EOHA 2026
Annual Scientific Meeting

International One Health Congress
18–20 MAY — MADRID (SPAIN)

PROCEEDINGS BOOK

EOHA
European One Health Association

CSIC
Consejo Superior de Investigaciones Científicas

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PREFACE

Dear Participant to the Annual Scientific Meeting of the European One Health Association (EOHA),

Dear One Health colleague,

It is a great pleasure for us to welcome you all to the 2026 edition of the EOHA Annual Scientific Meeting (ASM), hosted and co-organized by the Spanish National Research Council (CSIC) in Madrid! This ASM is the first one organized by the EOHA following a series of annual scientific meetings that took place between 2028 and 2022 within the framework of the One Health European Joint Project, in which the EOHA, formerly known as the Med-Vet-Net Association, participated. As members of the European One Health community, we were all looking forward to seeing each other, presenting our research results, sharing knowledge, exchanging ideas, and meeting new colleagues in an inspiring environment like Madrid. Events like these are essential for strengthening the One Health community in Europe and form a basis for future collaborations and partnerships.

During this week, we will learn about the latest developments in the field of One Health, through inspiring keynote lectures by internationally recognized One Health experts, oral and poster presentations on One Health research results by experts from the EOHA and beyond, as well as innovative One Health studies conducted by PhD students. The scientific sessions will be structured around four inspiring themes.

The first theme addresses the need to better integrate environmental sciences into One Health research and initiatives. The roots of our Association lie in collaboration between public health and animal health institutions, but contemporary global health challenges, including emerging zoonoses and antimicrobial resistance, are closely linked to environmental changes, ecological systems, and biodiversity, requiring more comprehensive One Health strategies.

The second theme focuses on research topics at the frontiers of One Health such as microbiome, genomics, pathogen evolution, AMR, cross species transmission. Topics for which inter- and transdisciplinary research collaboration across sectors and borders is of great added value, if not crucial. Subsequently, the third theme covers innovative solutions for One Health challenges and their implementation. We will learn from best practices for the implementation of new technologies, methodologies, vaccines, digital tools, and capacity building, to bridge research and practice.

The fourth theme addresses how science can benefit policy and society, taking into account related aspects such as risk communication, health economics, participatory research and policy evaluation. One Health research needs to be translated into One Health policy and should lead to the operationalization of the One Health approach in prevention, surveillance, preparedness and response. Moreover, One Health policy is necessary to facilitate One Health collaboration and data sharing across sectors and borders.

At least for a few days, Madrid will be the centre of the European One Health community. This ASM marks a milestone for One Health in Europe and will contribute significantly to the development of a One Health community that will be better prepared and more resilient against future threats.

Enjoy the meetings, enjoy the social interactions, enjoy One Health!

Arjen van de Giessen, President of the European One Health Association
and
Hein Imberechts, Vice-President of the European One Health Associationt

WELCOME

Dear colleagues and friends,

It is a real pleasure to welcome you to the first Annual Scientific Meeting (ASM) of the European One Health Association (EOHA), taking place in Madrid, Spain, from 18th to 20th May 2026.

This meeting is specially meaningful for the local organizing committee, as it represents the first international congress we have organized since the incorporation of our research institute (Animal Health Research Center, CISA-INIA) to the Spanish National Research Council (CSIC), the largest and most prominent public research institution in Spain. For this reason, we are delighted to hold our EOHA ASM at the historic CSIC headquarters. Located in the city center of Madrid, this unique venue offers well-equipped and historically significant spaces where science and culture can be enjoyed together.

From the very beginning, our goal has been to design a conference that truly embraces all components of the One Health concept, fostering genuine collaborative research and innovation to address global health challenges. Ultimately, we hope to contribute to turning scientific knowledge into real-world impact, reaching both policymakers and society —possibly the most rewarding outcome of our research.

Together with the fantastic EOHA management team, we have prepared an exciting scientific program featuring outstanding keynote speakers opening each thematic session, inspiring oral and poster presentations, and dynamic round-table discussions with leading experts addressing key topics around One Health. We have also placed special emphasis on giving visibility to early-career researchers, who will play a relevant role throughout the meeting. In addition, you will find a few surprises throughout the sessions to maintain a lively and friendly atmosphere.

In line with our commitment to sustainability, we have adopted an e-poster format and kindly invite you to join us in promoting the environmentally conscious values of the One Health community.

Of course, it is not all going to be science. We warmly encourage you to join the social events we have carefully organized, including the welcome Spanish wine reception on the first day and the conference dinner on the second day. Both events are designed to foster networking and scientific exchange, while enjoying some of our most popular gastronomy in beautiful locations in the heart of Madrid. And, do not forget to take some time to explore our vibrant city—after all, as we like to say here, *From Madrid to Heaven*!

Finally, we would like to sincerely thank everyone who has contributed to making this event possible: the EOHA management team (deep thanks Arjen, Hein, Arnaud, Anouk, and Ludo), the CSIC staff (Jorge, María, and technical and administrative teams), our committed sponsors (Longhorn Vaccines and Diagnostics, Werfen, BComing), the scientific, the young and the national committees, and our enthusiastic technical secretariat (Raquel and Horizcience team). We are also truly grateful to our national collaborators and to the nearly 200 speakers, authorities, panellists and delegates from 25 countries across Europe and beyond. Your participation is what makes this first EOHA ASM such a vibrant and international event.

We look forward to welcoming you all in Madrid!

Ana de la Torre and Jovita Fernández-Pinero

EOHA ASM 2026 co-chairs

Animal Health Research Center (CISA-INIA-CSIC), Valdeolmos, Madrid, Spain

COMMITEES

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Jovita Fernández-Pinero

CISA INIA CSIC

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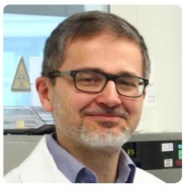
Animal and Plant Health Agency



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KEYNOTE & INVITED SPEAKERS

Ana María de Roda Husman -Keynote Speaker

Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), The Netherlands

Prof. dr. Ana Maria de Roda Husman PhD has over 20 years of experience as a principal investigator in environmental infectious diseases and antimicrobial resistance in the One Health context. She advises policy makers at the Dutch government, the European committee, WHO, ECDC and EFSA on environmental surveillance for public health, and possible intervention measures. She has published over 150 peer-reviewed papers in scientific journals. And has given many interviews for national and international media. She directs infectious disease research and policy advice at RIVM. She holds the chair of Global changes and environmentally transmitted infectious diseases at the Institute for Risk Assessment Sciences of Utrecht University. She has served as an expert for WHO since 2004 for the revision of the Guidelines for Drinking Water Quality. Ana Maria is the director of the WHO Collaborating Center for Risk Assessment of Pathogens in Food and Water. She has set up the Dutch nationwide wastewater and environmental surveillance programs for AMR, COVID-19 and other health determinants.

Bruno González Zorn-Keynote Speaker

Professor and Head of the Antimicrobial Resistance Unit (ARU) at the Complutense University in Madrid, Spain.

Prof. Bruno Gonzalez-Zorn is full Professor and Head of the Antimicrobial Resistance Unit (ARU) at the Complutense University in Madrid, a multidisciplinary laboratory he founded in 2005 and has brought One Health to the forefront of research on antimicrobial resistance.

In 2023 he was elected Dr honoris causa in Ghana for his continuous support of local Public Health, and he is the Chair of One Health in the Alliance Una Europa. His research focuses on the flux of antimicrobial resistance genes and bacteria between humans, animals and the environment. He gained his DVM in 1996 studying in Spain and Germany and his european PhD in 2001. After his Postdoc at the Pasteur Institute in Paris he received a Ramon y Cajal tenure-track contract from the Spanish Ministry of Science to return to Spain. In 2011 he was awarded the National Microbiology Award, from the Spanish Society for Microbiology, the National Antimicrobial Resistance Research Award for his research on mcr-1 and waste-water from the Ministry of Health in 2018, and in 2020 the Award for antimicrobial resistance alternatives from the Veterinary Royal Academy. In 2011 he was elected the first non-clinical member of the Scientific Advisory Board of the JPI AMR, co-authoring the first two Strategic Research Agendas.

He is the former President of the Molecular Microbiology Group of the Spanish Society for Microbiology and Head of Department. Gonzalez-Zorn has lead projects with the US, Latin America, Africa and Asia on molecular microbiology and the ecology of antimicrobial resistance, and has collaborated with Research Institutions world-wide. Gonzalez-Zorn works on the National Action Plan against Antimicrobial Resistance, and has advised Governments world-wide in the implementation of the One Health approach in their Action Plans.

Isabella Monne-Keynote Speaker

Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) – WOAH/FAO Reference Centres for Avian Influenza and Newcastle Disease, Italy.

Isabella Monne is a veterinarian, currently Head of the Viral genomics and transcriptomics laboratory at the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) which hosts the EU/FAO/WOAH Reference Laboratory (RL) for Avian Influenza and Newcastle Disease. Since 2016, she has served as a WOAH expert for avian influenza and Newcastle disease, supporting reference laboratory activities at the science–policy interface. Her work is strongly One Health–oriented, combining genomic surveillance and bioinformatics with field and epidemiological information across wildlife, poultry, and other susceptible hosts to understand viral evolution, transmission pathways, and determinants of host range and zoonotic risk, particularly for avian influenza. She leads and contributes to multiple national and international projects and has authored or co-authored 168 peer-reviewed publications.

Carlos Gonçalo Das Neves- Keynote Speaker

Chief scientist of European Food Safety Agency (EFSA)

Prof. Dr. Carlos das Neves is EFSA's Chief Scientist and has been a member of EFSA's senior management team since November 2022.

A Portuguese and Norwegian national, Carlos was Director of Research and Internationalisation at the Norwegian Veterinary Institute (NVI) before joining EFSA and previously served as Head of Virology and Head of Food Safety & Emerging Threats at the NVI. Additionally, he was a Full Professor at The Arctic University of Norway (UiT) from 2012 to 2025.

Carlos is a veterinarian (DVM – Technical University of Lisbon) and holds a PhD in veterinary sciences (Norwegian School of Veterinary Sciences). He also has a Postgraduate Certificate in Public Health from the London School of Hygiene and Tropical Medicine, and a Certificate in Public Policy Analysis from the London School of Economics and Political Science. In April 2024, he has been appointed as a member and co-chair of the One Health High-Level Expert Panel (OHHLEP), the scientific and strategic advisory group to the Quadripartite organisations – Food and Agriculture Organisation, UN Environment Programme, World Health Organization and World Organisation for Animal Health.

His areas of expertise include animal health, food safety, wildlife, emerging diseases, and One Health. He has led national and international research and development projects and has been a member of international panels and organisations related to his field of work. Carlos has several publications in peer-reviewed journals and books.

Ole Heuer- Keynote Speaker

Head of Unit for One Health Related Diseases at the European Centre for Disease Prevention and Control (ECDC)

Dr Ole E. Heuer is a Doctor of Veterinary Medicine (DVM) from the Royal Veterinary and Agricultural University in Copenhagen and holds a PhD in Epidemiology. As Head of Unit for One Health Related Diseases at the European Centre for Disease Prevention and Control (ECDC), he leads work on One Health, surveillance, and scientific advice across a broad range of infectious diseases. He held various pivotal scientific and managerial positions at ECDC including Head of Section Epidemic Prone Diseases and Public Health Emergency manager during the COVID-19 pandemic, before being appointed as Head of Unit Disease Programmes in 2024. Dr Heuer has chaired the EU Cross-Agency One Health Task Force involving five EU Agencies and he leads the implementation of the ECDC One Health Framework. His work is characterised by strong commitment and dedication to advancing public health through interdisciplinary and cross sectoral collaboration.

Ludovico Sepe- Keynote Speaker

European One Health Association (EOHA) – German Federal Institute for Risk Assessment (BfR)

Ludovico Sepe is a project manager passionate about One Health, with a background in molecular biology of infectious diseases. He works at the German Federal Institute for Risk Assessment (BfR) where he is involved in the European Partnership on Animal Health and Welfare, overseeing dissemination activities, as well as being Stakeholder Liaison Officer for the European One Health Association. He also assists the European One Health Association in running the Thematic Network on One Health called PEITHO. Ludovico has worked in a number of European and non-European countries, and is always happy to collaborate with multidisciplinary and diverse teams

Hein Imberechts- Round Table Chair

Vice-president of EOHA, Sciensano, Belgium

Hein Imberechts holds a degree of Veterinary Medicine from the University of Ghent and obtained a PhD in 1992 at the Free University of Brussels in Belgium.
From 2001 to 2015 he was the Head of Department of bacteriology at the Belgian reference laboratory for infectious animal diseases, now Sciensano. Since 2015 he is project manager at the Strategy & External Positioning service at Sciensano. He is member of the CWG on Animal Health and Welfare Research, of which he became Chair in 2019. Since 2024 he is member of the management team of the European Partnership on Animal Health & Welfare. Between 2018 and 2023, he was scientific coordinator of the One Health European Joint Programme together with ANSES in France. Since 2018, he is Vice-President of the European One Health Association.

Pablo Hervás-Round Table Chair

Vice-president of the Foundation Vet+i - Spanish Technology Platform for Animal Health

Pablo Hervás is the Vice-president of the Foundation Vet+i – Spanish Technology Platform for Animal Health, which objective is to promote Research, Development and Innovation in the Animal Health Sector.Since 2008 Pablo is working for the animal health industry in Spain. He is currently Technical and Public Affairs Director for the Spanish Animal Health Industry Association (Veterindustria), which is a member of AnimalhealthEurope and HealthforAnimals and the Spanish Platform for One Health. He is also Technical Director for the Spanish Petfood industry Association (ANFAAC).

Pablo is one of the coordinators of SomosGanadería, Spanish mirror Initiative of the European Livestock Voice.

During his career Pablo has been involved in strategies and policies regarding the one health concept in areas such as research and innovation, policy, training, communication, etc.

Pikka Jokelainen-Round Table Chair

Head of Function for One Health and International Collaborations at Statens Serum Institut (SSI). Denmark

Dr. Pikka Jokelainen (DVM, MPG, PhD, Adj. prof.) is Head of Function for One Health and International Collaborations at Statens Serum Institut, Denmark, which is a member organisation in the European One Health Association (EOHA). Dr. Jokelainen has published about 150 scientific articles, mainly in the areas of One Health, zoonoses, infectious disease preparedness, and science-policy interfaces. They hold several leading roles in large One Health and preparedness initiatives, including in EU-WISH on wastewater-based surveillance, Global Pathogen Analysis Platform on genomic data analysis, and OH4Surveillance on integrated One Health surveillance for zoonotic pathogens.

Ricardo Carapeto-Panellist

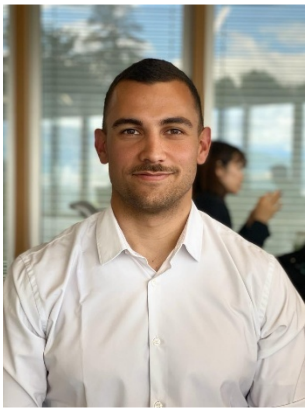
Spanish Medicines Agency (AEMPS)

Mr. Ricardo Carapeto is a veterinarian who has been working in Spanish Medicines Agency for the las 15 years. There, he specialised in the field of environmental risk assessment of medicines and AMR in the environment. Indeed, he is member of the European Committee of Veterinary Medicines at the European Medicines Agency (to whom he gives support in the field of environmental risks) and he is also Coordinator in the field of the environment of the National Action Plan Against Antimicrobial resistance (PRAN).

Jordi Figuerola-Panellist

Estación Biológica de Doñana (EBD-CSIC)

Jordi Figuerola holds a degree in Biology from the University of Barcelona and a PhD in Biological Sciences from the Autonomous University of Madrid. He is Research Professor at the Spanish National Research Council (CSIC) and works at Estación Biológica de Doñana. His main research focuses on understanding the environmental and evolutionary factors that affect the emergence and transmission of zoonoses, with particular attention to emerging mosquito-borne zoonoses. His studies on the ecology of West Nile virus transmission has been very influential in the development of current West Nile virus surveillance and monitoring programas in the country. He currently directs the ARBOPREVENT project, funded by the "la Caixa" Foundation, which aims to improve our understanding of the transmission ecology of West Nile virus and develop new strategies to enhance the surveillance and control of this and other mosquito-borne viruses. Currently is member of the Animal Health and Welfare panel of the European Food Safety Authority (EFSA)



Pablo Sagredo-Panellist

One Health Specialist

Pablo is a One Health Specialist at the United Nations Environment Programme (UNEP), based in Brussels, where he serves as the regional focal point for Europe and Central Asia. With a background in law and international cooperation, he works at the science–policy interface to advance the integration of environmental considerations into One Health approaches. Pablo collaborates closely with the Quadripartite (FAO, UNEP, WHO, and WOAH) and engages with European Union institutions to promote coordinated action on issues such as antimicrobial resistance, biodiversity loss, pollution, and climate change. His work focuses on strengthening cross-sectoral collaboration and translating global commitments into regional and national implementation.

Diana Teixeira-Panellist

Federation of Veterinarians of Europe

Isabel Masip-Panellist

VIT-CSIC

José Miguel Rubio Muñoz-Panellist

Director of the National Centre for Microbiology, ISCIII, Spain

José Miguel Rubio has been Director of the National Centre for Microbiology (ISCIII) since 2025. He holds a degree and a PhD in Biological Sciences from the Autonomous University of Madrid (Spain) and has been part of the Instituto de Salud Carlos III since 1997, where he has developed a strong career in parasitology and global health as Head of the Malaria and Emerging Parasitic Diseases Unit from 2007.

He completed his training at leading international institutions in the United Kingdom (1989–1992), Italy (1992–1993), Greece (1993–1994), and the Netherlands (1994–1996). He is currently a Visiting Scientist at FIOCRUZ-Amazonas (Brazil) and an external consultant for academic institutions in Egypt (Cairo University) and Malaysia (Institute of Medical Research). He also serves as an expert on several European committees, including the ECDC, and acts as an evaluator for European Commission health programmes.

He has authored more than 100 international scientific publications, as well as several book chapters, books and divulgate articles, and has participated in 60 competitive research projects, serving as PI in 22. He has been awarded five six-year research evaluation periods, the most recent in 2023.

Furthermore, he contributes to postgraduate programmes in microbiology and parasitology, has supervised seven PhD theses and several Master’s and undergraduate dissertations. He has coordinated several courses on Molecular Diagnosis in Tropical Diseases (2001–2019; ENS-ISCIII) and more recently the international course Parasitic Diseases & Malaria: Road Back from Molecular to Microscopy + AI (ESCMID, 2024 & 2026)

Enrique Navarro-Panellist

International relations of the Science in Parliament platform, Spain

Dr. Enrique Navarro is a senior researcher and Vicedirector at the Pyrenean Institute of Ecology (IPE-CSIC, Spain), with a long-standing career in freshwater ecology and ecotoxicology. His work has focused on the impacts of multiple stressors and emerging contaminants on aquatic ecosystems, linking mechanistic science with ecosystem-level assessment. He has also contributed to ecological status assessment frameworks and international cooperation on freshwater management.

Dr. Enrique Navarro also served as Director General for Research and Innovation of the Government of Aragón, where he oversaw regional science and innovation policy, funding, and strategic planning. He also worked at the science–policy interface, promoting the use of robust scientific evidence in public decision-making as a part of the Asociación Ciencia en el Parlamento. His experience bridges research excellence with institutional leadership and policy implementation.

Maite Martín Ibañez -Panellist

President of the One Health Platform, Spain and Professor at the Veterinary Faculty of the Universitat Autònoma de Barcelona

Maite Martín holds a Licentiate and a PhD in Veterinary Medicine from the Autonomous University of Barcelona (UAB). She served as Dean of the Faculty of Veterinary Medicine at UAB (2017-2022) and represented Spanish and Portuguese veterinary faculties on the ExCom of the European Association of Establishments for Veterinary Education. As President of the Conference of Deans of Spanish Veterinary Faculties (2020–2022), she was a key driver behind the creation of the Spanish One Health Platform (POH), an association launched in 2021 and oriented toward policy engagement for the implementation of One Health approach. Under her leadership, POH has established strong institutional partnerships, participated in policy-focused working groups, and become the organizer of the Spanish Annual One Health Meeting. The work developed by the POH has been recognized with several awards including RTVE's El Escarabajo Verde and the I Premio Prevención para un Futuro Saludable, acknowledging its impact on education, science communication, and public policy

Marie-Cécile Ploy-Panellist

Coordinator of EU-JAMRAI project, Limoges university, France

Marie-Cecile PLOY, PharmD, PhD, is a Professor of Microbiology at the Faculty of Medicine and Limoges Teaching Hospital, Limoges University, France. She is head of the Bacteriology-virology-hygiene department at the Limoges teaching hospital and director of the Inserm RESINFIT research unit on antimicrobials at the Limoges University (https://www.unilim.fr/resinfit/). She gained her PharmD in 1994 and her PhD on aminoglycoside resistance in 2000 (Institut Pasteur and Paris XI University). She had a postdoctoral position (2003-2004) in Didier Mazel'lab at the Institut Pasteur in Paris, France, where she focused her research on integrons.

She is part of numerous Committees on Antimicrobial resistance at the national level. She was the coordinator of the European Joint Action an Antimicrobial resistance and healthcare-associated infections (www.eu-jamrai.eu) from 2017 to 2021 and she coordinates the second Joint action, EU-JAMRAI 2, from 2024 to 2027.

She is an expert in numerous national and international research programmes on antimicrobial resistance.

She is vice-dean for research at the Faculty of Medicine, Limoges University

She is full member of the French Academy for Veterinary Medicine

Her research addresses the mechanisms and dynamics of mobilization and spread of antimicrobial resistance. Her main research topics are i) the role of the SOS response in antibiotic resistance acquisition and expression, and ii) the risk assessment of the antibiotic resistance dissemination in the environment.

