tokyo, Japan*
- *2010-2017: Medical doctor – Faculty of Medicine, Sam Ratulangi University, Indonesia*

Poster Abstracts

Dietary Exposure to PCBs: A Public Health Concern related to Type 2 Diabetes

Zahra Hejazi[1], Torsten Bohn[1]*

[1] Nutrition and Health Research Group, Department of Precision Health, Luxembourg Institute of Health
** Presenting author*

Polychlorinated biphenyls (PCBs), classified as persistent organic pollutants (POPs), are known for their lipophilicity and bioaccumulation in the food chain, leading to human exposure through diet. The European Food Safety Authority (EFSA) analyzed over 30,000 food and feed samples from 26 countries to evaluate PCB levels. Out of these, 10% and 3% of the samples contained above maximum levels of dioxin and dioxin-like PCBs and of non dioxin-like PCBs, respectively. In general, fish, meat, and dairy products had the highest contribution to dietary exposure to PCBs. One consequence of this exposure could be an increased risk for cardiometabolic diseases, such as type 2 diabetes (T2D), through oxidative stress, inflammation, and modulation of several transcription factors such as Nf-kB and nuclear receptors, for example RXR/PPARs that could act on the immune, and hormonal systems. Considering the importance of the topic, an ongoing PhD project at Luxembourg Institute of Health is focusing on the relationship between POPs and T2D, aiming to explore multiple exposure dimensions. Specifically, this project strives to unravel the potential mitigating role of healthy, balanced, and rich in micronutrient diet on this relationship. This is achieved by combining data from EFSA and food consumption patterns across European countries from the EPIC (European Prospective Investigation into Cancer and Nutrition) project. The project also emphasizes the need for effective strategies to monitor, regulate, and reduce PCB exposure to protect public health. Therefore, here we aimed to highlight the extent of PCB contamination in Europe and underscore the associated health risks.

Does the use of reclaimed wastewater for irrigation pose a risk to plants? Initial findings regarding plant viruses.

Leslie Ogorzaly[1], Héléna Wolf[1], Cécile Walczak[1], Malte Herold[1], Henry-Michel Cauchie[1]*

[1] LIST - Luxembourg Institute of Science and Technology
**Presenting author*

Growing interest in wastewater reuse raises concerns about plant pathogens in reclaimed water that can infect crops, causing yield losses and economic damage.
Firstly, we analysed twelve raw wastewater and ten surface water samples using shotgun metagenomics to detect plant viruses. Results revealed a high plant virus abundance in wastewater, with tomato brown rugose fruit virus (ToBRFV) consistently co-occurring with pepper mild mottle virus (PMMoV), cucumber green mottle mosaic virus (CGMoMV), melon necrotic spot virus (MNSV) and tomato mosaic virus (ToMV). These viruses primarily belong to the Tobamovirus genus (*Virgaviridae*), except MNSV (*Carmovirus, Tombusviridae*). Near-complete ToBRFV genomes were assembled from thirteen samples with adequate sequencing depth and coverage. Then, we implemented a targeted multiplex RT-ddPCR approach to specifically detect PMMoV, ToBRFV, CGMoMV, and MNSV. Using this more sensitive and specific method, the results from year-long sampling confirmed their widespread presence, detecting up to 10^9 genome copies/100 mL. Temporal analysis revealed seasonal fluctuations for CGMoMV and MNSV RNA, contrasting with stable ToBRFV and PMMoV RNA levels throughout the year.
This study provides the first comprehensive evidence of the occurrence of genome of diverse RNA plant viruses in Luxembourg's wastewater, including the economically devastating ToBRFV. Current research is evaluating the presence of these viruses in reclaimed water after treatment, which is crucial for developing safe reuse protocols. Future work will establish the virus infectivity in environmental waters and conduct comprehensive risk assessments for agricultural irrigation applications. Our preliminary findings emphasise the need for plant pathogen monitoring in water reclamation strategies, highlighting an underexplored dimension of wastewater reuse safety for food security.

Acknowledgement:
This study was supported by the Luxembourg National Research Fund (C21/BM/15793340/VIRALERT), and jointly by the Fond de la Gestion de l'Eau and the Health Directorate in the framework of the SUPERVIR Project.

Apple production in Luxembourg at risk?

Michael Eickermann[1], Matteo Ripamonti[1], Marine Pallez-Barthel[1], Alexander Weigand[2], Carmelo Rapisarda[3], Imen Kharrat-Jarboui[3], Wolfgang Jarausch[4], Hannes Schuler[5]*

[1] Luxembourg Institute of Science and Technology
[2] Musée national d'histoire naturelle Luxembourg
[3] Fondation Faune-Flore
[4] RLP AgroScience
[5] Free University of Bozen-Bolzano
** Presenting author*

The apple tree's ecological community also encompasses pest insects, including so-called psyllids, which represent a particularly intriguing insect group. Since 2018 the occurrence of over 60 psyllid species in Luxembourg is documented. In total, three psyllid species are found on apple trees in our region, which play a significant role in the transmission of plant pathogens known as phytoplasmas. These are bacterial-like agents that cause the so-called "apple proliferation" disease in apple trees. An infection leads to the sprouting of axillary buds, which produce slightly twisted shoots with a broom-like appearance. Fruits from affected trees remain small and are unsuitable for storage. In South Tyrol, particularly this psyllid-transmitted disease results in substantial economic losses. Currently, two research projects (VectoRise and PsyPhyPaths[2]) are underway in Luxembourg investigating the distribution of vector insects and the pathogens they transmit in the Greater Region. In addition to extensive insect monitoring, molecular genetic analyses will identify the specific pathogen strains and thus characterize the existing pathosystem in detail. Both projects have a significant impact on food security regarding apple production.

Funding: VectoRise is funded by the Fonds National de la Recherche. And the project PsyPhyPaths2 is funded by the Ministry of the Environment, Climate and Biodiversity of Luxembourg.

Rickettsia-infected Dermacentor reticulatus tick foci in Luxembourg

Patrick Reteng[1], Cédric Simon[2], Carlos Gamio[1], Aurélie Sausy[1], Aleksandra Krawczyk[1], Alexander M. Weigand[2], Judith M. Hübschen[1]*

[1] Clinical and Applied Virology Group, Department of Infection and Immunity, Luxembourg Institute of Health, Esch-sur-Alzette, Luxembourg
[2] Musée National d'Histoire Naturelle de Luxembourg, Luxembourg, Luxembourg
** Presenting author*

Historically absent in Luxembourg, the tick *Dermacentor reticulatus* (Fabricius, 1794) is now established in the country. This tick species is known as the vector of several pathogens, but so far, data about pathogen prevalence in the local *D. reticulatus* population were missing. To address this gap, 510 adult *D. reticulatus* ticks were collected from May to June 2024 in the South of Luxembourg. The ticks were identified morphologically and nucleic acids extracted from the ticks were screened with multiplex qPCRs for various tick-borne pathogens. *Rickettsia* sp. was the predominant pathogen found (58/510; 11.4%) and further analysis of partial *ompB* and *gltA* sequences revealed that the strains formed a cluster together with *R. raoultii*, which is capable of infecting humans and animals. The sequences obtained from ticks in Luxembourg are highly similar, suggesting limited genetic diversity of *R. raoultii* in the country. Interestingly, the prevalence of *Rickettsia* infection differed between collection sites, which could be attributed to environmental differences between locations. Higher infection prevalence was associated with presence of agricultural land connected to natural vegetation, while land heavily used for agriculture was associated with decreased prevalence. However, the discrepancy in prevalence might also be a result of the "founder effect," considering that *R. raoultii* is horizontally transmitted in the ticks. As the population of *D. reticulatus* is expected to further expand due to warming climate and movements of humans and animals, ongoing surveillance of tick distribution and associated pathogens is necessary to identify and monitor risk areas.

ALIsens® – a 3D Alveolar *In Vitro* Test System for the Screening of Inhalable Respiratory Sensitizers in the Food Industry

*Sabina Burla, Giovanna Radicchio, Arno C. Gutleb**

INVITROLIZE, Luxembourg
** Presenting author*

Allergic diseases represent a growing global health burden, with food and respiratory allergies contributing substantially to morbidity. Inhalation of sensitizers from food sources may prime the immune system for exacerbated responses upon ingestion, underscoring the urgent need for reliable allergenicity assessment of novel food proteins and additives. Current new approach methodologies (NAMs) for skin sensitization fail to discriminate respiratory sensitizers, highlighting the necessity of physiologically relevant models for the respiratory tract.

ALIsens® is available in various sizes from 6- to 24-well inserts to enable high-throughput screening (HTS). The model incorporates human alveolar type II epithelial (A549), endothelial (EA.hy926), and monocyte (THP-1) cell lines, fostering a tissue-like microenvironment through direct cell-cell interactions and paracrine signaling. Structural resemblance to the alveolar region was confirmed microscopically, and exposures were performed at the air-liquid interface (ALI) using a panel of known respiratory sensitizers and non-sensitizers.