Elsa Dibongue

General secretary of PREZODE

Ariane Vander Stappen

Head of Unit-One Health, Antimicrobial Resistance, DG SANTE, European Commission)

EOHA Annual Scientific Meeting 2026

Scientific Programme

Madrid, Spain | May 18–20, 2026

Venue: CSIC Headquarters, main building (C/Serrano, 117, Madrid)

Day 1 - 18 May 2026

14.00h - 14.30h	**OPENING CEREMONY** **Arjen van de Giessen** (President EOHA) **Carlos Gonçalo das Neves** (EFSA chief scientist and EFSA management team) **Ernesto Igartua Arregui** (Deputy coordinator of the LIFE area, Agricultural Sciences of CSIC.) **Ana de la Torre** (Congress chair CISA/INIA/CSIC) **Jovita Fernández-Pinero** (Congress chair CISA/INIA/CSIC)

SESSION 1 – MAIN HALL

Joining Environmental Sciences and Ecology with Human/Animal Health

14.30h - 15.00h	**KEYNOTE LECTURE 1 - One Health goes Environmental** **Ana Maria de Roda Husman**, Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), The Netherlands *Chair: Hein Imberechts, Vice-president of EOHA, Sciensano, Belgium*
15.00h - 16.00h	**PANEL DISCUSSION / ROUND TABLE 1.** **Environmental Health as the Missing Pillar of One Health** **CHAIR: Hein Imberechts**, Vice-president of EOHA, Sciensano, Belgium **PANELLISTS:** Ana Maria de Roda Husman (RIVM, Netherlands), Ricardo Carapeto (AEMPS, Spain), Carlos das Neves (EFSA), Jordi Figuerola (EBD-CSIC, Spain), Pablo Sagredo (United Nations Environment Programme -UNEP)
16.00h - 16.30h	COFFEE BREAK
16.30h - 18.30h	**SESSION 1** **Selected oral presentations** *Chairs: Mamuka Kotetishvili (OHI, Georgia) and Miguel A. Jiménez-Clavero (CISA-INIA-CSIC, Spain)* **16:30** -- “Towards synergy: better integration of the Environmental domain in One Health” - **De Cock, M. et al.** **16:45** -- “Scrub Typhus Outbreak in Sagalee Block, Arunachal Pradesh, India, September 2023: An Emerging Zoonosis” - **Monya, M. et al.** **17:00** -- “Host community traits driving Crimean-Congo hemorrhagic fever virus maintenance in Iberian ecosystems” - **Xavier, P. et al.**

Day 1 - 18 May 2026

	17:15 -- “Arbovirus monitoring in field collected mosquitoes in Emilia-Romagna (Italy, 2025)” - **Calzolari, M. et al.** **17:30** -- “Higher rates of Shiga toxin-producing E. coli (STEC) detection in groundwater wells associated with increasingly “vulnerable” hydrogeological settings” - **Burke, L. et al.** **17:45** -- “Antimicrobial resistance of public health relevance in wild ungulates of Andalusia, southern Spain” - **Ewbank, A. C. et al.** **18:00** -- “Impacts of Climate Change and Population Growth on Campylobacteriosis and Salmonellosis in England and Wales” - **Lo Iacono, G. et al.**
18.15h – 18:30h	**OFFICIAL CONFERENCE PHOTO**
18.30h - 20.00h	WELCOME SPANISH WINE (CLAUSTRO- MAIN ENTRANCE) Centro de Física "Miguel Antonio Catalán" C/Serrano, 123

Day 2 - 19 May 2026

SESSION 2

Research Topics at the Frontiers of One Health

09.00h - 09.30h	**KEYNOTE LECTURE 2 - The Coevolution of Antimicrobial Resistance and One Health** **Bruno González Zorn,** Professor and Head of the Antimicrobial Resistance Unit (ARU) at the Complutense University in Madrid, Spain. *Chairs: Shaun Cawthraw (APHA, UK) and Beatriz Romero (VISAVET-UCM, Spain)*
09.30h – 10.45h	**SESSION 2** **Selected oral presentations-Main Hall- AMR** *Chairs: Shaun Cawthraw (APHA, UK) and Beatriz Romero (VISAVET-UCM, Spain)* **09:30** --“Shared genes, different pressures: environmental AMR landscapes in Spain and Switzerland” - **Gionchetta, G. et al.** **09:45** -- “Divergent antimicrobial resistance trajectories across US food production and human clinical settings revealed by time-series and cross-correlation analysis” - **Carreño Gútiez, M. et al.** **10:00** -- “Nationwide Prevalence, Virulence, and AMR of Shiga toxin-producing Escherichia coli in Slaughtered camels, sheep, and goats in Saudi Arabia” - **Aljasir, S. et al.** **10:15** -- “Metagenomic deep learning to support dissemination risk assessment of antimicrobial resistance genes” - **Hu, K. et al.**

Day 2 - 19 May 2026

10:30 -- “Modeling the evolutionary trajectories of antimicrobial resistance genes and donor-recipient interactive networks underlying their transmission” - **Kotetishvili, M. et al.**

Selected oral presentations- Parallel Hall *(IQF Blas Cabrera, C/Serrano, 119)*- Viral Pathogens

Chairs: Ludovico Sepe (BfR, Germany) and Pilar Aguilera-Sepúlveda (CISA-INIA-CSIC, Spain)

09:35 -- “Early Spring Heat, Higher Summer Risk: Temperature-Curve Signals to Guide West Nile Virus Preparedness” - **Barbić, L. et al.**
09:50 -- “Strong1H: filling the gaps in surveillance of zoonotic influenza viruses and West Nile Virus in the Netherlands” - **Lempens, P. et al.**
10:05 -- “Comparative pathogenicity and host competence of Spanish West Nile virus strains in animal models” - **Llorente, F. et al.**
10:20 -- “Hepatitis E in Serbia – The Human–Animal Interface Within a One Health Framework” - **Lupulović, D. et al.**

10.45h – 11.15h

COFFEE BREAK

11.15h - 13.00h

SESSION 2

Selected oral presentations – Main Hall-Miscelaneous

Chairs: Angela Pista (INSA, Portugal) and Puerto Morales (ICMM-CSIC, Spain)

11:15 -- “Salmonella transmission dynamics in a pig slaughterhouse” - **Bloem, H. et al.**
11:30 -- “Changes in soil microbiota after the application of five organic wastes” - **Alija Novo, N. et al.**
11:45 – “Exploring airborne resistomes in two Japanese cities through PacBio long-read metagenomic sequencing” - **Ekhlas, D. et al.**
12:00 -- “Evaluation of routine One Health WGS-based surveillance of Salmonella Enteritidis and Typhimurium in the Netherlands” - **Kerkvliet, J. et al.**
12:15 -- “Bio-resonance and frequency-dependent resilience in the mouse gut microbiome” - **Gardner, B. et al.**
12:30 -- “Fish as bioindicators for monitoring aquatic ecosystem health status in a One Health perspective” - **Ossola, M. et al.**
12:45 -- “Integrating Aquamation and Composting for Sustainable One Health Management of Animal Waste in Arid Contexts” - **Barsi, F. et al.**

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Chairs: Virginia Filipello (IZSLER, Italy) and Giulia Gionchetta (IDAEA-CSIC, Spain)

11:20 --“Monitoring antimicrobial resistance in aquatic environments using wild coypu (Myocastocoypus) as sentinels: An Enterococcus-based approach” - **Massella, E. et al.**

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	11:35 – "Metagenomic Evidence for Localised Clinically Relevant ARG Hotspots Along a Coastal Wastewater-to-Beach Gradient" - **Sanchez-Carrillo, S. et al.** **11:50** --"Shotgun metagenomics of four Irish Integrated Constructed Wetlands reveals microbial dynamics in wastewater treatment" - **Tumeo, A. et al.** **12:05** -- "A One Health Approach into Aliarcobacter AMR Dynamics: A Comparative Analysis of MAGs and Isolates Across the Urban Wastewater System" - **Fornés Pérez, A. et al.** **12:20** -- "Association between veterinary antimicrobial sales data and antimicrobial resistance in commensal and 3GCR Escherichia coli in Spanish livestock" - **Serna, C. et al.** **12:35** --"Free-living amoebae as vectors of antimicrobial resistance in the agricultural environment: FLA microbiome and resistome in regenerated sludge" - **Machí Camacho, C. et al**.
13.00h – 14.30h	LUNCH/NETWORKING
14:00h – 14.30h	**e-POSTERS FLASH PRESENTATIONS COMPETITION**
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15.00h - 16.30h	**SESSION 3** **Selected oral presentations – Main Hall** *Chairs: Roberto La Ragione (U. Surrey, UK) and Aitor Nogales (CISA-INIA-CSIC, Spain)* **15:00** --"A rapid tool to assess the risk of emerging zoonotic signals at the human-animal interface" - **Vlaanderen, F. et al.** **15:15** -- "DatOHs: A modular data ecosystem for interoperable One Health surveillance and risk assessment" - **Hernández Jiménez, F. et al.** **15:30** -- "Evaluation of trained immunity induction by dpB in human monocytes" - **Sánchez Morales, L. et al.** **15:45** -- "Global Pathogen Analysis Platform" - **Wegener, H. C. et al.** **16:00** --"Pandemic Preparedness by Pathogen Detection (P3Dx): high-throughput central testing workflow using self-sampling and isothermal detection" - **Bordes, L. et al.** **16:15** --"Bacteriophage-Powered One Health Solutions for Safer Agri-Food Systems" - **Lasagabaster, A. et al.**

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16.30h – 17.00h	COFFEE BREAK
17.00h - 18.00h	**PANEL DISCUSSION / ROUND TABLE 2.** **Scaling Up One Health Solutions: From Research to Real-World Impact** **CHAIR: Pablo Hervás,** Vice-president of the Foundation Vet+i - Spanish Technology Platform for Animal Health **PANELLISTS:** Diana Teixeira (Federation of Veterinarians of Europe), Isabel Masip (VIT-CSIC), José Miguel Rubio Muñoz (Director of the National Centre for Microbiology, ISCIII, Spain), Isabella Monne (IZSVe – WOAH/FAO Reference Centres for Avian Influenza and Newcastle Disease), Bruno González Zorn (Head of the Antimicrobial Resistance Unit, UCM).
20.00h	CONGRESS NETWORKING DINNER (Optional) *Picalagartos, Gran Vía 21 (28013)*

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SESSION 4 – MAIN HALL
Science for Policy and Society

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09.00h - 09.30h	**KEYNOTE LECTURE 4** **Carlos Gonçalo das Neves**, chief scientist of European Food Safety Agency (EFSA) *Chairs: Nina Dam Otten (U. Copenhagen, Denmark) and Silvia Herrera (ISCIII, Spain)*
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11.00h – 11.30h	**KEYNOTE LECTURE: Advancing One Health in Europe: an EU agency perspective on evidence, approach and practice.** **Ole Heuer,** Head of Unit for One Health Related Diseases at the European Centre for Disease Prevention and Control (ECDC) *Chairs: Pikka Jokelainen (SSI, Denmark) and Marta Martínez (CISA-INIA-CSIC, Spain)*
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11.45h - 12.45h	**PANEL DISCUSSION / ROUND TABLE 3.** **Turning Evidence into Action: How to Make Science Matter in Policy** **CHAIR:** Pikka Jokelainen, Head of Function for One Health and International Collaborations at Statens Serum Institut (SSI). Denmark). **PANELLISTS:** Enrique Navarro (International relations of the Science in Parliament platform, Spain), Maite Martín Ibañez (President of the One Health Platform, Spain and Professor at the Veterinary Faculty of the Universitat Autònoma de Barcelona), Marie-Cécile Ploy (Coordinator of EU-JAMRAI project, Limoges university, France), Ole Heuer (Head of Unit for One Health Related Diseases at the European Centre for Disease Prevention and Control -ECDC), Elsa Dibongue (General secretary of PREZODE),

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	Ariane Vander Stappen (Head of Unit-One Health, Antimicrobial Resistance, DG SANTE, European Commission)

CLOSSING SESSION – MAIN HALL

12.45h - 13.15h	**BEST POSTER AND COMMUNICATIONS AWARDS / CLOSING CEREMONY** **Arjen van de Giessen** (President EOHA) **Ariane Vander Stappen (**Head of Unit-One Health, Antimicrobial Resistance, DG SANTE, European Commission) **A representative of CSIC** (TBC)
13.15h	LUNCH (Take away)

KEYNOTE LECTURES

Avian influenza as a stress test for One Health: how multidisciplinary research turns evidence into action

Ana Maria de Roda Husman, Centre for Infectious Disease Control (CIb), National Institute for Public Health and the Environment (RIVM), The Netherlands

The Coevolution of Antimicrobial Resistance and One Health

Bruno González Zorn, Professor and Head of the Antimicrobial Resistance Unit (ARU) at the Complutense University in Madrid, Spain.

Antimicrobial resistance (AMR) has emerged as one of the greatest global health threats of the 21st century, transcending the boundaries between human, animal, and environmental health. The One Health concept, which recognizes the interconnectedness of these sectors, has become central to understanding and combating the evolution and dissemination of resistance. This talk will explore the historical co-evolution of AMR and the One Health approach, highlighting how resistance predates the antibiotic era yet has been dramatically accelerated by anthropogenic antimicrobial use across medicine, veterinary practice, agriculture, and environmental contamination.

Special emphasis will be placed on the development of international collaborative frameworks such as Med-Vet-Net, which played a pioneering role in integrating medical, veterinary, food safety, and environmental perspectives in Europe. The presentation will examine how these interdisciplinary initiatives laid the foundations for current One Health surveillance and research strategies.

The lecture will further address the concept of “silent dissemination” of AMR: the unnoticed circulation of resistant bacteria, resistance genes, and high-risk clones across humans, animals, food chains, wildlife, and environmental reservoirs. Particular attention will be given to asymptomatic carriage, wastewater dissemination, plasmid-mediated transmission, and the role of global mobility and ecosystem interfaces in facilitating hidden transmission pathways.

By integrating historical perspectives, molecular epidemiology, and contemporary One Health surveillance strategies, this talk aims to provide a comprehensive overview of how AMR has evolved into a planetary health challenge and why coordinated, transdisciplinary action is essential to mitigate its future impact.

Avian influenza as a stress test for One Health: how multidisciplinary research turns evidence into action

Isabella Monne, Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) –
WOAH/FAO Reference Centres for Avian Influenza and Newcastle Disease, Italy

Highly pathogenic avian influenza has become a key test case for the practical implementation of One Health. The scale of virus circulation in wild birds, its repeated incursions into poultry, and the increasing detections in mammals make clear that prevention can no longer rely on fragmented surveillance or sector-specific responses. Under these conditions, research has real-world impact only if it helps detect threats earlier, characterize them faster, and support timely action.

Early warning now depends on the ability to look beyond conventional surveillance boundaries: into environmental contexts, across unexpected host species, and into settings where diagnostic capacity is limited. Horizon-scanning studies, field-adapted molecular tools, and real-time genomic characterization are reshaping how avian influenza can be monitored. Their value lies not only in detecting virus presence, but also in clarifying viral movement across space and species, tracking evolution, and enabling dynamic assessment of the risks posed by circulating strains. Real-time genetic characterization further extends this impact by supporting the predictive assessment of vaccine effectiveness across animal and human health, as well as early identification of viral changes potentially associated with altered susceptibility to antivirals.

In a scenario shaped by competing priorities such as food security, biodiversity protection, animal welfare, and public health, avian influenza remains a “One Health wicked problem”, and this is why innovation and innovative approaches to early detection and characterization matter: not because they solve it, but because they make it more governable.

KEYNOTE LECTURE 4

Carlos Gonçalo das Neves, chief scientist of European Food Safety Agency (EFSA)

KEYNOTE LECTURE: Advancing One Health in Europe: an EU agency perspective on evidence, approach and practice.

Ole Heuer, Head of Unit for One Health Related Diseases at the European Centre for Disease Prevention and Control (ECDC)

A renewed European commitment to One Health is increasingly recognised as essential for addressing complex, interconnected health threats like pandemics, antimicrobial resistance (AMR), the expansion of vector-borne diseases, and climate-driven shifts in infectious disease patterns. One Health has been further embedded as a core public health principle in Europe with increased cross sectoral collaboration at national level in several EU Member States and at EU level trough the EU Cross-Agency One Health Task Force strengthening interagency collaboration, providing strategic coordination and identifying research needs.

Recent evidence points to several high-impact threats, including AMR, vector-borne diseases, zoonotic food- and water-borne infections, underscoring the need for integrated surveillance and analytical capacity. Within this context, ECDC's work on One Health includes joint surveillance approaches, methodological developments, and cross-sectoral outbreak response, alongside efforts to support capacity building in Member States.

Examples from practice illustrate how One Health approaches are being implemented through coordinated platforms, local initiatives, and engagement with a broader range of stakeholders. Continued progress will depend on sustained investment, innovation, and trust, with further collaboration across sectors and disciplines needed to advance prevention and control of infectious diseases in a One Health approach.

Presentation of PEITHO – Platform for European Interdisciplinary, Transdisciplinary, Holistic One Health

Ludovico Sepe, European One Health Association (EOHA) – German Federal Institute for Risk Assessment (BfR**)**

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O-01 Towards synergy: better integration of the Environmental domain in One Health.

Bouman, A. [1]; de Cock, M. [1]; Thie, N. [1]

[1] National Institute for Public Health and the Environment, Centre for Infectious Diseases, Bilthoven, The Netherlands

Background: One Health is an integrated approach that recognizes the interconnectedness between human, animal, and environmental health in addressing complex public health challenges such as infectious disease emergence and spread. Despite the central role of the environment in shaping disease dynamics, the environmental domain is often underrepresented in One Health research, policy, and practice. This underrepresentation may limit the effectiveness and scope of One Health initiatives.

Objectives: This study aims to examine the underlying reasons for the marginalization of the environmental domain with the aim to better integrate the environmental domain within One Health. We focus on clarification of the definitions and scope of ‘environmental surveillance’ and ‘environmental health’ as used in the One Health scientific community, and map how the environment is currently included in One Health research. Next to that, we synthesize the benefits, opportunities, and challenges of integrating the environmental domain within One Health approaches.

Methods: A scoping review is currently being conducted to examine the literature on the inclusion of the environment and of environmental surveillance in One Health, with particular attention to discrepancies in terminology and practice. In addition, qualitative data will be collected for a more thorough understanding of underlying challenges through interviews and/or questionnaires with scientists and public health professionals active in the One Health field.

Expected results: This research will deliver a comprehensive overview of the position of the environment within One Health, highlight challenges and present opportunities for improved integration of the environmental domain in One Health.

O-02 Scrub Typhus Outbreak in Sagalee Block, Arunachal Pradesh, India, September 2023: An Emerging Zoonosis.

Michi Monya[1], P. Thiyagarajan[1], Vijaypal Singh[1], Preeti Madan[1], Abhay Kumar Sharma[2], Dr T. Nyodu[3], Monil Singhai[4], Ramesh Chandra[1], Dr L. Jampa[5] and Tanzin Dikid[1]

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Background: In August 2023, India's disease system surveillance generated a scrub typhus outbreak alert from Sagalee block in Arunachal Pradesh at the international border. We investigated to confirm and characterize the outbreak and provide recommendations.

Methods: We defined cases as scrub typhus positive by rapid diagnostic or ELISA in a resident (>6 months stay) of Sagalee block between January-September 2023. We confirmed the outbreak using a threshold of mean+2SD, from surveillance, hospital, and private laboratory data for the preceding three years. Cases were identified from the line lists and interviewed using a semi-structured questionnaire to collect demographic details, clinical features, and exposure history. Environmental assessments around case households assessed vegetation, proximity to forests or water bodies, domestic animals, and rodent activity. Rodents were trapped and examined for ectoparasites; rodent infestation rate and chigger index were calculated. Rodent sera were tested using Weil-Felix test.

Results: Scrub typhus cases increased in 2023 (n=53), exceeding the threshold (mean+2SD = 1.7+2.9). Among 42 interviewed cases, 67% were female and the median age was 40 years (IQR 28–50). Most were indigenous (95%), farmers (83%), and forest dependent (62%). Fever (100%) and headache (67%) were common symptoms; eschar was present in 12%. All except one patient recovered. All cases lived near forests, fields, water bodies, or dense vegetation. Rodent activity was reported by 95%, and none used personal protective measures while visiting forest nor used insecticide/rodenticide in surrounding habitat. Rodent infestation rate was 78% (18/23), chigger index was nine (207/23), and 44% (7/16) of rodents showed significant ($\geq$1:40) OXK titers.

Conclusion: This was the first documented scrub typhus outbreak in Sagalee block. Conducive vector habitats, high rodent and chigger infestation, human exposure behaviors, and rodent seropositivity completed the epidemiological triad. A one-health approach with integrated surveillance, rodent control, and community awareness is recommended.

Key words: One-health, Scrub typhus, India, Epidemiology

O-03 Host community traits driving Crimean-Congo hemorrhagic fever virus maintenance in Iberian ecosystems.

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Background: Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne zoonosis of significant public health concern, maintained in complex multi-host systems shaped by ecological, climatic, and anthropogenic drivers. In the Iberian Peninsula, changing land-use patterns and biodiversity loss may be reshaping host communities in ways that alter local transmission dynamics.

Objectives: We aimed to identify ecological and environmental predictors of CCHFV exposure in Iberian ecosystems and to evaluate how community composition, landscape structure, and climate jointly shape transmission risk at different spatial scales. Understanding how these factors interact is essential for developing One Health surveillance and preparedness strategies that protect both human and animal health.

Methods: We conducted a landscape-scale study across 18 Iberian sites, integrating serological surveillance of wild ungulates (n = 1,461; 69.4% wild boar and 30.6% red deer) with camera-trap monitoring of mammalian communities, land-cover analysis, and climatic variables. Two GLMM were fitted: a full-landscape model including all sites to identify broad predictors of exposure, and an endemic-area model restricted to sites with established transmission foci to explore fine-scale dynamics.

Results: Overall, 44.5% of sampled individuals tested positive for CCHFV antibodies, with site-level seroprevalence ranging from 1.5% to 81.4%. Across all sites, seroprevalence was positively associated with red deer abundance, underscoring the potential role of red deer as key amplifying host, forest cover, and precipitation seasonality, while small ruminant presence was linked to reduced exposure risk. Within endemic areas, higher mammalian diversity and greater lagomorph abundance were negatively associated with exposure, whereas warmer temperatures promoted circulation. This pattern suggests that more balanced host communities can reduce the efficiency of pathogen transmission.

Conclusions: This study highlights how community structure and environmental change jointly shape CCHFV ecology. The context-dependent nature of ecological drivers support integrated One Health strategies that conserve biodiversity, promote mixed grazing systems, and regulate wild ungulate populations to reduce CCHFV circulation in ecosystems undergoing socio-ecological transformation.

O-04 Arbovirus monitoring in field collected mosquitoes in Emilia-Romagna (Italy, 2025).

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Background:

Emilia-Romagna region experienced the circulation of West Nile virus (WNV) since 2008. For the early detection of virus circulation an entomological surveillance targeting *Culex pipiens* was set (as part of the Regional and National arbovirus surveillance). We take advantage of this plan to search WNV, Usutu virus (USUV) and Tahyna virus (TAHV) in all mosquitoes collected in a lapse of time.

Objectives:

Detection of different arbovirus in mosquitoes collected for WNV surveillance.

Methods:

Mosquitoes were collected by 98 georeferenced traps evenly distributed in the lowland area of the region. Attractive traps, baited with CO2 were used overnight every two weeks. Collected mosquitoes from July 22 to August 14 and in September 2-11 2025, were identified and pooled, with a maximum of 200 females per pool. Pools were tested with real-time PCRs targeting WNV, USUV and TAHV.

Results:

A total of 44,035 mosquitoes, belonging to 11 species, were collected, grouped in 954 pools and tested. The most collected species were *Cx. pipiens* (58.9 %) followed by *Aedes caspius* (32%), *Ae. albopictus* (5.7%) and *Ae. vexans* (3%). WNV was detected in 54 pools, USUV in 35, TAHV in 14. WNV and USUV were mainly detected in *Cx. pipiens* pools, with 50 and 35 respectively, but also in *Ae. caspius* and *Ae. albopictus*. Twelve TAHV/+ pools were recorded in *Ae. caspius* and 2 in *Cx. pipiens*.

Conclusions:

The obtained data demonstrate that *Cx. pipiens* is the main vector of WNV and USUV in the monitored area. The presence of other WNV-positive mosquitos does not demonstrate their vectorial competence and does not mean that they are playing a concrete vector role, but it may indicate their potential contribution as a bridging vector. *Aedes caspius* represents the main vector of TAHV, the detection of this virus deserves a more in-depth investigation, to better evaluate its potential pathogeny in study area.

O-05 Higher rates of Shiga toxin-producing *E. coli* (STEC) detection in groundwater wells associated with increasingly "vulnerable" hydrogeological settings.

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Background: Unregulated private groundwater supplies are widely used for drinking water in Ireland and represent an important transmission route for waterborne pathogens including Shiga-toxin producing *Escherichia coli* (STEC).

Objectives: To investigate the presence of six human infection-associated STEC serogroups in groundwater wells in three hydrogeologically distinct catchments during the peak human infection period.

Methods: Three sub-catchments of extreme, high and moderate groundwater vulnerability categories (according to Geological Survey Ireland) were selected for field studies. Groundwater wells (n=13-14 per catchment, 40 total) were sampled fortnightly from June to September 2025 and assessed for *E. coli* (MPN/100 mL) using Colilert 18®. For *E. coli* positive samples, 1L was filtered (0.45 µM), filters enriched in mTSB, and Shiga toxin (*stx1* and *stx2*) detection performed on DNA extracts by real-time PCR. Stx1/2-positive samples were assessed for six serogroup-associated genes by real-time PCR.

Results: *E. coli* was detected in 68/234 (29%) samples and STEC (*stx1/stx2*) in 28 (12%) samples. There was greater STEC detection in the extreme (n=20/82, 24%) vs the high (n=6/75, 8%; p=0.009, Fisher's Exact test) and moderate (n=2/77, 3%; p=<0.0001) vulnerability catchments. The overall STEC to *E. coli* detection ratio was 1:2.43, with ratios of 1:1.95, 1:3.16 and 1:5 in the extreme, high and moderate vulnerability catchments, respectively. Serogroups O157 (n=8 detections, 29% positivity in STEC samples), O145 (n=8, 29%), O104 (n=7, 25%) and O103 (n=6, 21%) were present, with 7 samples positive for multiple serogroups. O26 and O111 were not detected.

Conclusions: Frequent detection of viable *E. coli*, *stx1/2* genes, and genetic markers for 4 serogroups associated with hundreds of STEC enteritis cases annually in Ireland highlights the likely importance of groundwater wells in STEC transmission, particularly in hydrogeologically vulnerable catchments. Non-detection of the most common human infection serogroup, O26, may reflect different transmission pathways.

O-06 Antimicrobial resistance of public health relevance in wild ungulates of Andalusia, southern Spain.

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Background: Ungulates co-inhabit with extensive livestock, humans, and crop fields – scenarios under antibiotic pressure. We hypothesized that wild ungulates could be AMR environmental pollution indicators.

Objectives: Our goal was to (i) identify selected ARGs, heavy metals and biocides, and MGEs, and (ii) analyze, within each species´ home range, their exposure to anthropogenic sources using our geospatial analytical tool (Surveillance and Monitoring of Antibiotic Resistance in the Environment [SMART-E]).

Methods: Fecal samples from wild boar *Sus scrofa* (n=23), red deer *Cervus elaphus* (n=9) and fallow deer *Dama dama* (n=6), Andalusia, Spain, were analyzed using SmartChip PCR, for 23 genes: beta-lactams, macrolide-lincosamide-streptogramin B, phenicol, quinolone, sulfonamide, tetracycline, vancomycin, and polymyxins, heavy metals (copA, czcA, merA), biocide (qac), and MGEs (IncF-FIC and IncI1 plasmids, class 1 integron). The 16S rRNA gene was quantified for quality control. Exposure to anthropogenic sources (i.e., rivers downstream WWTP and agricultural plots fertilized with sludge and/or animal manure) within each species´ location was extracted (ArcGIS Pro 3.1).

Results: ARGs and multidrug-resistance were detected in 100% (38/38) of the individuals. Most relevant results: (I)ARGs against vancomycin and betalactams in red and fallow deer (100%;9/9 and 6/6), and in wild boar (95,65%[22/23] and 91,30%[21/23]), and to polymyxin in red (88,89%[8/9]) and fallow deer (83,33%[5/6]); (II)copA in red and fallow deer (100%;9/9 and 6/6), and wild boar (95,65%;22/23); and (III) IncI1_repl1 in red and fallow deer (100%;9/9 and 6/6), and wild boar (91,30%;21/23). All samples were biocide-negative. Spearman's rank correlation analysis showed a significant positive correlation between ARG prevalence and the presence of contaminated rivers ($\rho = 0.394$, $p = 0.05$) and manure-fertilized agricultural plots ($\rho = 0.333$, $p = 0.05$).

Conclusions: Our findings highlight anthropogenic sources as local indicators of environmental AMR contamination and support the use of wild ungulates as bioindicators of environmental impact. Co-funded: EU's Horizon 101136346 EUPAHW.

O-07 Impacts of Climate Change and Population Growth on Campylobacteriosis and Salmonellosis in England and Wales.

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Background: Salmonellosis and Campylobacteriosis are two foodborne diseases strongly influenced by weather and climate factors, as evidenced by their seasonal patterns and associations with temperature and precipitation. Climate change is expected to exacerbate these conditions by altering environmental factors, yet quantitative projections of its impact on disease burden remain limited.

Objectives:

- To provide high-resolution projections of the future incidence of Salmonellosis and Campylobacteriosis in England and Wales under different climate scenarios.
- To quantify the relative contributions of climate change and population growth to disease burden
- To identify potential seasonal shifts in incidence.

Methods: We integrated high-resolution meteorological projections from **UKCP18** with conditional-incidence estimates linking daily weather conditions (maximum air temperature, precipitation, and daylength) to laboratory-confirmed cases of Salmonellosis and Campylobacteriosis. The analysis was conducted under two Representative Concentration Pathways (RCP2·6 and RCP8·5) for the years 2025–2095. By isolating the effects of climate change from demographic changes, this approach provides a clearer understanding of future disease burden, with increased uncertainty for weather conditions outside historically observed ranges.

Results: Salmonellosis incidence is projected to increase by 35–50% relative to historical averages, with climate change alone contributing up to a 15% increase under RCP8·5 by 2095. These changes are driven by rising temperatures, altered precipitation patterns, resulting in a shift in seasonal peaks. In contrast, climate change is expected to have a limited impact on Campylobacteriosis incidence, with projected increases primarily attributed to population growth rather than climate factors.

Conclusions: This study provides the first high-resolution projections of foodborne disease burden under UK climate scenarios. The findings highlight the importance of integrating epidemiological and climate models to inform public health preparedness and adaptation strategies for mitigating future foodborne disease risks.

ORAL PRESENTATIONS·SESSION 2: RESEARCH TOPICS AT THE FRONTIERS OF ONE HEALTH

O-08 Shared genes, different pressures: environmental AMR landscapes in Spain and Switzerland.

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Background: Antimicrobial resistance (AMR) is a critical One Health challenge sustained by environmental reservoirs where antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) persist and disseminate. Anthropogenic pressures can strongly shape environmental resistomes, yet how geographical context influences resistance abundance versus dissemination potential remains poorly understood.

Objectives: This study aimed to compare the abundance, composition, and mobility potential of environmental resistomes across countries, environmental matrices, and impact gradients, and to assess the occurrence of core clinically relevant ARGs and priority pathogens.

Methods: We analyzed freshwater, freshwater biofilms, agricultural soils, and wastewater from impacted and non-impacted sites in Spain and Switzerland. High-throughput quantitative PCR targeting 205 ARGs and 37 MGEs was applied to pooled DNA samples representative of each matrix and condition. ARG-MGE correlations and pathogen-ARG co-occurrence networks were used as proxies for dissemination risk.

Results: ARGs and MGEs followed a consistent abundance gradient (wastewater > freshwater > soil > biofilm), with significantly higher richness and abundance in Spain across most matrices. Despite this, both countries shared a stable core resistome, indicating widespread dissemination of key resistance genes. Anthropogenic pressure strongly increased ARG and MGE abundance, particularly in Spanish soils, biofilms, and wastewater. In contrast, Swiss samples exhibited stronger ARG-MGE correlations, suggesting a higher relative potential for horizontal gene transfer despite lower gene loads. Thirty-nine clinically relevant ARGs and priority pathogens (*Acinetobacter baumannii, Pseudomonas aeruginosa, Klebsiella pneumoniae*) were detected, with distinct abundance and association patterns between countries.

Conclusions: Environmental AMR risk reflects not only resistance abundance but also gene mobility and ecological connectivity. Integrating resistome, mobilome, and pathogen data is essential for One Health surveillance and for anticipating AMR dissemination across environmental compartments.

O-09 Divergent antimicrobial resistance trajectories across US food production and human clinical settings revealed by time-series and cross-correlation analysis.

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Background: Multidrug-resistant (MDR) *Enterobacteriaceae* and resistance to WHO-classified critically important antimicrobials (CIA) threaten treatment efficacy and food safety. In 2017, FDA Guidance #213 prohibited medically important antimicrobials for growth promotion in US food-producing animals, providing a natural experiment to evaluate policy effectiveness across the One Health continuum. However, comprehensive temporal analyses linking resistance patterns across this regulatory transition remain limited.

Objectives: We compared temporal antimicrobial resistance patterns in zoonotic and non-zoonotic *Enterobacteriaceae* across bacterial genera, host species, and *Salmonella* serotypes, evaluating MDR trends (resistance to ≥3 antimicrobial classes) in food-producing animals and retail meat (2005-2023), and CIA resistance across food-producing animals, retail meat, and human clinical isolates (2005-2025).

Methods: Surveillance data from 814,000+ isolates in NARMS were analyzed using time-series, change point detection, and cross-correlation analyses with 3- and 6-month lags, stratified by genus, host, zoonotic status, and serotype.

Results: Non-zoonotic bacteria exhibited markedly higher MDR prevalence than zoonotic bacteria in food production (50.4% vs 12.0%) and retail meat (82.9% vs 14.6%), particularly *Enterococcus* and *Escherichia*. Significant declining MDR and CIA resistance emerged in retail meat and food-producing animals ($p<.05$), with multiple post-2016 change points coinciding with FDA Guidance #213 implementation. Conversely, CIA resistance in human clinical isolates increased significantly for both zoonotic (0.6%) and non-zoonotic (0.1%) bacteria. Cross-correlation analyses revealed strong farm-to-retail associations for *Enterococcus* MDR (0-1 month lag), validating direct food chain transmission. However, food-to-human CIA correlations were limited to zoonotic *Salmonella* (12-month lag). *Salmonella* Infantis in poultry showed strong farm-to-retail CIA signals ($r=0.646$, $p<.05$, 0-month lag).

Conclusions: Antimicrobial resistance in food-producing animals closely tracked retail meat trends, demonstrating FDA Guidance #213 effectiveness. However, human clinical resistance followed independent trajectories uncorrelated with food production improvements, indicating distinct sector-specific drivers. Results support comprehensive One Health surveillance and aggressive antimicrobial stewardship interventions targeting human healthcare alongside continued food production improvements.

O-010 Nationwide Prevalence, Virulence, and AMR of Shiga toxin-producing Escherichia coli in Slaughtered camels, sheep, and goats in Saudi Arabia.

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Background: Shiga toxin-producing *Escherichia coli* (STEC) poses significant foodborne disease risks globally. In Saudi Arabia, camels, sheep, and goats represent nearly 90% of slaughtered animals; however, data on the occurrence of STEC in these animals remain limited.

Objectives: This nationwide study assessed STEC prevalence, serogroups, virulence, and antimicrobial resistance (AMR) across slaughtered camels, sheep, and goats in Saudi Arabia.

Methods: Paired fecal (pre-slaughter) and carcass (post-slaughter) samples were collected from camels (n=550), sheep (n=552), and goats (n=552) at slaughterhouses in six provinces, along with equipment swabs (n=41; total N=1,695). Presumptive STEC colonies were isolated on CHROMagar STEC and confirmed by qPCR targeting *stx* genes. Serogroup distribution, virulence genes (*stx1*, *stx2*, *eaeA*), and antimicrobial susceptibility were determined.

Results: Overall, 901 samples (53.2%) yielded presumptive STEC colonies, of which 382 (42.4% of presumptive; 22.5% of total) were confirmed by qPCR, including 226 fecal, 153 carcass, and 3 equipment isolates. Among fecal samples, STEC prevalence was significantly higher in sheep (34.1%) than in camels (22.9%) and goats (25%) (p=0.08). Carcass contamination was highest in camels (22.5%), followed by sheep (19.6%) and goats (13.4%) (p=0.09). Notably, 56.9% of STEC-positive carcasses originated from animals with negative fecal samples, indicating substantial cross-contamination during processing. The serogroup O103 was predominant in both fecal (3.15%) and carcass (3.9%) samples, significantly exceeding O157 (0.97% each). Virulence profiling showed *stx1* prevalence (21.8–30.4%) exceeding *stx2* (0.36–1.1%) across species (p=0.006). The *eaeA* gene was detected in 16–24.6% of fecal and 8–12% of carcass isolates (p=0.001). Antimicrobial testing (n=127) revealed high resistance to tetracycline and ampicillin, with 94.5% of isolates exhibiting multidrug resistance.

Conclusions: Animals intended for slaughter in Saudi Arabia harbor diverse STEC serogroups with concerning AMR profiles. Extensive processing-related cross-contamination highlights critical food safety gaps requiring improved slaughterhouse hygiene, expanded molecular surveillance, and strengthened antimicrobial stewardship.

O-011 Metagenomic deep learning to support dissemination risk assessment of antimicrobial resistance genes.

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Background: Genomic surveillance has become a powerful tool for identifying antimicrobial resistance (AMR) determinants that predict antimicrobial susceptibility. However, most studies emphasize mobile genetic elements, while comprehensive integration of full genomic context from metagenomic data to assess antimicrobial resistance gene (ARG) dissemination risk remains limited.

Objectives: To investigate genomic drivers of resistance spread across the One Health continuum, we leveraged metagenomic data to develop a deep learning model that could score ARG dissemination risk per sample.

Methods: We annotated 778 metagenome samples of both ARGs and other coding regions, identifying 461 ARGs with a total of 33,382 occurrences. A pseudo-pan-genome graph was constructed to connect all samples carrying a specific ARG, with each node representing a coding region. We learned node-level aggregation functions across all the graphs, through unsupervised training using three Graph Neural Network architectures: GraphSAGE, Graph Attention Networks (GAT), and Graph Isomorphism Networks (GIN). Based on learned aggregator functions, we extracted an embedding for each ARG node. Furthermore, we quantified the dissemination risk for each ARG across four aspects: the number of samples containing the ARG, its frequency across samples, the number of species associated with contigs containing the ARG, and the number of countries from which samples containing the ARG were collected. Finally, these embeddings were used to train a multilayer perceptron to predict the four-dimensional ARG dissemination risk score.

Results: Our work develops an aggregative scoring scheme that provides a per-sample risk metric of AMR threat.

Conclusions: Given a new metagenomics or genomics sample, we are developing a pipeline that performs assembly, predicts the species, annotates ARGs, and subsequently generates a score reflecting the ARG dissemination risk. Ongoing analysis explores the predictive genomic context underlying AMR spread by examining the weights in the learned GAT model.

O-012 Early Spring Heat, Higher Summer Risk: Temperature-Curve Signals to Guide West Nile Virus Preparedness.

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Background: West Nile virus (WNV) is a mosquito-borne zoonosis in which temperature influences vector abundance, biting rates, and viral replication, shaping seasonal transmission intensity. Temperature-based indicators could support One Health early warning and preparedness.

Objectives: To assess whether interannual temperature variability is associated with annual human neuroinvasive WNV cases and annual acute equine WNV infections from 2015 to 2024.

Methods: Monthly temperatures (2015–2024) from four monitoring locations were analysed as within-year trajectories using Fourier seasonal smoothing of 12 monthly points. Outcomes were annual human neuroinvasive WNV case counts and acute equine infections defined by IgM antibody detection. From fitted curves, we derived degree-days above 10°C and 15°C and seasonal onset (first upward crossing). Associations were evaluated using Spearman correlations with permutation-based inference and count regression (negative binomial for humans; Poisson sensitivity analyses for equine outcomes). Month-window analyses identified periods predictive of burden.

Results: Human WNV cases showed a strong temperature signal. Degree-days were positively associated with annual human burden (degree-days >10°C: $\rho \approx 0.83$, permutation $p \approx 0.004$; degree-days >15°C: $\rho \approx 0.68$, $p \approx 0.036$), consistent with longer and/or more intense warm-season conditions. Month-window analyses identified spring warming as the principal predictor: April and especially May temperatures were positively associated with annual human case counts, with May showing the largest effect sizes (incidence rate ratios >2 per +1°C). Because WNV transmission peaks in summer, April–May temperature elevations plus higher degree-day accumulation provide an early-warning signal for the forthcoming season. Acute equine infections did not show robust associations with temperature-curve metrics, potentially reflecting differences in vector exposure/contact structure and other unmeasured factors.

Conclusions: From 2015 to 2024, annual human WNV burden was best explained by temperature regime characteristics—particularly April–May warming and accumulated warm-season thermal exposure—supporting spring temperature anomalies as a practical early-warning indicator to guide intensified anti-epidemic measures in high-risk seasons.

O-013 Modeling the evolutionary trajectories of antimicrobial resistance genes and donor-recipient interactive networks underlying their transmission.

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Background: The escalating emergence and global transmission of antimicrobial resistance pose critical challenges to One Health initiatives spanning human, animal, and environmental health. Enhanced understanding of the evolutionary trajectories of key antimicrobial resistance genes (ARGs) and specific donor–recipient microbial networks driving their dissemination across natural populations of human and animal pathogens is therefore essential.

Objectives: This study aimed to model the dominant evolutionary forces shaping the ARGs *tetM*, *tetW*, and *msrA*, and reconstruct donor–recipient bacterial networks driving their dissemination across diverse genera, including clinically and veterinary relevant pathogens.

Methods: Large GenBank datasets (*tetM*: 2,838 protein coding sequences [CDSs]; *tetW*: 161 CDS; *msrA*: 601 CDS) were analyzed using nucleotide diversity and neutrality statistics (π, Tajima's D, Fu's Fs, d_N/d_S), codon-based selection tests (PAML, HyPhy/FUBAR/MEME/aBSREL), recombination detection (RDP4 suite, GARD, SplitsTree, PHI), linkage disequilibrium metrics, conserved-region mapping, and GC-adjusted null models for synonymous codon optimization at fourfold-degenerate sites.

Results: Strong pervasive purifying selection dominated evolution of all three genes ($d_N/d_S \approx 0.15–0.58$; negative Tajima's D/Fu's Fs), preserving critical functional motifs (GTPase elements in TetM/TetW; nucleotide-binding domains in MsrA). Genetic recombination modeling revealed extensive, recombination-driven interspecies and intergeneric donor–recipient networks that facilitate the multidirectional transmission of *tetM*, *tetW,* and *msrA* across a wide range of species and genera. Evidence of post-transfer synonymous codon optimization was statistically significant ($p \leq 0.04$) for *tetM* in *Enterococcus faecium*, *Enterococcus faecalis*, *Streptococcus oralis*, *Streptococcus agalactiae*, and *Acinetobacter baumannii*, and for *tetW* in *Streptococcus suis*.

Conclusions: Purifying selection maintains core resistance functionality of *tetM*, *tetW,* and *msrA*, while recombination networks—often centered on pathogenic species—drive their wide dissemination. Synonymous codon usage optimization constitutes an additional under-recognized mechanism facilitating successful integration and long-term persistence of *tetM* and *tetW* in certain bacterial pathogens.

O-014 Strong1H: filling the gaps in surveillance of zoonotic influenza viruses and West Nile Virus in the Netherlands.

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Background: Zoonotic influenza viruses and West Nile Virus (WNV) are considered priority pathogens for One Health surveillance in the Netherlands as well as in Europe.

Objectives: In the Strong1H project (2023-2026), we aim to strengthen One Health surveillance of zoonotic influenza viruses and WNV in the Netherlands by targeted/risk-based sampling of populations complementary to existing surveillance components.

Methods: Samples from wild boar were tested for antibodies against Influenza A virus (IAV) using NP-ELISA and further serotyped using Luminex technology. Samples from domestic outdoor pigs, wild mammals, and the environment were collected and tested for IAV using PCR. PCR-testing for WNV was done on samples from wild birds and wild mammals. PCR-positive samples were sequenced. IAV sequences were shared in a national One Health data sharing platform, enabling joint analysis with IAV sequences from the surveillance in domestic indoor pigs and comparison with human, avian, and mammalian reference sets.

Results: Antibodies against IAV were detected in 18.5% of the 2585 samples from wild boar collected between 2017-2025 and antibodies against H5N8 and H5N1 were identified. Non-invasive saliva samples were collected on twenty-five outdoor pig farms. All samples tested negative. In 2025, two red foxes investigated in Strong1H tested H5N1-positive (DI.2 genotype). Surface water samples collected in the winters of 2024-25 and 2025-26 frequently tested positive on a pan-influenza PCR; however, H5-PCR positives were rare, detected only once. Two dead wild birds tested WNV-positive (lineage 2) and their sequences clustered with other WNV-positive cases (horse, mosquito) in the Netherlands in 2025.