Cell viability was assessed by resazurin assay 24 h post-exposure, and dose–response curves were generated for apical, basolateral, and integrated compartments. Flow cytometry of CD54, CD86, and TSLPr was conducted at non-cytotoxic concentrations (≥75% viability). The system successfully distinguished respiratory sensitizers from non-sensitizers and correctly identified pro-haptens frequently misclassified by other NAMs.

These findings demonstrate that ALIsens®, the 3D model for the alveolar barrier provides a physiologically relevant and scalable in vitro platform for predicting respiratory sensitization. The approach holds promise for efficient hazard assessment of food components and chemicals, addressing a critical gap in current regulatory testing strategies.

Transforming food systems through fermentation: Microtarians SIS as a catalyst for One Health innovation

Cuenca-Ortolá M[1], Gandía M[1], Filice S[2], Gamero A[1], Cilla A[1]*

[1] Bionutest group, Department of Preventive Medicine and Public Health, Food Sciences, Toxicology and Forensic Medicine, University of Valencia, Spain
[2] Microtarians SIS, Social Impact Company, Luxembourg
** Presenting author*

The Microtarians SIS initiative promotes a low-tech, community-driven approach to food fermentation. It supports circular food systems by upcycling local, often wasted resources into high-value functional products and improving the nutritional profiles of Traditional Mediterranean Recipes (TMR).

Within the framework of the MEDIET4ALL project and in collaboration with the University of Valencia, this study investigates the potential of fermentation to enhance the antioxidant properties of traditional plant-based ingredients (black garlic, lemon, and kombucha), aiming for their functional integration into TMR.

Through comparative analyses of Total Antioxidant Capacity (TAC) and total polyphenols (TP) between homemade (HM) and industrial (IN) fermentation processes, our results consistently show superior antioxidant profiles in HM products.

Notably, ORAC values for black garlic reached 182,587 µM Trolox/100g DW in HM samples versus <100,000 µM in IN counterparts (+80% increase). Fermented lemon exhibited 363,294 µM Trolox/100g DW, reflecting a +275% increase relative to fresh and industrial references. Kombucha samples displayed 4717 mg GAE/100g DW total polyphenols, approximately 10-fold higher than typical industrial samples (400-500 mg GAE/100g DW).

These enhancements are attributed to the preservation of microbial diversity, absence of pasteurization, and reduced processing steps inherent to HM fermentation, which foster bioactive compound release.

In conclusion, fermentation is a key determinant in optimizing antioxidant properties of functional foods. We advocate for the co-creation of a doctoral research program combining nutritional biochemistry and circular economy to validate and scale up the Microtarians SIS initiative.

Surveillance of highly pathogenic avian influenza in wild mammals in Luxembourg for zoonotic risk prevention

Chantal J. Snoeck[1], Aurélie Sausy[1], Lena de Baets[2], Louis Kox[3], Jill Gaasch[3], Guillaume Fournier[2], Marianne Jacobs[4], Manon Bourg[2], Caroline Merten[2], Judith M. Hübschen[1]*

[1] Clinical and Applied Virology Group, Department of Infection and Immunity, Luxembourg Institute of Health
[2] Luxembourg Veterinary and Food Administration (ALVA)
[3] Centre de Soins pour la Faune Sauvage, Natur&Emwelt
[4] Administration de la Nature et des Forêts (ANF)
** Presenting author*

Highly pathogenic avian influenza (HPAI) viruses have been repeatedly detected in wild birds in Europe for the past decade and are regularly transmitted to poultry upon direct or indirect contact. In Luxembourg, several occurrences of HPAI in domestic and wild birds have been detected over the past 2 decades of surveillance. Recently, the number of HPAI events in wild mammals has drastically increased in Europe and the Americas, especially in carnivores preying on sick or dead birds, mammals kept for fur production and sea mammals. Besides animal health and wildlife conservation issues, increased circulation of HPAI strains in mammals provides more opportunities for HPAI viruses to acquire specific mutations for adaptation, increasing the pandemic risk. Surveillance is thus crucial to identify and monitor emerging threats. In parallel with surveillance in birds, screening of wild carnivores was thus initiated in 2022 in Luxembourg, with more than 300 animals from all over the country tested since then. Red foxes, well represented in HPAI positive cases in Europe likely due to their preying behavior, constitute the main species tested in Luxembourg, followed by invasive raccoons. No HPAI virus has been detected so far in wild mammals in the country, despite occasional HPAI cases in wild and domestic birds during the 2021-2022 and 2022-2023 seasons. However, the situation is highly dynamic and requires continuous monitoring for both animal and public health.

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