Conclusions: By combining expertise and data from the veterinary, environmental, and human sectors, and by sampling underrepresented reservoirs such as wildlife and the environment, our project contributes to integrated One Health surveillance. Using this as a model, a roadmap for sustainable One Health surveillance in the Netherlands will be developed.

O-015 Comparative pathogenicity and host competence of Spanish West Nile virus strains in animal models.

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Background: West Nile virus (WNV) incidence and geographical range in Europe have steadily increased over the past three decades, with two genetic lineages (L1 and L2) circulating. In Spain, L1 was first identified in 2007 and has spread throughout southwestern Spain, with human and equine cases reported since 2010. In contrast, L2 was first detected in Catalonia (northeastern Spain) in 2017. The epidemiological situation has changed in recent years. Large outbreaks in southwestern Spain caused a high number of human and equine cases in 2020 and 2024, while the number of cases in northeastern Spain remained low. These contrasting epidemiological patterns may reflect biological and ecological differences. In particular, the risk of disease outbreaks may depend, among other factors, on intrinsic properties of circulating strains, such as their pathogenicity and the reservoir competence of avian hosts.

Objectives: To evaluate the pathogenicity in mammals and the host competence in avian reservoirs for Spanish WNV strains.

Methods: Mice and red-legged partridges were inoculated with different WNV isolates, obtained between 2012 and 2022, and monitored for clinical signs, mortality and analytical parameters such as viral load and presence of neutralizing antibodies.

Results: Southwestern isolates (L1) showed higher pathogenicity in mice compared with northeastern strains (L2). The higher virulence of L1 isolates was observed across all strains obtained between 2012 and 2021. Additionally, host competence in partridges was higher for southwestern strains compared with northeastern isolates.

Conclusions: These findings highlight the importance of a One Health approach for assessing pathogenicity and outbreak risk of WNV strains. Lineage 2 strains circulating in Catalonia may represent a lower risk for humans and horses compared with L1 isolates from southwestern Spain. Variations in disease incidence in different years are likely driven by factors unrelated to the intrinsic properties of the virus, such as fluctuations in mosquito populations.

O-016 Hepatitis E in Serbia – The Human–Animal Interface Within a One Health Framework.

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Background: Hepatitis E virus (HEV) genotype 3 is a zoonotic pathogen widely distributed in Europe, with domestic pigs and wild boars recognized as major reservoirs. Human infections are often asymptomatic but may cause severe disease in immunocompromised individuals. In Serbia, increasing evidence from human, livestock, slaughterhouse, and wildlife studies indicates endemic HEV circulation at the human–animal–environment interface.

Objectives: To summarize and integrate available human and animal data on HEV in Serbia within a One Health framework, highlighting epidemiological links across sectors.

Methods: Human data included detection of anti-HEV IgG antibodies in blood donors using ELISA. Animal investigations comprised serological testing by ELISA in backyard and intensive pig farms, as well as in wild boars. Molecular analyses included detection of HEV RNA in liver samples from slaughtered pigs and in slaughterhouse environmental swabs using real-time RT-PCR.

Results: Anti-HEV IgG antibodies were detected in approximately 15% of blood donors, indicating substantial exposure in the general population. In pigs, seroprevalence reached 34.6% in backyard systems and 40.66% in intensive farrow-to-finish farms, with farm-level values ranging from 31% to 54%. Molecular investigations at slaughterhouses detected HEV RNA in 29% of pig liver samples, with the highest prevalence (44%) in pigs younger than three months, and viral RNA present on 22% of environmental swabs. In wildlife, approximately 52.25% of tested wild boars were seropositive, confirming enzootic circulation.

Conclusions: Both serological and molecular evidence in humans, domestic pigs, slaughterhouse environments, and wild boars confirm endemic HEV circulation in Serbia. These findings indicate ongoing viral transmission at the human–animal interface and underscore the need for coordinated One Health surveillance linking public health, veterinary, food safety, and wildlife sectors to reduce zoonotic risk.

O-017 Exploring airborne resistomes in two Japanese cities through PacBio long-read metagenomic sequencing.

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Background: Although current research acknowledges the transmission of antimicrobial resistance (AMR) across different sectors within the One Health framework, the role of air as a potential transmission pathway remains poorly characterized. Here, we conducted a longitudinal airborne AMR surveillance study using a PacBio long-read metagenomic approach.

Objectives: This study aimed to explore and quantify the abundance and diversity of airborne AMR determinants in both cities, identify mobile genetic elements (MGEs) that carry AMR genes (ARGs), and reconstruct metagenomic-assembled genomes (MAGs) to identify airborne ARG-carrying taxa.

Methods: Air samples (>200) were collected from the rooftops of the Kumamoto University and the Toyama University Hospital across all four seasons (2017-2018) using high-volume air samplers (500 L/min) with quartz fiber filters. DNA was extracted via an in-house phenol-chloroform extraction protocol. Metagenomic long-read sequencing was performed on the PacBio Sequel II platform. Sequencing reads were pre-processed, ARGs were quantified, and their counts normalized to account for sequencing depth and bacterial abundance (CPM). An assembly-based approach was used to identify ARG-carrying MGEs and to reconstruct MAGs.

Results: Both locations exhibited distinct airborne resistome profiles. In Kumamoto, the most abundant AMR classes conferred resistance to tetracyclines, MLSP (Macrolide-Lincosamide-Streptogramin B), and aminoglycosides, whereas in Toyama, resistance to tetracyclines, beta-lactams, and multidrug efflux systems predominated. ARG counts peaked in winter in both cities, with similar seasonal patterns observed for ARG richness and beta diversity. ARG-carrying MGEs were mostly plasmids, with few integrons or viruses. Reconstruction of 5,440 MAGs, including 75 medium- to high-quality genomes carrying at least one ARG, allowed identification of taxonomic contributors to airborne AMR reservoirs.

Conclusions: Our findings highlight the potential of PacBio long-read sequencing for airborne AMR surveillance, provide novel insights into the seasonality and location-specificity of airborne resistomes, and support the inclusion of air sampling in One Health AMR monitoring frameworks.

O-018

Evaluation of routine One Health WGS-based surveillance of *Salmonella* Enteritidis and Typhimurium in the Netherlands.

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Background: Non-typhoidal *Salmonella enterica* is the second most prevalent cause of bacterial gastro-enteritis in the Netherlands. The main causative serovars are Enteritidis (SE), Typhimurium (ST) and monophasic Typhimurium (mST).

Objectives: We aimed to assess the completeness of current One Health *Salmonella* WGS-based surveillance for public health by measuring overlap and genomic diversity between human and food production chain (FPC) isolates.

Methods: We analysed 3973 clinical *Salmonella enterica* isolates (SE:2531, ST:732, mST:710), and 1035 FPC isolates (SE:479, ST:306, mST:250) using cgMLST (3,002 genes) and average-linkage hierarchical clustering (5 allele cutoff) collected for national *Salmonella* surveillance since 2019. We quantified clustering and genomic overlap of clusters between clinical and FPC sources. We used rarefaction and Dirichlet re-sampling to assess potential under-representation of sources in our surveillance efforts.

Results: SE analysis revealed 339 clusters (80% of isolates), of which 58 (17%) comprised both clinical and FPC isolates. ST showed 139 clusters (64% of isolates), of which 35 (25%) contained both clinical and FPC isolates. mST showed 146 clusters (65% of isolates), of which 44 (30%) had both clinical and FPC isolates. Mixed clusters of SE primarily contained poultry isolates (60% of mixed clusters), ST primarily cattle (51%) and mST swine (23%). Mixed clusters showed the highest proportion of temporal persistent (> 1 year) clusters (SE:86%, ST:74%, mST:57%). Rarefaction and resampling analyses indicated that an increase in (m)ST isolates in the swine reservoir yields moderate cluster increases.

Conclusions: Our analysis demonstrates that many FPC isolates could be linked to clinical clusters, while a substantial fraction of clinical clusters remain unconnected to FPC isolates, highlighting gaps in sampling strategies or limited availability of FPC isolates. Increased sampling, especially from swine reservoirs, is likely to yield the greatest improvement. These findings underscore the value of evaluating routine One Health surveillance to improve public health outcomes.

O-019 *Salmonella* transmission dynamics in a pig slaughterhouse.

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Background: Consumption of contaminated pork is a major *Salmonella* transmission route to humans, with the slaughter process playing a critical role in both dissemination and control. Identifying transmission routes within slaughterhouses is essential for targeted interventions to reduce public health risks.

Objectives: This study aimed to shed more light on *Salmonella* transmission in a pig slaughterhouse by sampling individual pigs and genetically characterizing isolates using whole genome sequencing (WGS).

Methods: Sampling was conducted in a Dutch slaughterhouse on seven days in 2025. The same individual carcasses were sampled at three stages: pre-scalding, post-flaming, and post-slaughter. Pigs originated from fourteen farms across the Netherlands. Carcass swabs (shoulder, cutting surfaces) and cecal contents were cultured for *Salmonella*. WGS data of isolates were analyzed by multilocus sequence typing (MLST) and SeqSero2 to determine sequence types (ST) and serovars. Phylogenetic analysis was performed using core genome MLST (cgMLST; cluster threshold ≤7 allelic differences).

Results: *Salmonella* prevalence was highest on carcasses pre-scalding (72.7%; 80/110), but drastically reduced post-flaming (1.0%; 1/98) and post-slaughter (shoulder: 1.0%; 1/103, cutting surfaces: 2.0%; 2/102). Cecal samples showed a prevalence of 19.8% (20/101). In total, seven serovars were identified, predominantly *S.* Derby (57.4% of isolates), *S.* Senftenberg (18.5%), monophasic *S.* Typhimurium (10.2%), and *S.* Brandenburg (10.2%).

S. Derby and *S.* Brandenburg were mainly found on carcasses pre-scalding, with genomic clusters spanning multiple batches and days, indicating environmental cross-contamination during transport, lairage and/or pre-scalding processes. *S.* Senftenberg and monophasic *S.* Typhimurium were mostly detected in cecal samples, although cecal isolates clustered with carcass isolates from pigs from different farms and days, suggesting that pigs infected during primary production entering the slaughterhouse contribute to cross-contamination.

Conclusions: Hygiene measures during slaughter effectively reduce *Salmonella* carcass contamination. However, persistent clusters pre-scalding indicate ongoing environmental cross-contamination in early processing stages and the importance of farm biosecurity to prevent *Salmonella* introduction.

O-020 Changes in soil microbiota after the application of five organic wastes.

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Background: In Ireland, approximately 84 million tonnes of farm animal waste and 70,000 tonnes of dry human sewage sludge are generated annually, all of which is reused as a soil fertiliser after appropriate treatment. Organic wastes support soil fertility and contribute to circular and sustainable agriculture systems. However, they may also introduce human and animal pathogens.

Objectives: The aim of this study was to investigate the temporal effect of applying bovine, ovine and porcine slurry, broiler waste and wastewater treatment sludge (WWTS) on the soil microbiota when applied to a sandy clay loam temperate permanent grassland soil.

Methods: In this field study, 18 plots (1m^2) were prepared, and each waste was randomly applied in triplicate at a nitrogen-based rate, mimicking splash plate spreading. Soil cores (10 cm depth) were extracted at times (t) = 0, 1, 3, 6 and 10 weeks. Microbial composition using full-length 16S rRNA sequencing and daily temperatures and rainfall were monitored.

Results: *Planctomycetota*, *Pseudomonadota* and *Bacillota* dominated in soil communities, *Bacteroidota* in bovine and pig slurry, *Campylobacterota* in ovine slurry, *Actinomycetota* in poultry waste, and *Chloroflexota* and *Bacteroidota* in WWTS. At both phylum and genus levels, soil microbial populations were either not disturbed (ovine and porcine slurry) or returned to baseline levels within one week (bovine slurry), or after sampling at t = 6 weeks (WWTS) or 10 weeks (poultry waste).

Conclusions: To the authors knowledge, this study is the first to characterise the bacterial microbiota when organic wastes are applied to soil using a full-length sequencing technology. The results demonstrated that the extent of disruption to the soil microbiota differed depending on the specific waste with poultry waste causing the most changes, requiring 10 weeks for remediation. Long-term shifts can reduce microbial diversity by favoring stress-tolerant taxa, which then weakens nutrient cycling and carbon–nitrogen enzyme activity.

O-021 Bio-resonance and frequency-dependent resilience in the mouse gut microbiome.

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Background: Gut microbiota support host health, particularly through colonisation resistance against pathogens. Yet, their interactions and temporal dynamics remain hard to resolve from compositional sequencing data, especially under external perturbations such as antibiotics. While the strength of perturbations is a known factor, the frequency with which they occur may determine whether a community recovers or shifts to an alternative configuration.

Objectives: Develop a mechanistic model of gut microbiome dynamics.

- Investigate under which conditions gut communities exhibit natural frequencies (the characteristic oscillation rates the system expresses after a small disturbance).
- Explore the effect of perturbation frequency on community dynamics.
- Test for bio-resonance, where perturbations near natural frequencies cause amplified changes in species abundance.

Methods: Synthetic and genus-level mouse microbiome dynamics were modelled using a generalised Lotka-Volterra system. Growth rates, interactions and perturbation susceptibilities were estimated via Bayesian linear regression on biomass-scaled 16S rRNA profiles. Natural frequencies were obtained analytically. Frequency-dependent responses were assessed by applying sinusoidal perturbations of fixed amplitude and quantifying amplification of community responses.

Results: Forcing near a natural frequency produced amplified deviations, consistent with bio-resonance. In an antibiotic-perturbed gut dataset resolving the 10 dominant genera including *Clostridioides difficile*, periodic perturbations with equal cumulative dosage yielded contrasting outcomes: some schedules sustained pathogen persistence, whereas others drove the community across a threshold into a state associated with clearance of the pathogen.

Conclusions: Population resilience is frequency-dependent: the same perturbation intensity can be benign or destabilising depending on how often it is administered. Linking community-specific natural frequencies to susceptibility provides a basis for optimising patient-specific treatment schedules that maximise clearance while minimising collateral dysbiosis and the opportunity for resistance to emerge. This principle may also extend to other complex population systems, providing a framework for optimising interventions across diverse ecological and health contexts.

O-022 **Fish as bioindicators for monitoring aquatic ecosystem health status in a One Health perspective.** Martina Ossola[1], Michele Macrelli[1], Giovanni Sala[1], Damiano Accurso[1], Marco Farioli[2], Cristian Salogni[1]

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Background: Fish are effective bioindicators of aquatic ecosystem health status, reflecting anthropogenic pressure, pathogen exposure, and consumer risk.

Objectives: To assess potential risks for human and aquatic-dependent wildlife in the heavily anthropized Lake Varese (Northern Italy), five commercially and ecologically relevant species were investigated: pike (*Esox lucius italicus*), pike-perch (*Sander lucioperca*), European perch (*Perca fluviatilis*), tench (*Tinca tinca*), and wels catfish (*Silurus glanis*).

Methods: A total of 59 specimens sampled during 2024 underwent morphological and anatomopathological examinations, bacteriological cultures, parasitological investigations involving transillumination and molecular identification (ITS region), and virological screening for major fish pathogens using EPC and BF2 cell lines. Per- and polyfluoroalkyl substances (PFASs) and heavy metals (Cd, Hg, Pb) were quantified in skeletal muscle using LC-MS/MS and ICP-MS QQQ, respectively.

Results: Among the detected biological agents, zoonotic pathogens were identified. Bacterial growth was detected in 49.2% of specimens; 93.1% of isolates were *Aeromonas* spp. (*A. sobria*, *A. caviae*, *A. hydrophila*) and 6.9% *Pseudomonas* spp.. *Mycobacterium hiberniae*, a non-tuberculous mycobacterium, was isolated from wels catfish. *Eustrongylides excisus* was detected in 16.9% of fish, involving all species except tench, representing the first report in Lake Varese. No viral pathogens were detected. Heavy metals were within EU regulatory limits. EU-regulated PFASs were generally below legal limits, except for PFOS in three larger pike specimens, which showed slightly elevated but non-alarming concentrations. Non-EU-regulated PFASs were detected at generally low levels, although higher cumulative concentrations were observed in pike-perch, showing values up to one order of magnitude higher than those of other species.

Conclusions: Species-specific bioaccumulation trends, evidence of PFAS circulation in the environment, and the detection of zoonotic bacterial and parasitic agents support the need for continuous, site-specific surveillance in freshwater ecosystems. Fish confirm their role as effective bioindicators for integrated environmental and human health risk assessment in heavily anthropized environments.

O-023 Integrating Aquamation and Composting for Sustainable One Health Management of Animal Waste in Arid Contexts.

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Background: In Sahrawi refugee camps, located in the Algerian Sahara, the management of slaughterhouse waste and livestock by-products represents a major public health and environmental challenge. Uncontrolled disposal in drylands promotes pathogen persistence, soil contamination, and loss of valuable organic resources. Within the One Health framework, human, animal, and environmental health are strictly interconnected, and ecosystem degradation directly affects community wellbeing and food security. Addressing organic waste management is essential to mitigate zoonotic risks and enhance local resilience in resource-limited humanitarian settings.

Objectives: The project aims to implement an integrated aquamation and aerobic composting system for the safe and sustainable treatment of animal by-products, reducing sanitary and environmental risks while generating agronomic resources to support local food production. A complementary objective is to strengthen local technical capacity through theoretical-practical training, fostering operational autonomy and long-term sustainability.

Methods: Animal by-products from poultry slaughtering are treated through alkaline aquamation using potassium hydroxide, effectively inactivating pathogens and producing a nutrient-rich aqueous solution. The resulting liquid is incorporated into an aerobic composting process together with poultry manure, plant residues, and lignocellulosic biomass. Process control includes monitoring physical and chemical parameters, compliance with hygiene standards, and capacity-building activities for local operators.

Results: The integrated system effectively reduced health and environmental risks associated with uncontrolled disposal of animal waste, converting hazardous materials into a stabilized and safe product. The resulting compost improves fertility of arid soils, enhances water retention, and supports agroecological production. Training activities showed high engagement among participants and rapid acquisition of practical operational skills.

Conclusions: The integration of aquamation and composting represents an effective One Health solution in humanitarian and arid contexts, simultaneously addressing public health, environmental protection, and food security. Transforming sanitary waste into an agricultural resource promotes circular resource use, strengthens the resilience of refugee communities, and contributes to the development of more sustainable food systems.

O-024 Monitoring antimicrobial resistance in aquatic environments using wild coypu (*Myocastor coypus*) as sentinels: An *Enterococcus*-based approach.

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Background: Surface waters facilitate the spread of antimicrobial resistance (AMR) from anthropogenic and zootechnical settings to environments with lower antimicrobial selective pressure, including wildlife. Monitoring waterborne AMR is crucial for a One Health approach, complementing human and animal AMR surveillance.

Objectives: This study aims to: (i) monitor aquatic AMR pollution using the wild coypu (*Myocastor coypus*) as sentinel species and enterococci as bacterial indicators; (ii) assess the potential role of wild coypu as reservoir and/or vector of AMR to the environment, other animals and humans. The project was funded by the Italian Ministry of Health (IZSLER-13/23-RC).

Methods: Between December 2024 and April 2025, 90 wild coypu carcasses/faeces were collected along the Reno River, Italy. *Enterococcus* spp. were isolated using standard microbiological analysis and identified by MALDI-TOF. AMR profiles were assessed by the broth microdilution method and results interpreted using the EUCAST epidemiological cut-off.

Results: A total of 95 *Enterococcus* strains were isolated. Seven different species were detected, mostly *Enterococcus hirae* (56/95) and *Enterococcus faecium* (18/95). Overall, 81/95 isolates were resistant to at least one antimicrobial. The highest resistance rate was observed for quinupristin/dalfopristin (77/95). Concerning resistance levels were observed for critical antimicrobials for humans, including daptomycin (24/95), linezolid and erythromycin (11/95 each). Resistance to other antibiotics was detected in less than 10% of isolates. Notably, 9/95 strains were multidrug-resistant, showing resistance from three to five different antimicrobial classes. These isolates belonged to four species (*Enterococcus casseliflavus*, n=4; *Enterococcus faecium*, n=2; *Enterococcus hirae*, n=2; *Enterococcus faecalis*, n=1).

Conclusions: These preliminary findings suggest that wild coypu may (i) act as effective sentinels of AMR in aquatic environments, (ii) promote AMR persistence in the natural settings and heighten exposure for other wild animals, and (iii) enable the transmission of AMR *bacteria* to humans and domestic animals due to their increasing synanthropy.

O-025 Shotgun metagenomics of four Irish Integrated Constructed Wetlands reveals microbial dynamics in wastewater treatment.

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Background: Over the past 20 years, the Integrated Constructed Wetland (ICW) concept has been applied in Ireland for wastewater treatment, offering a nature-based solution for reducing pollutants and antimicrobial resistance (AMR) in effluents and receiving environments. However, wastewater microbial communities remain inadequately characterised and their dynamics across treatment largely unexplored.

Objectives: We present the first culture-independent investigation of four Irish ICWs, aiming to advance our understanding of microbial dynamics in wastewater treatment. By reconstructing influent and effluent microbial taxonomic and functional profiles, we provide insights into ICWs efficacy in mitigating microbial pollutants, antimicrobial resistance genes (ARGs), and we uncover previously uncharacterised microbial diversity.

Methods: Influent and effluent samples were collected in biological triplicates from four ICWs of agricultural, animal, industrial, and municipal wastewater influents. Samples were filtered to select for bacterial biomass, followed by eDNA extraction and shotgun metagenomic sequencing. Nine positive and three negative controls were included for filtering and sequencing. Bioinformatic analyses including quality-control, assembly, taxonomic/functional assignment, and binning were performed with SqueezeMeta. GTDB-Tk was used to confirm taxonomic placement of high-quality metagenome-assembled-genomes (HQ-MAGs). Decontamination, and statistical analyses were conducted in R using decontam and vegan packages. Assembled contigs were screened for ARGs, virulence-, and plasmid-associated sequences.

Results: Treatment drove statistically significant shifts in taxonomic and functional profiles. Effluent populations exhibited generally higher richness than corresponding influents yet were more similar to one another across locations. Results revealed multi-log-scale increases in the relative abundance of environmental genera (*Legionella*, *Methylotenera*, *Thiothrix*) alongside reductions in common faecal indicators (*Bacteroides*, *Lactococcus*, *Prevotella*), and >80% removal of ARGs. Taxonomic placement of recovered HQ-MAGs uncovered 19 previously uncharacterised taxa, including three potentially novel genera.

Conclusions: Collectively, our findings show that ICWs can drive shifts in wastewater microbial communities and markedly reduce ARGs. Additionally, our metagenomic approach uncovers a reservoir of previously uncharacterised microbial diversity that warrants further investigation.

O-026 Metagenomic Evidence for Localised Clinically Relevant ARG Hotspots Along a Coastal Wastewater-to-Beach Gradient.

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Background: Antimicrobial resistance (AMR) is an escalating One Health threat driven by antimicrobial use and environmental dissemination of resistance determinants. Coastal zones are key sentinels because they integrate human and agricultural wastewater inputs with exposure via recreation and seafood consumption.

Objectives: The aim was to profile the resistome —including clinically relevant ARGs (antibiotic resistance genes) and host–ARG associations—along a wastewater-to-beach gradient on Ireland's west coast.

Methods: We generated 60 shotgun metagenomes (triplicates) from 1-L surface-water samples collected at four sites on six dates in spring and winter 2021: seawater at a raw effluent discharge point (B), seawater from two beaches flanking the discharge (A, C), and an adjacent freshwater stream (F). Quality-filtered reads were taxonomically classified (Kraken2/Bracken) and annotated for ARGs (AMR++) using stringent thresholds. Reads were also screened against a curated panel of clinically relevant ARGs (CARPDM) to distinguish priority signals from background resistomes.

Results: Host–ARG relationships followed a clear spatial gradient (B > F > A/C). A shared core was dominated by *Alpha-*, *Gamma-* and *Epsilonproteobacteria* linked to MLS (**Macrolides-Lincosamides-Streptogramins**) resistance. Beaches (A, C) also showed *Actinomycetes* and *Alpha-/Betaproteobacteria* associated with aminoglycosides, elfamycins, tetracyclines, fluoroquinolones and rifampin. Location B was dominated by *Gammaproteobacteria* linked to β-lactam, multi-metal and drug/biocide resistance, whereas location F was characterised by drug/biocide resistance across *Proteobacteria* and prominent *Betaproteobacteria*–fluoroquinolone/rifampin associations. Clinically relevant ARGs were detected only at locations B and F, dominated by tetracycline and MLS resistance determinants (tet(O), tet(T), tet(X3–X4), mphE/msrE, erm), with additional OXA-type β-lactamase, sul1/sul2, dfr and qac signals mapping mainly to *Enterobacterales* and other pathogenic genera, including ESKAPE members.

Conclusions: AMR was pervasive across the system, but clinically relevant ARGs were restricted to effluent and freshwater sites and were not detected at beaches, supporting targeted mitigation and routine surveillance at discharge points and upstream sources.

O-027 A One Health Approach into *Aliarcobacter* AMR Dynamics: A Comparative Analysis of MAGs and Isolates Across the Urban Wastewater System.

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Background: The genus *Aliarcobacter* has gained recognition as a group of emerging foodborne and waterborne pathogens. Urban wastewater treatment plants (WWTPs) and sewage networks act as critical reservoirs for these bacteria and their associated antimicrobial resistance genes (ARGs). Understanding their distribution and genomic characteristics is essential under the One Health framework to assess potential public health risks.

Objectives: This study aims to characterize the diversity and resistance profiles of *Aliarcobacter* populations within a complex urban sewage system and its receiving WWTP by integrating insights from Metagenome-Assembled Genomes (MAGs) and the genomic profiles of environmental isolates.

Methods: Wastewater samples were collected from different points of a sewage network (including hospital-impacted points) and a municipal WWTP over a two-year period, comprising six sampling campaigns. Short-read shotgun metagenomics was employed for the reconstruction and refinement of *Aliarcobacter* MAGs. In parallel, *Aliarcobacter* strains were isolated from the same locations and characterized via Whole Genome Sequencing (WGS).

Results: Medium and high-quality *Aliarcobacter* MAGs were successfully recovered through metagenomic binning. Functional annotation revealed a niche-specific distribution of ARGs, with specific resistance markers predominantly detected in hospital-impacted and WWTP effluent samples compared to other points in the network. The analysis of the isolates' genomes was compared to the metagenomic findings.

Conclusions: Our findings underscore the role of wastewater infrastructure as a hotspot for emerging pathogens and provide high-resolution data on the environmental circulation of resistance determinants. This study emphasizes the importance of integrating metagenomic surveillance to monitor antimicrobial resistance (AMR) dissemination in urban ecosystems.

O-028 Association between veterinary antimicrobial sales data and antimicrobial resistance in commensal and 3GCR *Escherichia coli* in Spanish livestock.

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Background: Antimicrobial resistance (AMR) in food-producing animals is a major One Health concern. Antimicrobial use can select for resistant bacteria in livestock, which may disseminate through the food chain and affect animal and human health. Surveillance of commensal *Escherichia coli* provides a sensitive indicator for tracking population-level resistance dynamics.

Objectives: To quantify resistance frequencies, identify multidrug-resistance (MDR) phenotypes, and test whether reductions in veterinary antimicrobial sales in Spain are associated with changes in the resistance profiles of *E. coli* across livestock species.

Methods: We analyzed caecal samples collected at slaughter from broilers, turkeys, pigs, and cattle in Spain (2014-2023). The dataset comprised 7,532 isolates from the EU-regulated monitoring programme, including indicator (commensal) *E. coli* and selectively enriched third-generation cephalosporin-resistant (3GCR) *E. coli*. Minimum inhibitory concentrations for 14 antimicrobials were classified as wild type (WT) or non-wild type (NWT) using EUCAST ECOFFs. Binary WT/NWT profiles were clustered using multivariate Bernoulli mixture models. Associations between cluster membership and national veterinary antimicrobial sales were tested with multinomial logistic regression.

Results: Across species, NWT proportions were consistently high for ampicillin, tetracycline, sulfonamides, trimethoprim, chloramphenicol and fluoroquinolones, while NWT to last-resort agents remained rare in both datasets. Indicator isolates clustered into five resistotypes spanning a gradient from low resistance to MDR, with and without fluoroquinolone resistance. 3GCR isolates formed four analogous clusters. Over time, high-resistance clusters decreased and low-resistance clusters increased, most clearly in poultry. Spain reduced total veterinary antimicrobial sales by approximately 70% from 2014 to 2022, and higher sales were associated with higher odds of membership in MDR and fluoroquinolone-associated clusters, with the strongest associations in poultry.

Conclusions: Reductions in veterinary antimicrobial sales in Spain coincided with a population-level shift toward less resistant commensal *E. coli* and, to a lesser extent, 3GCR *E. coli* across livestock species. Similar clusters in both subsets suggest shared underlying ecological dynamics.

O-029 Title of the Abstract: Free-living amoebae as vectors of antimicrobial resistance in the agricultural environment: FLA microbiome and resistome in regenerated sludge.

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Background: Antimicrobial resistance (AMR) is one of the most serious threats we face in the 21st century. The dissemination of AMR in the environment plays a relevant role in the clinical area, since agriculture can act as a bypass that connects the environmental area with the population health. In recent years, the potential role of free-living amoebae (FLA) is being studied as reservoirs and vectors of AMR.

Objectives: This study aimed to analyse FLA microbiome and resistome, focusing specifically on carbapenem resistance and ARGs, within FLA populations from regenerated sludge.

Methods: A total of 40 sludge samples from two different treatment processes were analyzed using a multidisciplinary approach combining molecular and culture-based techniques. FLA populations and their associated microbiome were characterized by 18S and 16S rRNA amplicon sequencing, respectively. In parallel, the intracellular resistome of FLA was assessed using high-throughput quantitative PCR (HT-qPCR) by quantifying the presence of ARGs. Additionally, culture-based detection and phenotypic characterization of viable carbapenem-resistant bacteria (CRB) associated with the FLA populations were performed.

Results: FLA such as *Vermamoeba vermiformis* and *Naegleria* spp. were detected. The FLA-associated microbiome exhibited high bacterial diversity, with a predominance of the genera *Stenotrophomonas*, *Aeromonas*, and *Pseudomonas*, among others. Most of the viable CRB belonged to *Pseudomonas*, *Klebsiella*, *Stenotrophomonas*, *Acinetobacter,* and *Ochrobactrum*, among others. HT-qPCR analysis revealed a high prevalence of ARGs within the intracellular resistome of FLA, with *intI1_1, intI1_2* and *intI1_3* being the most abundant genes detected, indicating a strong potential for horizontal gene transfer.

Conclusions: This study provides evidence that FLA present in regenerated sludge act as reservoirs of antibiotic-resistant bacteria and ARGs. These findings underscore the potential risks associated with the agricultural reuse of treated sludge and emphasize the need to incorporate FLA monitoring into AMR surveillance strategies within a One Health framework.

ORAL PRESENTATIONS · SESSION 3: INNOVATIVE SOLUTIONS FOR ONE HEALTH CHALLENGES

O-030 Global Pathogen Analysis Platform.

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Abstract: There's an urgent need to strengthen integrated one-health pathogen surveillance by linking disparate surveillance systems, providing access to state-of-the-art online bioinformatic and epidemiological analysis services that function in LMICs, developing secure data storage, sharing and collaboration services, while securing users full ownership and control over their data.

The Global Pathogen Analysis Platform (GPAP) is the world's first globally accessible, AI-powered platform designed to turn pathogen data from across human, animal, plant, and environmental systems into standardized, actionable intelligence at scale. GPAP closes a critical gap between the growing volume of genomic and surveillance data and the limited capacity to rapidly analyze, compare, and interpret that data for decision-making, particularly in low- and middle-income countries.

Funded by the Novo Nordisk Foundation and established by the Technical University of Denmark in collaboration with the University of Copenhagen, the Statens Serum Institut, and a global consortium convened with the World Economic Forum's Health Security Initiative, GPAP combines advanced bioinformatics and analytical AI with a federated, user-controlled data model. It provides free access to state-of-the-art analytical tools, alongside optional secure services for data storage, sharing, and collaboration, while ensuring full ownership and control of data remain with users. GPAP strengthens preparedness by enabling earlier detection of emerging pathogens and variants, faster comparison of signals across countries and sectors, and the generation of timely, decision-ready insights. These capabilities rely on robust inference and analytical methods that support surveillance, estimation, and validation across One Health domains.

GPAP also delivers day-to-day value for industry by enabling earlier risk detection, faster incident investigation, and improved continuity planning. Sectors such as food and agriculture, biotechnology, diagnostics, manufacturing, and logistics can use GPAP insights to reduce disruptions, protect workforces, and safeguard supply chains against biological risks.

GPAP is based on existing and widely used bioinformatic online services, such as *ResFinder* and *VirulenceFinder,* developed and operated by the Center for Genomic Epidemiology at the Technical University of Denmark.

O-031 Pandemic Preparedness by Pathogen Detection (P3Dx): high-throughput central testing workflow using self-sampling and isothermal detection.

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Background: The capacity to rapidly deploy large-scale diagnostic testing is essential for effective pandemic control. During the COVID-19 pandemic, diagnostic tests became widely available only after several months, largely due to equipment and personnel shortages in conventional PCR workflows and limited opportunities to implement novel diagnostic technologies during an ongoing crisis.

Objectives: In the P3Dx program we designed a high-throughput diagnostic testing workflow on existing infrastructure that can be rapidly deployed and scaled-up within weeks of the emergence of a novel pathogen, ensuring operational readiness and broad accessibility of diagnostic testing during early pandemic phases without interfering with conventional PCR based diagnostics.

Methods: The P3Dx consortium connects researchers, policymakers, and industry partners across the human, veterinary, and plant health sectors to streamline the implementation of innovative diagnostic solutions for pandemic preparedness. Stakeholders and experts on automation, logistics, assay design, legislation and epidemiology are actively involved in the design process.

Results: Core design principles include maximum use of automatization, integration of self-sampling strategies to increase testing uptake, extraction-free, LAMP-CRISPR molecular detection (scope*Dx*®) to minimize and diversify use of labware, thereby reducing dependency on vulnerable supply chains and costs per test. As a use case, a scope*Dx*® assay was designed to detect a conserved region of the influenza A M-segment.

Conclusions: The P3Dx high-throughput diagnostic testing platform provides a rapid, scalable, and cost-efficient solution for pathogen detection in a pandemic setting. It is designed to enable broad population testing and high test uptake in the earliest phases of an outbreak. By applying a One Health approach, the platform is integrated into veterinary diagnostics, primarily focusing on pathogens that may have zoonotic potential. This should support flexible and efficient routine testing within veterinary surveillance diagnostics during interpandemic phases, while at the same time ensuring readiness for rapid deployment during a pandemic crisis.

O-032 Bacteriophage-Powered One Health Solutions for Safer Agri-Food Systems.

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Background: Bacteriophages are increasingly recognized as precise, sustainable biocontrol agents capable of targeting pathogenic and spoilage-associated bacteria across agri-food systems. Their strong host specificity with negligible impact on non-target microbiota position them as valuable complementary tools to hygiene measures, processing interventions and antimicrobial strategies providing residue-free and microbiota-preserving interventions applicable from primary production to food processing. Their application contributes directly to integrated One Health strategies, addressing food safety, rising antimicrobial resistance and climate-related pressures at the human–animal–environment system.

Objectives: This work aims to highlight the scientific advantages of phage biocontrol and its potential to strengthen food safety and One Health strategies through the development of targeted, scalable and field-adaptable applications that may act as an additional barrier within existing control programs.

Methods: Advancing phage-based solutions from laboratory proof-of-concept to operational scale requires systematic phage isolation and robust characterization, rational formulation and cocktail design, manufacturing scale-up, and validation under real or simulated agri-food conditions.

Results: AZTI has developed a collection of over 300 bacteriophages targeting *Listeria monocytogenes*, *Campylobacter spp*., and *Vibrio spp*. enabling the design of robust phage-based formulations adapted to diverse agri-food environments and applications. Within ongoing initiatives, such as the BIOTEGANIA project, we are developing end-to-end pipelines encompassing phage isolation and characterization, cocktail engineering, pilot-scale validation and criteria for personalised interventions to combat pathogenic bacteria relevant for food safety and animal and human health, demonstrating the translational potential of phage-based biocontrol. This presentation outlines key scientific principles and implementation pathways required to accelerate the transition of phage-based biocontrol from laboratory environments to scalable, field-ready One Health solutions.

Conclusions: Bacteriophages represent maturing, evidence-based biocontrol tools capable of enhancing the agri-food system resilience and supporting the deployment of scalable, One Health-aligned innovative solutions.

O-033 A rapid tool to assess the risk of emerging zoonotic signals at the human-animal interface.

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Background: This study describes a quantitative Rapid Risk Assessment Tool (RRAT) for zoonotic signals, such as those evaluated within the Dutch Signalling Forum for Zoonoses (SO-Z). This multidisciplinary committee systematically collects signals of potentially (re-)emerging zoonotic pathogens at the human-animal interface. Signals from surveillance activities and field observations are discussed to assess risks and determine whether escalation, further investigation, or advice to professionals and policymakers is warranted. While qualitative risk assessment criteria are available, a quantitative RRAT is needed to strengthen the risk assessment procedure.

Objectives: To develop a RRAT to support experts in deciding whether zoonotic signals warrant upscaling. It also highlights the relative importance of signals, enabling more transparent and consistent risk communication.

Methods: Based on a scientific literature review, quantitative risk factors were selected to score signals assessed by the SO-Z between July 2011 and December 2025. These factors included pathogen characteristics, geographic spread, animal involvement, human health impact, and signal dynamics. Using SMOTE (Synthetic Minority Over-sampling Technique) and XGBoost (Extreme Gradient Boosting) analysis, we identified non-trivial patterns underlying expert decisions to upscale signals. These patterns were subsequently translated into a classification tool.

Results: A total of 443 SO-Z signals were analysed, of which 48 were escalated. Distribution of herds, pathogen characteristics, geographic origin, companion animal involvement, and signal repetition were associated with increased likelihood of upscaling. To distinguish multiple levels of association for upscaling, a RRAT was developed with three threshold values: A) most sensitive threshold (100% sensitivity and 24% specificity); B) most discriminating threshold (69% sensitivity and 72% specificity); C) most specific threshold (31% sensitivity and 94% specificity).

Conclusions: The RRAT is quick and easy to use. However, it does not replace experts' judgments; rather, it supports them by providing data-driven insights for upscaling zoonosis control measures and enabling more transparent risk communication.

O-034 DatOHs: A modular data ecosystem for interoperable One Health surveillance and risk assessment.

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Background: Digital transformation is reshaping surveillance by enabling large, heterogeneous datasets to be integrated into operational decision-support tools. While the growing volume of information supports more informed decisions, it also creates major challenges for coherent integration across sources. In our research group, we routinely work with diverse One Health data streams and identified the need for a single, organised platform to access and analyse them consistently across diseases.

Objectives: To develop and demonstrate a shared digital infrastructure that automates data integration and analytics to power interoperable One Health dashboards for multiple diseases (e.g., highly pathogenic avian influenza and antimicrobial resistance).

Methods: We designed a cross-cutting architecture based on modular Python pipelines that automatically extract epidemiological, microbiological, environmental, and territorial data from APIs, official repositories, and laboratory information systems. Data are cleaned, harmonised, and standardised before storage in relational databases. Graph databases are used to represent trade networks, mobility patterns, and epidemiological connectivity. Interactive dashboards were implemented using Python Shiny to support exploration and dissemination of curated outputs.

Results: Using the shared architecture, interoperable dashboards were deployed to support risk assessment and situational awareness across diseases. Users can explore spatial and temporal patterns, identify potential high-risk areas, and download harmonised datasets for further analysis. The modular design enables reuse of ingestion, processing, and visualisation components, reducing duplication and simplifying updates as new data sources or diseases are incorporated. You can check the tool in the following website: https://datohs.github.io/

Conclusions: A unified data ecosystem can be reused across surveillance domains, accelerating the development of transparent and reproducible digital tools. By strengthening interoperability and collaboration across veterinary, environmental, and public health sectors, this framework supports more agile, evidence-based One Health surveillance.

O-035 Evaluation of trained immunity induction by dpB in human monocytes.

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Background: Trained immunity refers to the long-term functional reprogramming of innate immune cells, leading to enhanced responses upon secondary stimulation. DpB is a BCG porcine-derived immunomodulator that has shown protective and immunomodulatory effects in animal models of SARS-CoV-2, *Streptococcus suis* and *Salmonella* spp. However, its capacity to induce trained immunity in human innate immune cells has not been investigated yet. Given the growing interest in trained immunity-based strategies, evaluating the effects of dpB in human monocytes may support the development of innovative complementary prophylactic tools within One Health.

Objectives: To assess whether dpB can induce trained immunity in human monocytes.

Methods: Monocytes were isolated from buffy coats of healthy human donors by Percoll density gradient centrifugation and trained with different concentrations of dpB, BCG (5 µg/mL) as positive control and RPMI as a negative control. At day 7, cytokine production (IL-6 and TNF-α) following LPS (10 ng/mL) restimulation was measured. Cytotoxicity (LDH release) was also assessed at 24h post training. Based on these results, dpB at 10 µg/mL was selected for further experiments, including phagocytosis assays (n=4), lactate production (n=8) and fumarate measurements (n=2).

Results: Dose response analyses showed that dpB at 10 µg/mL induced cytokine responses within the range observed for BCG at 5 µg/mL. No cytotoxic effects were detected at any dpB concentration. Metabolic assays did not reveal statistically significant differences in lactate or fumarate levels; however, a trend like the one from BCG was observed following dpB stimulation. Phagocytosis assays demonstrated enhanced macrophage training on day 6 in 2 out of 4 donors treated with dpB.

Conclusions: These preliminary results demonstrate that dpB can induce trained immunity in human monocytes as well as its safety, as no cytotoxic effects were observed. Although metabolic and functional assays showed variable responses between donors and did not reach statistical significance, dpB showed trends comparable to BCG. Further studies with a larger number of donors and additional analyses are needed to define the role of dpB in training human monocytes.

O-036 SMART-E: A Spatial Digital Framework for Standardized Environmental AMR Surveillance.

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Background: Environmental antimicrobial resistance (AMR) is increasingly recognised as a One Health priority, yet surveillance and risk assessment remain limited by heterogeneous data and an incomplete understanding of key emission sources. Moreover, the lack of standardized spatial approaches to characterise environmental pressure at the sample level hinders comparability across studies and regions.

Objectives: To develop and validate a scalable spatial digital framework that standardizes the characterization of environmental pressure, enabling comparable and integrative AMR analyses across heterogeneous surveillance contexts.

Methods: SMART-E (Surveillance and Monitoring of Antimicrobial Resistance in the Environment) was developed as a pilot framework in Spain with scalability across Europe. The tool compiles indicators of anthropogenic AMR emission to the environment derived from existing datasets and dedicated geoprocessing, i.e. rivers receiving wastewater treatment plant (WWTP) effluents, agricultural plots fertilized with sewage sludge from WWTPs, and agricultural plots fertilized with animal manure. SMART-E combines geostatistical modelling and geographic information system (GIS) automation within an ArcGIS Pro (ESRI, Redlands, CA) environment, integrating data from public sources and validated spatial layers produced by national and European environmental agencies.

Results: The framework generates uniformly processed datasets linking AMR-related observations with multidimensional environmental pressure profiles. These outputs support statistical analyses exploring associations between AMR presence or prevalence and environmental pressures across species, regions, and sampling strategies, fostering interdisciplinary research at the human–animal–environment interface.

Conclusions: By prioritizing the consistent spatial extraction of predefined pressure indicators rather than source identification, SMART-E provides a robust and scalable tool for One Health surveillance. It enhances the integration of environmental context into AMR studies, facilitates comparability across case studies, and supports evidence generation relevant for research, surveillance, and policy-oriented interpretation.

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O-037 Antimicrobial Resistance by metaGenomics Overview in a Sewage system (ARGOS).

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Background: Antimicrobial resistance (AMR) poses a significant threat to global public health. The World Health Organization has therefore advocated for a “One Health” approach recognizing the interconnectedness of human, animal, and environmental health. Under this context, sewage systems play a critical role in disseminating antimicrobial resistance genes (ARGs) into the environment, yet limited information is available for most wastewater infrastructures in Spain. Here, we present the ARGOS (Antimicrobial Resistance by metaGenomics Overview in a Sewage system) project—the first large-scale metagenomic investigation of AMR within Madrid’s sewage network, managed by Canal de Isabel II.

Objectives: We aim to build a comprehensive map of AMR situation across the network by characterizing the resistome across multiple sampling stations by quantifying the presence, diversity, and abundance of ARGs; identifying AMR hotspots within the wastewater system; and assessing the effectiveness of wastewater treatment plants (WWTPs).

Methods: Since July 2025, monthly sampling has been conducted at 30 stations across the wastewater system, including WWTPs, hospital effluents, and regular sewage network points. Shotgun metagenomic sequencing is applied to characterize microbial communities and ARG profiles. Concentrations of antibiotics are quantified using ultra-high-performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS). Furthermore, qPCR assays are performed in hospital and WWTPs samples to quantify ARGs.

Results: Preliminary analyses showed that the sewage microbiome is dominated by bacteria from the families *Arcobacteraceae* and *Burkholderiaceae*, both including relevant pathogenic species. Clustering analysis revealed that hospital samples form a distinct group compared to the rest of the stations, characterized by higher diversity of ARGs and variants.

Conclusions: These findings indicate the important role that hospitals play in introducing novel AMR mechanisms into sewage systems. The insights generated by ARGOS will inform targeted AMR surveillance strategies and provide essential baseline data for policies aimed at mitigating the environmental spread of AMR.

O-038 Organo-Functionalized Polyoxometalate Materials as Multifunctional Platforms for Antimicrobial Control and Environmental Remediation in a One Health Framework.

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Background: Antimicrobial resistance, biofouling, and environmental pollution are interconnected One Health challenges linking environmental, animal, and human health. Stone heritage, water systems, and metallic infrastructures act as reservoirs for microbial colonization, facilitating biodeterioration, microbiologically influenced corrosion, and dissemination of resistance determinants. Organo-functionalized polyoxometalates (POMs) are hybrid redox-active metal–oxo clusters whose tunable chemistry and intrinsic biological activity make them promising candidates for multifunctional antimicrobial and environmental materials.

Objectives: To engineer modular POM-based hybrid materials as innovative solutions for (i) long-term prevention of environmental biofilms, (ii) mitigation of microbiologically influenced corrosion, and (iii) development of pollutant removal devices, while evaluating their ecological impact and potential to influence resistance gene dynamics.

Methods: We synthesized polyoxometalate–ionic liquids (POM-ILs) and covalent POM–polypeptide hybrids (“POMlymers”) via organo-functionalization and on-POM polymerization strategies. Materials were characterized structurally and physicochemically, then applied as coatings on limestone, chalk, brick, and metal substrates. Antimicrobial performance was evaluated against phototrophic and heterotrophic environmental microorganisms, including bacteria, cyanobacteria, algae, and moulds, using culture-based assays, microscopy, and in situ exposure trials (up to three years). Gene-level analyses assessed shifts in microbial community composition and resistance markers. POM-functionalized porous substrates were fabricated and tested for universal pollutant removal from aqueous media.

Results: POM-IL coatings provided sustained inhibition of specialist colonizers, including Cyanobacteria, Chlorophyta, and Ascomycetes, under real environmental conditions (TRL 5–6). Treated substrates showed reduced biofilm formation and improved resistance to environmental corrosion. However, selective pressures were associated with increased prevalence of resistance genes in generalist taxa such as Pseudomonadota. POM-functionalized porous devices demonstrated efficient and versatile pollutant adsorption, supporting their application in water purification contexts.

Conclusions: Organo-POM materials represent adaptable, multifunctional platforms addressing microbial control and pollutant remediation across environmental interfaces. Integrating antimicrobial efficacy with ecological risk assessment is essential to ensure that advanced materials contribute positively to One Health, minimizing unintended resistance selection while protecting environmental and public health.

O-039 Sensitivity analysis of factors influencing the ecology of mosquitoes involved in the transmission of Rift Valley fever virus.

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Background: Vector-borne diseases are a major global health concern, with Rift Valley fever (RVF) serving as a key example due to its impact on both human and animal health. Predicting and controlling such diseases requires understanding how environmental factors shape mosquito ecology.

Objectives: Due to mosquito abundance, distribution, and behavior being influenced by ecological conditions, identifying the drivers of these dynamics is essential for anticipating transmission risk. This study aims to assess the sensitivity of ecological factors governing the ecology of mosquitoes, using a deterministic, compartmental model of RVF transmission in Kenya.

Methods: We performed sensitivity analyses on ten parameters influencing mosquito population dynamics: four species-specific parameters for *Culex* spp. and *Aedes* spp., and two shared parameters. Species-specific parameters included oviposition area scanned, egg-laying suitability, eggs laid, and maximum egg density. Shared parameters accounted for livestock population size and its effect on vector fecundity and gonotrophic cycles. Parameter ranges were informed by a scoping literature review. Using Sobol sensitivity analysis, we evaluated parameter importance under two environmental scenarios: (i) constant temperature and water body area, and (ii) periodically varying conditions, employing a time-dependent Sobol framework.

Results: Results revealed species-specific differences in parameter influence. For *Culex* spp., uncertainty in the area scanned for oviposition was highly influential, while for *Aedes* spp., the the proportion of area that eggs are laid on and the maximum density of eggs emerged as dominant.

Conclusions: These findings highlight the need for improved empirical data on spatial oviposition patterns across water bodies, as current evidence remains limited. By identifying the ecological parameters that most critically shape mosquito population dynamics and/or influence model outputs (e.g., due to large uncertainties in parameter knowledge), and thereby the transmission potential of RVF, this work supports more targeted vector surveillance and strengthens public health decision-making in RVF-endemic regions.

O-040 Silencing Pathogens: Anti-Quorum Sensing Antibodies to Control Pseudomonas aeruginosa Pathogenicity.

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Background: Antimicrobial resistance is a major global crisis, associated with Pseudomonas aeruginosa, a WHO-designated high-priority risk pathogen. Antibiotics often fail against multidrug-resistant strains, underscoring the critical need for new therapeutic approaches. One promising strategy involves targeting bacterial Quorum Sensing (QS), a cell-cell communication system that regulates virulence, biofilm formation, and pathogenicity.

Objectives: Disrupting communication with monoclonal antibodies targeting relevant QS molecules can attenuate bacterial virulence without directly affecting growth, while also interfering with the communication process itself.

Methods: A cell-based *in vitro* assay was used to evaluate the effects of two QS molecules, including Pseudomonas quinolone signal (PQS), a signaling molecule, and 2-heptyl-4-quinoline N-oxide (HQNO), a virulence factor. Cytotoxicity curves were built in two different murine macrophages and two monoclonal antibodies against PQS and HQNO were developed in-house. The protective effect of these QS-specific antibodies was examined by co-treating cells with them and the corresponding QS targets. Additionally, immunomodulatory effects were assessed by measuring a panel of cytokines.

Results: HQNO exhibited a lower LD_{50} and a steeper dose-response cytotoxicity curve compared to PQS, consistent with its role as a virulence factor. On the contrary, PQS showed a higher LD_{50} and a less pronounced slope. Co-treatment with the specific monoclonal antibodies provided complete protection by neutralizing both molecules cytotoxic effect (Fig.1). HQNO triggered a stronger immune response, resulting in a cytokine increase, whereas PQS induced a milder effect. Although antibody treatment alone increased cytokine levels, co-treatment with QS molecules restored cytokine production to near baseline levels.

Conclusions: These findings demonstrate that QS molecules differentially affect cell viability and immune responses, with HQNO showing stronger activity than PQS. QS-specific monoclonal antibodies effectively neutralized these effects, highlighting their potential as therapeutic agents. Future studies will evaluate co-infection models involving other pathogens, optimize antibody performance through nanocarrier delivery systems, and ultimately validate the approach in *in vivo* mammalian models.

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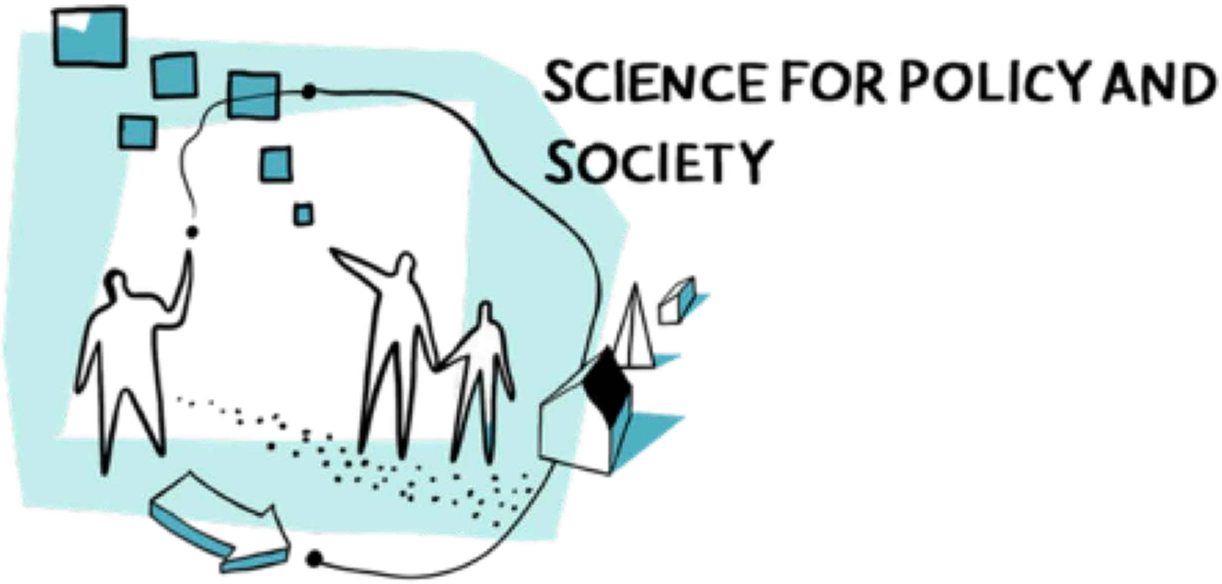

O-041 EU-JAMRAI 2: Fostering the integration of environmental approaches to strengthen a One Health response to antimicrobial resistance in Europe .

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Background: The European Joint Action on Antimicrobial Resistance and Healthcare-Associated Infections (EU-JAMRAI) represents Europe's largest coordinated effort to address antimicrobial resistance (AMR) through a One Health approach. EU-JAMRAI 2 has recognised the added value of environmental approaches, proactively including them into its operational strategy.

Objectives: To advance the operational integration of environmental approaches into European AMR strategies under a One Health approach.

Methods: EU-JAMRAI's work packages (WPs) were structured around AMR priority areas, in alignment with the EU Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach (2023/C 220/01). The WPs on antimicrobial stewardship (AMS), infection prevention and control (IPC), and surveillance each incorporated a dedicated environmental task with defined objectives and associated activities. Through the grant agreement, a collaborative network of 37 institutions from 21 countries—including government agencies, research centers, and universities—was established and organized into working groups to develop and implement these tasks.

Results: This collaborative work has helped advance the definition of environmental AMS and IPC principles, identify best practices that reduce the release and spread of AMR determinants in the environment, and establish priority objectives and targets for environmental AMR surveillance, including surface-water monitoring to further human-risk assessment and raw wastewater monitoring to track AMR trends. The implementation of these outcomes will be further strengthened through a pilot surveillance programme and capacity-building interventions embedded within a Community of Practice that combines an online learning platform with in-person activities – including workshops, peer to peers and mentorships –.

Conclusions: EU-JAMRAI 2 will accelerate the operational integration of the environmental dimension into AMR frameworks by delivering guidance to support the incorporation of environmental measures into national AMR action plans across Europe, thereby strengthening their One Health implementation.

O-042 Alternatives to Antimicrobials in Sub-Saharan Africa: A Regional Review of Evidence, Innovation Pathways, and Policy Trajectories.

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Background: Antimicrobial resistance (AMR) poses a critical threat to animal health, public health, and food security globally, with Sub-Saharan Africa (SSA) experiencing the world's highest AMR-attributable mortality despite comparatively low antimicrobial consumption. Livestock systems in the region remain highly vulnerable due to weak veterinary infrastructure, limited diagnostic capacity, widespread infectious disease pressure, and reliance on antimicrobials for prevention and treatment. Alternatives to antimicrobials (ATAs), including vaccines, probiotics, phytogenics, bacteriophages, competitive exclusion products, biosecurity measures, nutritional interventions, and emerging nanotechnologies, offer promising pathways to reduce antimicrobial use (AMU) and mitigate AMR risks.

Objectives: To review current evidence, innovation pathways, and policy trajectories for alternatives to antimicrobials in sub-Saharan Africa.

Methods: This review synthesizes evidence from scientific and grey literature, insights from four InnoVet-AMR 2.0 research projects, national policy briefs from Ethiopia, Kenya, Nigeria, and Tanzania, and deliberations from the 2025 WOAH Regional Workshop on Vaccination and ATAs. We present a consolidated analysis of ATA availability, use, regulatory environments, barriers, and emerging innovations across SSA.

Results: Findings show that while vaccination remains the most widely adopted ATA, uptake of probiotics, plant-based products, and microbial-based interventions is growing, particularly in poultry and aquaculture. Regulatory gaps, limited field validation, low awareness, and affordability barriers remain major constraints. Conversely, enabling factors include improving policy alignment, expanding research capacity, traditional knowledge systems, strengthening extension services, and increasing private-sector engagement.

Conclusions: Coordinated regional action, strengthened regulatory systems, increased investment in ATA research and commercialization, and integration of ATAs into national AMR strategies are essential to advancing sustainable livestock health systems in SSA.

O-043 Towards cross-border Vector Surveillance from the Mediterranean to the Alps: A Technical Approach to Harmonization.

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Background: The project *One Health surveillance and Vector monitoring for cross-border pathogens* (OH SURVector) is a cross-border One Health initiative (2024-2026) co-funded by the European Commission aiming to scale up vector surveillance across five European countries: Austria, Czeck Republic, Greece, Hungary, and Slovakia. As a Five-Member State Consortium we see it as our duty and a great opportunity to contribute our experience to European-wide surveillance harmonization efforts and to create impact towards better preparedness of health systems to reduce risks for humans and animals and the environment.

Objectives: Within this project task our objective is to develop an approach to explore harmonization potential within a project and understand what can hinder harmonization.

Methods: Through an iterative eight-month process (September 2024 – May 2025), experts from different institutions and work packages (WP) within the Consortium collaborated to identify opportunities for harmonization while respecting national contexts. First, a working group was set up, which consisted of one nominated person for each WP: field work tick collection, field work mosquito collection, laboratory activities, data and analysis, and communication and dissemination. From there on this working group explored the harmonization potential in five steps: 1) online group discussion, 2) design of a standardized matrix, 3) in person workshop to fill in/out the matrix, 4) data cleaning, and 5) analyses and interpretation of results.

Results: WP groups evaluated 23 surveillance characteristics, of these, 19 (83%) showed potential for harmonization, while 4 (17%) did not—primarily due to climatic/geographic differences, entrenched laboratory protocols, or varying institutional mandates. Notably, mosquito collection methods were already largely harmonized. Minimum criteria were defined for key characteristics to ensure baseline compatibility (e.g., morphological species identification using shared keys), with flexibility for additional methods based on national capacities.

Conclusions: Harmonization will enhance data comparability, outbreak preparedness, and cross-border collaboration. Establishing minimum criteria is proposed as a first step toward broader standardization. This approach balances standardization goals with the need for adaptability and flexibility.

O-044 OneHealthSecure project: multisectoral cooperation for sustainable vector-borne disease prevention and response in the Mediterranean, Black Sea and Sahel regions.

Elisa Pérez-Ramírez[1], Pilar Aguilera-Sepúlveda[1], Jovita Fernández-Pinero[1], Jordi Figuerola[2], Jean-Claude Manuguerra[3], Florence Fournet[4], Flavia Riccardo[5], Paolo Calistri[6], Guy Hendrickx[7], Vanessa Lagal[8], Miguel Ángel Jiménez-Clavero[1,9]

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Background: Globalization, climate change and rapid urbanization have created fertile ground for the emergence and spread of zoonotic diseases. Among these threats, vector-borne diseases (VBD) represent a growing concern due to their expanding geographic distribution and impact on human and animal health. Addressing VBD requires coordinated action across human, animal and environmental sectors. OneHealthSecure (OHS) is a multisectoral project funded by the European Commission (2024-2027) aiming to strengthen preparedness and response capacities against viral VBD in 23 EU-neighboring countries.

Objective: The main aim of the OHS project is to consolidate a sustainable multisectoral network of reference laboratories as well as health and environmental institutions and to enhance One Health surveillance and response capacities against vector-borne viruses in the Mediterranean, Sahel and Black Sea regions.

Methods: OHS builds on the legacy of MediLabSecure, a 10-year capacity-building project (2014–2024) that significantly strengthened regional capacities for virus detection, vector control and integrated surveillance in these regions. OHS further develops this unique One Health network by addressing remaining gaps in VBD preparedness. Particular emphasis is placed on strengthening collaboration with the environmental sector and promoting community engagement in prevention and control measures.

Results: OHS has established an extended international network bringing together, in each beneficiary country, institutions from complementary sectors involved in VBD management, including human and animal virology, entomology, public health, veterinary services, modelling and environmental sciences. The network involves more than 400 experts from 120 national reference laboratories and health and environmental institutions. The project supports cross-sectoral and cross-border collaboration in diagnostics, integrated surveillance, vector control and One Health operationalization.

Conclusions: Beyond training, OHS supports participating institutions in implementing concrete One Health initiatives at national level. By fostering local ownership and multisectoral collaboration, the project promotes the transfer of knowledge, tools and best practices to national authorities and contributes to strengthening political commitment to the One Health approach in beneficiary countries.

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POSTER THEME 1: JOINING ENVIRONMENTAL SCIENCES AND ECOLOGY WITH HUMAN/ANIMAL HEALTH

P-01 Role of migratory bird associated ticks in pathogen dispersal: a two-year field study in Northern Italy.

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Background: The epidemiological significance of ticks and their associated pathogens for human and animal health has increased substantially in recent decades. Migratory birds act as key vectors hosts, facilitating the transport and long-distance dispersal of ticks and the pathogens they harbor across geographical barriers

Objectives: This study aimed to investigate the diversity of ticks infesting migratory birds in Northern Italy and to determine the prevalence of bacterial and viral pathogens they carry.

Methods: Birds were captured during the post-breeding migration period (August - November) in 2023 and 2024. A total of 463 ticks were collected and morphologically and molecularly identified using MALDI-Tof technique. Ticks were screened for bacterial pathogens (*Borrelia* spp., *Anaplasma* spp., *Rickettsia* spp., *Coxiella burnetii*, *Francisella* spp., *Neoehrlichia mikurensis*) and viral agents (tick-borne encephalitis virus [TBEV], Crimean–Congo hemorrhagic fever virus [CCHF], West Nile virus [WN], Usutu virus [USUTU], Phleboviruses) using real-time PCR.

Results: The most frequently sampled bird species were *Fringilla coelebs* and *Fringilla montifringilla*.
Identification of the tick specimen revealed the presence of *Ixodes ricinus* (95.3%), *I. caledonicus* (3.5%), *I. arboricola* (0.6%), and *Ixodes acuminatus* (0.6%). Overall, 54% of ticks tested positive for at least one pathogen: 26% for *Borrelia spp.,* 19% for *Rickettsia spp.,* 4% for *Neoehrlichia mikurensis,* and 1.4% for *Anaplasma phagocytophilum*. All specimens tested negative for *Coxiella burnetii,* TBEV, CCHF virus, WN virus, USUTU virus, and Phleboviruses. Within the *Borrelia burgdorferi sensu lato* complex, *B. burgdorferi s.l.*, *B. afzelii* were predominated followed by *B. miyamotoi*. Rickettsial species identified included *Rickettsia helvetica* and *R. monacensis*.

Conclusions: These findings underscore the pivotal role of migratory birds in the long-distance dispersal of pathogenic and potentially zoonotic *Borrelia* and *Rickettsia* species. The data provides critical insights into the epidemiology of tick-borne diseases and highlights the importance of integrating avian surveillance into public and veterinary health monitoring programs.

P-02 Pathological study of Passeriformes infected by Haemosporida in the Community of Madrid.

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Background: The order Passeriformes, commonly referred to as passerines, comprises approximately 6,500 species and is one of the most diverse and ecologically vital groups of birds worldwide. These species fulfill crucial roles in ecosystem functioning and may also serve as indicators of environmental and public health. Nevertheless, passerine populations face increasing threats from both natural and human-induced pressures, endangering their survival. Among these threats, parasites in the order Haemosporida are particularly significant due to their potential impact on host health, fitness, and population dynamics.

Objectives and Methods: This study aimed to determine the incidence of Haemosporida parasites in wild passerine birds and to describe the related macroscopic and histological lesions to better understand their development. Additionally, the study assessed whether post-mortem findings could serve as supplementary or alternative diagnostic tools for PCR and blood smear analysis. A total of 34 passerines from the Community of Madrid were examined through complete necropsy.

Results: Macroscopic and histopathological lesions were recorded, and molecular diagnosis was conducted using PCR (14 positive cases) and genomic sequencing (9 positive cases), followed by statistical analysis. An overall prevalence of 26.5% for Haemosporida parasites was identified: 8.8% involved *Plasmodium* spp., 11.8% involved *Leucocytozoon* spp., and 8.8% involved *Haemoproteus* spp. Macroscopic lesions were significantly more common ($p<0.05$) in parasitized birds, especially affecting the liver, lungs, kidneys, and spleen. However, no significant histological differences ($p>0.05$) were found between parasitized and non-parasitized groups.

Conclusions: These findings suggest that macroscopic and histopathological examination alone is insufficient to establish hemoparasites as the definitive cause of death. Although compatible parasitic structures can confirm infection, additional immunohistochemical techniques are required to accurately identify the predominant genera and strengthen diagnostic reliability.

The authors acknowledge the financial support provided by the Ministry for Ecological Transition and the Demographic Challenge with Public Utility Founds but does not express the opinion of the Ministry.

P-03 **Presence of red foxes and *Echinococcus multilocularis* contamination on soft fruit production sites in the Dutch province of Limburg.**

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Background: *Echinococcus multilocularis* is considered the most impactful foodborne parasite in Europe, yet data on *E. multilocularis* contamination of locally grown produce in endemic areas are scarce. Following the detection of *E. multilocularis* DNA on 2/14 soft fruit samples from the Dutch endemic region of Limburg in an international multi-center study, a larger-scale follow-up study was conducted.

Objectives: This study investigated fox presence and the occurrence of *E. multilocularis* contamination of fruits and soil on commercial soft fruit production plots in Limburg.

Methods: During the 2024 harvest season, 220 soft fruit samples and 220 soil samples were collected from 14 production sites. Producers filled in a questionnaire on farm characteristics, and camera traps were used to record wildlife activity. Fruit and soil samples were processed to isolate eggs, followed by DNA isolation and *E. multilocularis*-specific qPCR, with confirmation by COX1 PCR and Sanger sequencing.

Results: *E. multilocularis* DNA was detected in 10/220 (4.5%) soft fruit samples, all at low concentrations. Positive fruit and/or soil samples were obtained from 9/14 production sites, including two sites located north of the currently known endemic area. Fox activity was recorded on 6/14 sites, where in some cases foxes were observed actively foraging on fruits.

Conclusions: This study confirmed the presence of *E. multilocularis* DNA on commercially grown soft fruits in an endemic region. It is unknown how contamination occurred and whether the DNA originated from infectious or non-infectious eggs; therefore, food safety implications remain unclear. However, the presence of foxes on production sites indicates the potential for *E. multilocularis* contamination of fresh produce. These findings highlight the importance of preventive measures to reduce foodborne exposure from locally-grown fresh produce in endemic areas. Additionally, measures focused on keeping foxes out of production sites, to the extent possible, are advisable to minimize contamination risk.

P-04 Social and environmental conditions associated with leishmaniasis in rural contexts of Nariño and Risaralda (Colombia). Ennue Fajardo Rosas.

Abstract: Leishmaniasis, a vector-borne disease, mainly affects vulnerable populations with limited access to health services, requiring intersectoral action for prevention. Cutaneous leishmaniasis, its most common form, causes skin ulcers that can leave permanent scars, disability and social stigmatisation. Its transmission is associated with adverse rural conditions, such as inadequate housing, risky practices (sleeping outdoors) and economic activities such as agriculture. In addition, human displacement due to conflict or deforestation facilitates transmission in zoonotic cycles. This study analysed non-climatic social and environmental conditions associated with cutaneous leishmaniasis in Tumaco-Nariño and Pueblo Rico-Risaralda through a cross-sectional design, using data from the Centro Internacional de Entrenamiento e Investigaciones Médicas (CIDEIM) (2012). The response variable was leishmaniasis infection (active lesions, 7 asymptomatic infection or immunological memory). Exposures such as socio-demographic conditions, housing conditions, cohabitation with animals, risk activities, and nearby habitats were assessed. Bivariate analyses were performed considering two levels: individual and household. Based on the variables that showed P-value <0.25 in the bivariate analysis and support in the literature, the final multilevel logistic regression model was developed, finding two explanatory models, one with the variable of awning use and the other with the variable of distances and walking time in the bush. The findings indicate that having the firepit located outside acts as a protective factor in both model 1 (aOR 0.139; 95%CI) and model 2 (aOR 0.063; 95%CI). On the other hand, age increases the chance of infection, observed in model 1 (aOR 1.051, 95%CI) and model 2 (aOR 1.055, 95%CI). In addition, not using an awning in model 1 (aOR 4.409, 95%CI) and walking intermediate distances into the bush in model 2 (aOR 3.800, 95%CI) increase the chance of infection. Possible differences between rural areas were found in relation to gender, occupation and awning use. This study identifies household and individual factors to be considered in the design of interventions and helped to establish baselines for future comparisons of social and environmental factors in rural areas endemic for leishmaniasis taking into account contextual factors from a multilevel approach.

P-05 From wildlife health to tourism sustainability: One Health insights from the first parasitological survey in Mosi-oa-Tunya National Park.

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Background: Wildlife–livestock interfaces in African ecosystems are critical hotspots for gastrointestinal parasite transmission. In Mosi-oa-Tunya National Park (Zambia), wild herbivores and domestic cattle share grazing areas and water points, creating continuous cross-species exposure. Although detected parasites are not zoonotic, high burdens may reduce wildlife fitness, affect livestock productivity, and indirectly impact human communities through diminished food security and compromised tourism revenue—particularly relevant in Zambia, where iconic species such as the remaining rhinoceroses hold substantial economic importance.

Objectives: To conduct the first *in situ* coprological assessment of gastrointestinal parasites in key wildlife species and cattle in Mosi-oa-Tunya National Park, and to evaluate the epidemiological links and potential One Health implications.

Methods: A total of 62 fecal samples were collected in August 2025 from eight species: impala (7), buffalo (4), giraffe (2), elephant (4), warthog (4), rhino (18), zebra (12), and cattle (5). Coprological analyses (Modified McMaster, flotation, sedimentation, larval migration) were performed on site. Egg per gram (epg) counts and parasite genera were recorded. Statistical analyses included Chi-square, Fisher's exact, and Kruskal-Wallis tests.

Results: Gastrointestinal nematodes (GIN) were present in all species, with rhinos and zebras showing the highest burdens (>1200 epg). *Strongyloides* occurred primarily in elephants, impalas, and warthogs. Cattle harbored GIN and *Toxocara vitulorum*, confirming epidemiological linkage with sympatric wildlife. Significant differences were observed in parasite presence ($p < 0.001$) and GIN intensity among species ($p < 0.001$). Ruminants acted as primary reservoirs, while omnivores contributed to parasite diversity.

Conclusions: Shared parasite profiles at the wildlife–livestock interface reveal substantial One Health challenges despite the absence of zoonotic species. High parasite burdens may compromise wildlife health, livestock productivity, and the ecosystem services that support local livelihoods and tourism. In situ surveillance and capacity building provide a sustainable framework for early detection and mitigation of parasitic risks in protected areas.

P-06 Passerine Migration as a Hidden Pathway of Antimicrobial Resistance Connectivity in South America.

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Background: Antimicrobial resistance (AMR) is a major global health challenge driven by antimicrobial use in humans and livestock and sustained by the environment that can facilitate resistance persistence and spread. Although migratory birds are recognized as potential vectors across large spatial scales, research has focused primarily on waterfowl, leaving the role of passerines—the most diverse and abundant avian order—largely unexplored in AMR ecology. Given their ecological plasticity, ground-foraging behavior and frequent use of forest, agricultural and peri-urban habitats, passerines may act as overlooked connectors at the wildlife–livestock–human interface. In South America, the genus Turdus provides a suitable comparative model due to its wide distribution and diversity of migratory strategies.

Objectives: We evaluated whether migratory Turdus species function as ecological connectors between areas of contrasting anthropogenic AMR pressure in South America.

Methods: Breeding and wintering distributions were derived from ensemble ecological niche models. A AMR source layer was generated integrating human and livestock densities, as an indirect proxy of Anthropogenic AMR pressure. This layer was restricted to forested areas (>50% cover) to define AMR hotspots (low, medium, high), which were extracted within seasonal ranges to assess spatial overlap and connectivity.

Results: AMR exposure patterns differed among species. Turdus subalaris overlapped extensively with high-intensity hotspots in both breeding and wintering areas. Turdus nigriceps showed asymmetric exposure, with high-pressure wintering zones but comparatively low-impact Andean breeding habitats. Turdus flavipes encountered anthropogenic pressure in both seasons, linking urban wintering hotspots with livestock-associated breeding areas through altitudinal migration.

Conclusions: Migratory passerines do not play a uniform role in AMR dynamics; their epidemiological relevance is species-specific and shaped by movement ecology and habitat context. Forest-associated thrushes may act as ecological connectors between distinct anthropogenic AMR landscapes, underscoring the need to integrate species-level ecological traits into One Health frameworks addressing environmental resistance circulation.

P-07 One Health Approaches for Health Challenges in Urban Environments. Y. Y. Hwang

UNU-MERT

Background: Human, animal, and environmental health has created challenges for cross-sectoral collaboration. High population density, close human–animal interactions, and environmental pressures in cities can amplify the risk of infectious disease emergence, zoonotic spillover, and environmental health hazards. A One Health framework in cities is essential to address these interconnected risks effectively.

Objectives: To examine the application of One Health approaches in urban settings, highlighting integrated surveillance, risk mitigation, and cross-sectoral interventions.

Methods: Urban health studies, epidemiological reports, and case studies was conducted to identify health risks at the human–animal–environment interface in urban ecosystems. Strategies for surveillance, risk reduction, and multisector collaboration were developed.

Results: Urban environments faces elevated risk of zoonotic transmission, vector-borne diseases, and environmental contamination. Effective interventions include integrated surveillance systems, environmental management, urban planning incorporating health considerations, and cross-sectoral governance involving public health, veterinary, and environmental stakeholders. Evidence indicates that coordinated One Health approaches improve early detection, outbreak response, and health resilience in urban areas.

Conclusions: Addressing health challenges in urban settings requires a One Health perspective that integrates human, animal, and environmental health considerations. Policy frameworks and collaborative interventions are critical to enhance urban health security and mitigate emerging risks.

Keywords: One Health; Urban health; Zoonotic diseases; Environmental health; Surveillance; Cross-sectoral collaboration

P-08 Microbial contamination dynamics across two Irish sub-catchments - effects of geology, hydrometeorology and infrastructure.

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Background: Shiga toxin-producing *Escherichia coli* (STEC) causes mild to severe gastrointestinal infections. Crude incidence rates in Ireland are consistently among the highest in the EU. Groundwater wells, used by over 720,000 Irish residents, represent a key exposure route. Microbial testing is optional and well construction unregulated.

Objectives: To investigate spatiotemporal dynamics of *E. coli* and STEC in groundwater wells across two hydrogeologically diverse sub-catchments over two years and assess likely environmental and infrastructural contamination drivers.

Methods: Groundwater wells were sampled fortnightly; the Black River sub-catchment (n=14 wells, 341 samples) was investigated in 2023/2024, and the Little Brosna sub-catchment (n=12 wells, 256 samples) during 2024/2025. *E. coli* was quantified using Colilert-18®, while quantitative real-time PCR was employed to detect O157 (*rfbE*) and O26 (*wzx*) serogroup markers. Statistical associations between contamination and environmental, climatic, and infrastructural variables were subsequently examined.

Results: In the karstic Black River sub-catchment, *E. coli,* O157 and O26 were detected in 48%, 63%, and 26% of samples, respectively. In the non-karstic Little Brosna sub-catchment, *E. coli* was detected in 7% samples, while no STEC serogroup markers were detected. Serogroup detection was associated with sub-catchment type, with both O157 and O26 detected exclusively in the Black River sub-catchment (Fisher's exact test $p < 0.001$). Shallow wells were more likely to have *E. coli* present in both catchments (Black River: $U = -5.501$, $p < 0.001$; Little Brosna: $U = -5.821$, $p < 0.001$). The absence of a waterproof seal at the wellhead was also significantly associated with *E. coli* contamination (Black River: $\chi^2 = 9.585$, $p = 0.002$; Little Brosna: $\chi^2 = 40.145$, $p < 0.001$).

Conclusions: Subsurface geology and well infrastructure are important static factors for microbial contamination risk. Regulating borehole construction to mandate adequate depth and waterproof seals should be considered to safeguard public health.

P-09 Living environment-related risk factors for zoonotic pathogen infection in humans and animals.

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Background: Zoonotic diseases represent a significant public health threat, with approximately 60% of emerging infectious diseases being zoonotic in origin. The emergence and transmission of zoonoses are shaped by complex interactions between hosts (humans and animals), pathogens, and the environment. Climate change and ongoing environmental transitions are altering these dynamics by influencing our shared living environment.

Objectives: This study aims to identify and characterize factors within the living environment that affect the risk of zoonotic disease transmission to both humans and animals. By synthesizing evidence linking environmental factors to zoonotic risks, we try to identify research gaps and showcase the role of the environment within One Health research.

Methods: We are conducting a systematic literature review on this topic.

Expected results: This review will produce a comprehensive overview of environmental factors—such as climate variables, green urban spaces, and animal habitats—associated with zoonotic disease risks for both humans and animals. The results can identify potential high-risk environmental factors and research gaps. This can be used to inform policy makers on how to make the living environment more ‘zoonoses proof’, to support surveillance strategies in the context of climate change and ongoing environmental transitions, and to guide future research.

P-010 Diversity and antimicrobial susceptibility patterns of clinical and environmental *Salmonella enterica* serovars in Western Saudi Arabia.

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Background: The diverse environmental distribution of *Salmonella* makes it a global source of human gastrointestinal infections.

Objectives: This study aimed to detect *Salmonella* spp. and explore their diversity and antimicrobial susceptibility patterns in clinical and environmental samples.

Methods: Pre-enrichment, selective enrichment, and selective plating techniques were adopted for the *Salmonella* detection whereas the API 20E test and Vitek Compact 2 system were used to confirm the identity of isolates. *Salmonella* serovars were subjected to molecular confirmation by 16S rDNA gene sequencing. Disc diffusion method and Vitek 2 Compact system determined the antibiotic susceptibility of *Salmonella* serovars. Multiple antibiotic resistance index (MARI) was calculated to explore whether *Salmonella* serovars originate from areas with heavy antibiotic usage.

Results: Results depicted low *Salmonella* prevalence in clinical and environmental samples (3.5%). The main detected serovars included *Salmonella* Typhimurium, *S. enteritidis*, *S.* Infantis, *S.* Newlands, *S.* Heidelberg, *S.* Indian, *S.* Reading, and *S.* paratyphi C. All the detected *Salmonella* serovars (27) exhibited multidrug resistance to three or more antimicrobial classes. The study concludes that the overall *Salmonella* serovars prevalence was found to be low in environmental and clinical samples of Western Saudi Arabia (Makkah and Jeddah). However, antimicrobial susceptibility patterns of human and environmental *Salmonella* serovars revealed that all isolates exhibited multidrug-resistance (MDR) patterns to frequently used antibiotics, which might reflect antibiotic overuse in clinical and veterinary medicine.

Conclusions: It would be suitable to apply and enforce rules and regulations from the One Health approach, which aim to prevent antibiotic resistance infections, enhance food safety, and improve human and animal health, given that all *Salmonella* spp. detected in this investigation were exhibiting MDR patterns.

P-011 Distinct Genomic Features and Codon Adaptation in Temperate versus Virulent Bacteriophages of *Listeria monocytogenes.*

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Background: Bacteriophages are critical mediators of bacterial population dynamics in natural, agricultural, and food-associated ecosystems, impacting human and animal health. In *Listeria monocytogenes*, both virulent and temperate phages shape ecological balance, drive evolution, and contribute to the pathogen's persistence. Although phage lifestyles are well-characterized, genome-wide differences—particularly in gene content and synonymous codon usage affecting translation efficiency—remain poorly understood.

Objectives:
This study aimed to characterize genome-wide differences in gene content and synonymous codon usage between virulent and temperate *L. monocytogenes* phages, providing insights into lifestyle-specific adaptations in translational efficiency and codon optimization.

Methods: We analyzed 1,516 genes from 10 virulent and 686 genes from 10 temperate phages. Metrics including gene length, codon adaptation index (CAI), effective number of codons (Nc), total GC content, and positional GC content (%GC1, %GC2, %GC3) were computed. Differences were evaluated using Welch's t-test and the Mann–Whitney U test. Principal component analysis and Pearson correlation analysis examined codon usage patterns and associations.

Results: Temperate phages had smaller genomes (41,023 ± 3,225 kb) and shorter genes (555 ± 647 nt) than virulent phages (101,089 ± 44,030 kb; 629 ± 584 nt). CAI was higher in temperate phages (0.711 ± 0.045), indicating stronger host codon adaptation, while virulent phages showed higher GC content (35.84 ± 2.99%) and greater codon usage bias (Nc = 44.80 ± 5.86), particularly at the third codon position. CAI and %GC3 were strongly negatively correlated ($r = -0.77$ to -0.97).

Conclusions: Differences in genome composition and codon usage reflect phage lifestyle, with temperate phages favoring host-adapted codons and virulent phages favoring biased codons most likely for rapid protein synthesis. These findings provide a framework for codon usage–based biomarkers to rapidly distinguish phage lifestyles and inform synthetic biology strategies to enhance phage-based therapeutics, diagnostics, and biocontrol.

P-012 Assessing the impact of meteorological conditions on Legionnaires' disease reported incidence in Greece: a 17-year time-series analysis.

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Background: *Legionella pneumophila is* transmitted to humans by inhalation of contaminated aerosols and may cause severe pneumonia, Legionnaires' disease (LD). LD incidence has been increasing globally, and meteorological conditions have been proposed as important drivers. Evidence from Greece remains limited.

Objectives: To investigate the effects of temperature, precipitation, relative humidity and wind speed on LD incidence.

Methods: We conducted a retrospective time-series study including sporadic LD cases exposed in Greece from 2008 to 2024, identified through the National Surveillance System and the European Legionnaires' Disease Surveillance Network. We excluded healthcare-associated and cruise ship-associated cases, cases exposed abroad, and cases exposed in multiple regions. We obtained atmospheric data from the Multi-Source Weather dataset and resident and tourism population data from Hellenic Statistical Authority. We fitted Negative binomial models to estimate the association between meteorological variables and weekly LD counts. We also fitted distributed lag non-linear models (DLNMs) to evaluate non-linear and delayed meteorological effects. Results are presented as adjusted incidence rate ratios (aIRR) with 95% confidence intervals (95%CI).

Results: LD incidence showed an increasing trend (IRR per year=1.08, 95%CI:1.06–1.10, $p<0.001$) with summer seasonality. In adjusted negative binomial models, LD incidence was positively associated with precipitation (aIRR=1.10, 95%CI:1.04–1.15, $p<0.001$). A significant temperature-relative humidity interaction was observed (aIRR=1.005, 95% CI: 1.003–1.007), with the association most pronounced at mid-range relative humidity (65–73%) and temperatures above 16.4°C and attenuated at lower and higher humidity levels. There was no association with wind speed. DLNMs showed a non-linear temperature effect on LD incidence, with significant delayed effects, peaking at 6 weeks before exposure (30 °C, aIRR:1.80, 95%CI:1.12-2.87).

Conclusions: In Greece, LD risk increased following rainy weather and certain temperature-humidity combinations. Warm temperature exhibited delayed effects for up to 6 weeks. Our findings support enhancing water-system maintenance during high-risk periods and highlight the potential for weather-informed early warning systems.

P-013 Mountain sentinels: The Pyrenean capercaillie (*Tetrao urogallus aquitanicus*) as an indicator of environmental antibiotic contamination in the Pyrenees, northeastern Spain.

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Background: The endangered Pyrenean Capercaillie (*Tetrao urogallus aquitanicus* [PC]) co-inhabits with extensive livestock. Although antibiotics were previously detected in their feces (fluorquinolones, tetracyclines and phenicols), the occurrence and diversity of genes against antibiotics (ARGS), heavy metals and biocides, and mobile genetic elements (MGEs), remain unknown. We hypothesized that PCs could be indicators of environmental contamination.

Objectives: Our goal was to (i)investigate the presence and concentration of selected genes in PC feces, and (ii)use SMART-E tool (Surveillance and Monitoring of Antibiotic Resistance in the Environment]) to analyze PC exposure to anthropogenic sources.

Methods: Twenty-one fecal samples (2020 and 2022), were tested for 23 genes using SmartChip PCR: beta-lactams, macrolide-lincosamide-streptogramin B [MLSB], phenicol, quinolone, sulfonamide, tetracycline, vancomycin, and polymyxins, heavy metals (*copA*, *czcA*, *merA*), biocides (*qac*), and MGEs (IncF-FIC and IncI1 plasmids, class 1 integron intI1_1). Exposure to anthropogenic sources (i.e., rivers downstream WWTP and agricultural plots fertilized with sludge and/or animal manure) within the species´ location was extracted from SMART-E.

Results: The 16S rRNA gene was quantified for quality control. ARGs were detected in 95.2% (20/21) of birds: 81.0% (17/21) were multidrug-resistant and 4.8% (1/21) were ARGs-negative. The most prevalent ARG classes were beta-lactams (90.5%,19/21), vancomycin (85.7%,18/21), sulfonamides (76.2%,16/21) and polymyxins (*mcr-1*,71.4%,15/21). Quinolone and MLSB genes were not detected. Heavy metal genes were found in 85.7% (18/21) of PCs: copper (*copA*; 85.7%,18/21), cadmium/zinc/cobalt (*czcA*;57.1%,12/21), and mercury (*merA*,9.5%,2/21). IncI1_repI1 was found in 76.2% (16/21), and intI1_1 33.3% (7/21) of PCs. All samples were biocide- and IncF-FIC-negative. No significant correlation between ARG prevalence and anthropogenic sources was identified.

Conclusions: We detected high vancomycin and polymyxin prevalences (last-resort antibiotics against nosocomial infections), heavy metal genes (that co-select ARGs), and intI1_1 (a DNA environmental pollutant and anthropogenic impact proxy). We highlight PCs as environmental contamination indicators in high mountain ecosystems, and suggest resistance markers for future epidemiological studies. Co-funded: EU's Horizon 101136346 EUPAHW.

P-014 Ecological Environmental? AMR Surveillance: How anthropogenic factors influence the spread of antimicrobial resistance in Catalonian wildlife.

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Background: Antibiotic resistance is often viewed as a problem affecting humans and domesticated animals who consume antibiotics. However, wildlife—though seemingly isolated—also experiences the consequences of human antibiotic use. Anthropogenic impacts on the environment significantly contribute to the spread of antimicrobial resistance (AMR), an often-neglected form of pollution.

Objectives:

1. To detect and characterize antimicrobial resistant genes in bacteria from wildlife from Catalonia, as a proof of concept for wildlife-based environmental AMR surveillance.

2.To identify patterns and potential hotspots of AMR-positive wildlife linked to anthropogenic environmental sources.

3. To demonstrate visually communicate AMR surveillance data in support of One Health monitoring, surveillance and policy making.

Methods: Rectal or cloacal swab samples from 310 individual wildlife collected in Catalonia between 2017-2021, were PCR-tested for antimicrobial resistant bacteria and genes. Using ArcGIS to map AMR gene presence and AMR-PCR-positive prevalence by wildlife category. ArcGIS was used to map the presence of AMR resistance gene Extended-Spectrum Beta Lactamase (ESBL), carbapenem (CARB)-, colistin (COL)-, tetracycline (TET)-, erythromycin (ERY)-resistance) and AMR-PCR-positive prevalence by animal category. Samples were geolocalized at municipality level.

The SMART-E dashboard was used to identify anthropogenic sources of AMR pollution, including downstream rivers affected by wastewater treatment plant (WWTP) discharge points and crop areas where manure and sludge are applied. Correlations between AMR prevalence and anthropogenic emission sources were analyzed. at the municipality level for municipalities with $n > 10$ (Spearman's rank correlation, $p < 0.05$).

Results: We identified (132/289; 45.6%) AMR-PCR-positive individuals (ESBL=113, TET=11, ERY=3, TET+ERY= 4, COL=1). A positive correlation was detected between downstream rivers affected by WWTP discharge points and AMR prevalence (Spearman's $\rho = 0.394$, $p = 0.05$).

Conclusions: Our results identified environmental areas of high and low AMR prevalence in Catalonia, their link to anthropogenic influence, and potential as AMR hotspots, which will inform future epidemiological and wildlife-based environmental AMR surveillance studies.

POSTERS THEME 2: RESEARCH TOPICS AT THE FRONTIERS OF ONE HEALTH

P-015 **Bacterial antibiotic resistance in West Africa drinking water sources – an invisible threat.** Adriano A. Bordalo[1,2], Ana Machado[1,2]

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Bacterial resistance in drinking water sources of West Africa represents a critical public health crisis, where the confluence of poverty, inadequate sanitation, and antibiotic misuse, particularly related to malaria and diarrhea treatments, creates a perfect storm. Our research exposed the alarming prevalence of antibiotic-resistant bacteria in water sources, mostly shallow hand-dug wells, in rural communities where the majority of population lives. The findings were stark. High levels of fecal contamination, indicated by elevated counts of E. coli and enterococci, confirmed that 80% (n> 1,000) of the water used by the communities was contaminated with human and/or animal waste, therefore unfitted for human consumption. More disturbingly, the systematic isolation of multidrug-resistant strains of these and other bacteria, demonstrated widespread resistance to common antibiotics like ampicillin, tetracycline, and sulfamethoxazole. The significance of our work lies in its direct linkage of environmental contamination to clinical threat. Indeed, the aquatic environment acts as both a reservoir and a breeding ground for resistance. Factors such as the widespread, unregulated sale of antibiotics and the lack of sewage treatment allows resistant bacteria to develop in the human gut and then cycle back into the water supply. The findings highlight that in these settings, drinking water is not just a vehicle for classic waterborne diseases like cholera, but also a potential source of untreatable infections. In conclusion, the research provides irrefutable evidence that the drinking water in many West African communities is a major pathway for the spread of antibiotic resistance, and underscore the urgent need for integrated solutions under the umbrella of the One Health concept, that combine improved water sanitation with stricter controls on antibiotics prescription/availability, to avert a future where common infections become fatal.

P-016 Beyond Antibiotics: Long-term exposure to sodium nitrite could select for antimicrobial resistance in *Salmonella* Typhimurium.

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Background: The impact of foodborne illnesses on Public Health has been aggravated by the emergence of antimicrobial resistant (AMR) bacteria. *Salmonella enterica*, a major pathogen in the food industry, has shown the ability to develop resistance to antimicrobials beyond antibiotics.

Sodium nitrite is a preservative commonly used in meat products to extend shelf life and help guarantee Food Safety. However, the potential for its continuous use to contribute to resistance, as observed with antibiotics, remains unclear.

Objectives: This work evaluates the effect of sodium nitrite on the emergence of resistant variants in *Salmonella* Typhimurium populations and identifies the genes related to the development of resistance phenotypes.

Methods: An adaptive laboratory evolution assay (ALE) was performed using five evolution lineages by exposing *S*. Typhimurium to a sub-inhibitory concentration of sodium nitrite for 30 days. Isolates were characterized phenotypically by determining their minimum inhibitory concentration (MIC) against the preservative and analyzing their growth fitness in the presence and absence of the antimicrobial through kinetic modelling. Finally, isolates exhibiting increased resistance were sequenced to identify their genetic changes.

Results: Results demonstrate that evolved *S*. Typhimurium strains exhibited an increase in MIC by 20-70% for sodium nitrite, compared to the parental strain. Furthermore, growth kinetic analysis provides evidence that these evolved isolates possess enhanced fitness at 150 mg/L of nitrites, showing a shorter lag phase compared to their parental strain. Genotypic characterization revealed common mutations in genes such as *ubiB* (flavin mononucleotide reductase), *rrlH* (23S ribosomal RNA), and *flhA* (flagellar biosynthesis protein).

Conclusions: This study suggests that *S*. Typhimurium can develop resistance to sodium nitrite after prolonged exposure *in vitro* through specific mutations in genes related to metabolism (*ubiB*), protein synthesis (*rrlH*) and motility (*flhA*). Further study of the causes and potential impacts of these resistances on Food Safety is required.

P-017 Hepatitis E virus transmission within two Dutch pig farms.

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Background: Hepatitis E virus (HEV) is a zoonotic pathogen that can cause hepatitis in humans, with genotype 3 mainly linked to the consumption of contaminated pork. Domestic pigs are considered the main reservoir in the Netherlands, where a high prevalence of viremic pigs has been reported at slaughter. Farm management practices may influence HEV transmission dynamics and the infection status of pigs at slaughter, thereby affecting public health risks.

Objectives: This study aimed to investigate HEV transmission on Dutch pig farms.

Methods: Longitudinal sampling was conducted on one farrow-to-finish and one finisher farm in the Netherlands between 2025 and 2026. Two pig batches per farm were followed at 3-5 time points until slaughter (farrow-to-finish: 5 sows with 3 piglets each; finisher: 8 pens). Individual fecal swabs, pooled pen droppings, and environmental swabs were tested for HEV RNA using RT-PCR.

Results (preliminary): On the farrow-to finish farm, HEV fecal shedding in batch 1 was first detected at 15 weeks of age (13.3% individual samples; 0% pooled), peaked at 19 weeks (93.3% individual; 100% pooled), and declined at 24 weeks (25% pooled). Sampling of batch 2 is ongoing at the time of abstract submission.

On the finisher farm, batch 1 remained HEV negative at all time points. In batch 2, fecal shedding was first detected at 18 weeks (62.5% pooled) and decreased at 21 weeks (37.5% pooled). Environmental swabs collected after cleaning and disinfection were HEV positive in 37.5% of pens prior to batch 1, but negative prior to batch 2.

Conclusions: HEV fecal shedding was only observed during the growing-finishing phase on both farms. Detection of HEV RNA in the environment after cleaning highlights the importance of hygiene measures to reduce viral persistence and within-farm circulation. Serological analysis and genomic sequencing will be used to confirm infection status and more accurately trace these transmission pathways.

P-018

Characteristics of *Vibrio* spp. strains possessing a *fosG/fosC*2-related fosfomycin resistance glutathione transferase-gene – a growing concern for aquacultures?.

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Background: *Vibrio* bacteria are ubiquitous in marine and estuarine environments and it is expected that climate change will create increasingly good conditions for them to flourish in. They can carry, acquire and transfer different antimicrobial resistances (AMR). We identified a *fosG/fosC*2-related fosfomycin resistance glutathione transferase-gene in 43 *Vibrio* spp. strains from Europe and Asia. Fosfomycin-resistant *Vibrio* spp. have not yet gotten much attention, but may be of increasing importance in the future.

Objectives: To determine genetic variation in *fos*-gene derivates with respect to its impact on the fosfomycin phenotype.

Methods: Pulsed-field gel electrophoresis (PFGE) was performed with the restriction enzymes S1 and Sfi1. We tested for phenotypic antimicrobial resistances to 24 substances with agar disc diffusion according to CLSI standards. Long-read whole-genome sequencing (WGS) was performed using Oxford Nanopore Technologies (ONT). The *fosG/fosC*2-related fosfomycin resistance glutathione transferase-gene was confirmed by PCR.

Results: Interestingly, the phenotypic resistance testing revealed a high fosfomycin tolerance in all tested *V. cincinnatiensis*, while all other species showed a low tolerance. No link between plasmids and the location of the fosfomycin resistance gene was found. In total, thirteen variants of the *fos*-gene were identified. Notably, different gene variants were found to cause either a resistance or susceptible phenotype while exhibiting the same amino acid sequence. This means that besides the *fos*-gene other factors also contribute to the phenotypic resistance.

Conclusions: *Vibrio* spp. strains resistant to fosfomycin have the possibility to become a detriment to aquacultures worldwide and can thus affect the food chain, local ecosystems and consumer health. Especially with the climate change of water bodies worldwide. Further investigation is needed to specify why the same amino acid sequence can result in phenotypic resistance for some strains while not for others.

P-019

Higher resistance without major fitness costs: evolutionary outcomes of ampicillin and gentamicin selection in *Salmonella* Typhimurium.

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Background: Antimicrobial resistance (AMR) can reshape bacterial physiology, influencing tolerance to environmental stresses, persistence, and virulence. Resistant variants of foodborne pathogens may exhibit cross-protection to stresses while retaining or even enhancing virulence. However, phenotypic outcomes depend on the specificity, number, and functional impact of acquired mutations, leading to distinct adaptive trajectories.

Objectives: To compare resistance levels, mutational patterns, and growth fitness in *Salmonella* Typhimurium LT2 (SeT) RVs evolved under both constant and increasing doses of ampicillin (AMP) and gentamicin (GEN).

Methods: Adaptive laboratory evolution (ALE) was conducted for 10 days with AMP and GEN under two selective regimens: constant sublethal doses (0.5× the minimum inhibitory concentration, MIC; Assay 1), and stepwise increasing concentrations (increased 1.85-fold per day; Assay 2). RVs were isolated from independent lineages (n=3 per antibiotic under constant exposure; n=5 under increasing exposure). MICs were determined by broth microdilution, and whole-genome sequencing (WGS) identified mutations and their functional associations. Growth kinetics were assessed by optical density measurements to estimate maximum growth rates (μmax).

Results: All RVs showed increased MICs compared with SeT. Under Assay 1, AMP and GEN resistance increased 4- or 8-fold. In contrast, Assay 2 produced markedly higher resistance, reaching 16- to 256-fold for AMP and up to 16-fold for GEN. WGS revealed fewer, target-specific mutations in Assay 1 RVs, whereas Assay 2 RVs accumulated more mutations linked to metabolic functions, suggesting broader physiological adaptation. Growth curve analysis showed μmax values largely comparable to SeT, with only occasional slight reductions.

Conclusions: Stepwise increasing antibiotic exposure selected higher resistance levels and broader genomic adaptations than constant sublethal exposure. Despite these differences, most RVs showed growth rates similar to the parental strain, indicating limited fitness costs. The frequent occurrence of metabolism-related mutations in RVs with higher MICs suggests physiological adaptations that may influence stress tolerance, persistence, and virulence, warranting further investigation.

P-020 Exploring the zoonotic potential of antimicrobial-resistant Clostridium perfringens isolated from poultry: a preliminary study.

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Background: *Clostridium perfringens* (*Cp*) is a Gram-positive, anaerobic, spore-forming bacterium commonly associated with necrotic enteritis in poultry, causing intestinal infections and considerable economic losses. The ability of *Cp* to produce endospores enables long-term environmental persistence and dissemination through soil, water, animal feed and foodstuffs. Moreover, *Cp* is frequently isolated from poultry meat implicated in foodborne outbreaks in humans, representing a relevant public health concern.

Objectives: In this context, the present study aims to investigate antimicrobial resistance (AMR) in *Cp* from a One Health perspective, considering the increasing involvement of this microorganism in human gastrointestinal infections.

Methods: Between 2023 and early 2026, 118 *Clostridium spp.* strains were isolated by standard microbiological methods from multiple organs collected during poultry necropsy. Identification was performed by MALDI-TOF. Antimicrobial susceptibility testing was carried out using the broth microdilution method. Results were interpreted according to CLSI guidelines or, when unavailable, to EUCAST breakpoints.

Results: MALDI-TOF analysis confirmed 60/118 isolates were *Cp*. The AMR profiles revealed variable resistance rates. Resistance was most frequently observed to tilmicosin (90.32%) and lincomycin (51.61%), followed by bacitracin (38.71%), tiamulin (37.10%), tylosin (35.48%), valnemulin (24.19%), doxycycline (20.97%), penicillin (19.35%) and ampicillin (11.29%).

Conclusions: Although most of the antibiotics investigated are not classified as critically important for human, the resistance patterns should not be overlooked. From a One Health perspective, these findings highlight the need to monitor AMR in animal pathogens, as resistance bacteria and genes may be transmitted to humans either directly through contact with animals or indirectly through the consumption of animal-derived products. Further studies are required to characterise the resistance genes involved and to evaluate their potential dissemination along the food chain.

P-021

Evolution of *tet(W)*: Selection, Recombination-Driven Dissemination, and Post-Transfer Synonymous Codon Optimization.

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Background: The ribosomal protection gene *tet(W)* is a widely distributed determinant of tetracycline resistance across diverse bacterial taxa and environments. It belongs to a monophyletic family of at least 12 gene classes that confer resistance by preventing tetracycline binding to the ribosome. Its frequent association with mobile genetic elements suggests extensive horizontal gene transfer (HGT), yet the structure of donor–recipient networks of this gene transmission, and the relative roles of selection and recombination in its evolution remain incompletely understood.

Objectives: This study aimed to reconstruct the evolutionary history of *tet(W)* by examining genetic diversity, recombination, selection, and synonymous codon usage across allelic variants from multiple bacterial species and genera, with emphasis on human and animal pathogens, using a globally representative dataset.

Methods: A total of 161 *tet(W)* sequences were retrieved from GenBank, curated, and aligned using ClustalX. Homologs were identified via megaBLAST with a CARD reference sequence. Genetic diversity, selection, and polymorphism were assessed using MEGA, DnaSP, PAML, and HyPhy. Genetic recombination was assessed using RDP4, GARD, SplitsTree, and phylogenetic methods. Codon usage adaptation was evaluated using codon adaptation index optimization and exact binomial testing.

Results: *tet(W)* showed high sequence conservation (92.3%), strong transition bias, and low synonymous nucleotide diversity ($\pi s = 0.01064$). Neutrality tests indicated an excess of rare variants, while episodic diversifying selection was detected at three codons. Fourteen conserved regions partially overlapped known functional motifs in this gene. Linkage disequilibrium analyses suggested moderate intragenic recombination, and combined analyses revealed extensive interspecies and intergeneric transfer of *tet(W)*. Codon optimization supported post-transfer synonymous codon adaptation in *Streptococcus suis*.

Conclusions: *tet(W)* evolution is dominated by purifying selection and interspecies recombination, with its transmission occurring through complex, multidirectional networks. Post-transfer synonymous codon adaptation of *tet(W)* in specific hosts may contribute to the persistence and global dissemination of tetracycline resistance.

P-022 Selection of glutaraldehyde-resistant genetic variants of *Salmonella* Typhimurium after repeated lethal treatments.

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Background: Cleaning and disinfection procedures (C&D) are essential in the food industry to control contamination by pathogens such as *Salmonella* spp. Exposure to antimicrobial agents may drive the emergence of resistance (growing under pressure) or tolerance (surviving lethal treatment). While extensively documented for antibiotic resistance, adaptive responses to industrial biocides such as glutaraldehyde remain insufficiently characterized.

Objectives: The purpose of this study was to determine whether cyclic exposure to lethal glutaraldehyde concentrations can lead to the emergence of resistant genetic variants (RVs) in *Salmonella enterica* Typhimurium (SeT).

Methods: An adaptive laboratory evolution assay (ALE) was conducted in five evolutionary lineages (SeT_GL_1-SeT_GL_5). Initially, the parental SeT was subjected to a lethal treatment: 8,000 mg/L of glutaraldehyde for 15 min. Survivors were recovered, grown, and re-exposed, repeating this cycle daily for ten days. One colony per lineage was selected and evaluated for glutaraldehyde resistance, determined by Minimum Inhibitory Concentration (MIC), and for glutaraldehyde and heat tolerance, based on survival following lethal treatments. Then, whole-genome sequencing (WGS) was performed to identify mutations on RVs.

Results: All RVs demonstrated a significant increase ($p < 0.05$) in glutaraldehyde tolerance, exhibiting approximately 2 $\log_{10}$ less inactivation than SeT under the same lethal treatment. Additionally, all RVs showed a two-fold increase in MIC, reaching 9,600 mg/L. No significant differences in thermotolerance were observed. WGS identified mutations in genes related to cell motility (*cheZ*, *fliM*, *flhB*), transporters (*ycjE*), metabolism (*rfbJ*), and virulence (*traS*, *sifB*). Co-occurring mutations within each RV prevent attributing the phenotype to a specific genetic change or a group of changes; therefore, functional validation is required.

Conclusions: Repeated short-term exposures to high glutaraldehyde concentrations, mimicking industrial applications, can lead to the selection of RVs with enhanced biocide tolerance and resistance. This adaptation could compromise the efficacy of C&D, highlighting the need for optimized protocols to prevent the emergence of biocide-resistant pathogens.

P-023 Wastewater surveillance of antibiotic resistance genes and bacteria in hospital effluents.

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Background: Wastewater surveillance is becoming a standard technique for the surveillance of pathogens and antimicrobial and virulence-related genes at population scales. However, there are few studies showing a direct relationship between clinically relevant resistant genes and bacteria and those detected in waste-waters.

Objectives: This study aims at characterizing carbapenem-resistance genes and bacteria in hospital wastewaters and compare them to clinical and isolates from the same waters.

Methods: We obtained 12 wastewater samples along 2 years which were subjected to metagenome sequencing. Carbapenem-resistant clinical isolates in the week previous to water sampling were subjected to whole genome sequencing and the same procedure was applied to isolates obtained after culturing wastewater concentrates.

Results: We assembled 895 genomes (MAGs) from wastewater samples, with a high prevalence of aquatic bacteria, such as *Aliarcobacter* and *Aeromonas* species. We obtained complete genomes from 174 clinical and 145 environmental isolates. Clinical isolates were rich in *Escherichia coli* and *Klebsiella pneumoniae*, whereas environmental ones were more diverse, with a mixture of aquatic and clinical species, but low prevalence of *Aliarcobacter* and *Aeromonas* species. We identified 16,456 ARGs (average 457 per sample) with a high prevalence of efflux pumps, followed by beta-lactamases. Among these, ESBLs (mainly of the OXA family in wastewaters and CTX-Ms, SHVs and SGMs in clinical samples) and penicillinases were the most abundant resistance genes. Wastewaters shared only 34% ARGs with clinical isolates whereas 44.5% were found in wastewaters (metagenomes or isolates) exclusively. About 16% of the total ARGs were only found in clinical isolates, but these included the most clinically relevant.

Conclusions: Hospital wastewaters are rich in ARGs also present in clinical samples but they include a large proportion of exclusive ARGs. Thus, they are potential reservoirs for further dissemination of resistance but they do not represent an accurate picture of current ARGs in the hospital.

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P-024 Circulation of Crimean-Congo Hemorrhagic Fever Virus (CCHFV) in wild ungulates in the Community of Madrid, 2022-2025

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Background: Crimean-Congo haemorrhagic fever (CCHF), caused by an RNA virus is a widely distributed disease transmitted mainly by *Hyalomma* spp. ticks. Although infected animals remain asymptomatic, they develop a transient viremia capable of infecting feeding ticks, thereby contributing to viral maintenance in nature. Serological surveys worldwide have detected CCHFV antibodies in numerous wild species, with ungulates showing the highest seroprevalence. Thus, wildlife plays a key epidemiological role and represents an indirect risk to human health. In Spain, CCHF is considered an emerging zoonosis, with 20 confirmed human cases and six fatalities reported since 2013. In this context, continuous epidemiological surveillance is essential to understand viral circulation and assess potential public health risks.

Objectives: The aim of the present study was to evaluate CCHFV circulation in wild ungulates including Iberian ibex, red deer, fallow deer, wild boar, and roe deer-in the Community of Madrid between 2022 and 2025.

Methods: Antibodies against CCHFV were analyzed in a total of 162 liver exudate samples using a commercial ELISA (IDvet, France). Statistical analyses were performed using WINPEPI version 11.65 and IBM SPSS Statistics version 29.0.2.0.

Results: Of the 162 samples analyzed, 49.3% (95% CI: 41.3-57.3) tested positive. All animal species showed at least one seropositive individual, with prevalence ranging from 31.2% (95% CI: 14.1–55.6) to 76% (95% CI: 56.6–88.5), the latter observed in fallow deer, which showed significantly higher values. Significant differences were detected between years ($p = 0.013$), including a marked decrease in 2025 ($p = 0.006$). Seroprevalence also varied significantly among sampling locations.

Conclusions: These findings confirm active CCHFV circulation in wild ungulates in the Community of Madrid, with fallow deer showing the highest exposure. The heterogeneous distribution observed suggests localized endemic areas and highlights the importance of ongoing wildlife surveillance to better assess the potential risk to human health.

P-025 Molecular evidence of *Leishmania infantum* circulation in non-traditional wildlife hosts from Central Spain.

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Background: Leishmaniosis is a vector-borne disease caused by protozoan parasites of the genus *Leishmania* and transmitted by sandflies. In Europe, domestic dogs are the main hosts; however, infections have been increasingly reported in wild mammals, including carnivores, ungulates, lagomorphs, rodents and bats. The role of non-traditional wildlife hosts in the maintenance and transmission of *Leishmania* spp. remains insufficiently investigated in Central Spain. Systematic surveillance is essential to clarify parasite circulation, identify potential reservoirs, and support evidence-based control strategies.

Objectives: This study aimed to assess the presence of *Leishmania infantum* infection in wild ungulates, wild carnivores and bats from the Madrid Region using ear skin samples, and to evaluate their potential involvement in parasite circulation in natural ecosystems.

Methods: Between 2024 and 2025, 200 wild mammals from various municipalities in the Madrid Region were sampled. Species included bats, foxes, raccoons, cervids, wild boars, carnivores, and other wild mammals. Ear skin samples were analyzed by real-time PCR (qPCR) to detect *L. infantum* DNA.

Results: *L. infantum* DNA was detected in 6/200 animals (3.0% prevalence, IC 95%: 1.38-6.39), including four red foxes (*Vulpes vulpes*), a roe deer (*Capreolus capreolus*) and a Vietnamese pig (*Sus scrofa domesticus*). All other species tested negative.

Conclusions: These findings indicate that several wild mammal species, particularly red foxes, a roe deer and a Vietnamese pig, harbor *L. infantum* infection in Central Spain. Detection in red foxes and roe deer aligns with previous reports from Europe, including Spain, suggesting that these species may contribute to parasite maintenance in endemic areas. Although the role of suids in *Leishmania* spp. epidemiology remains unclear, this finding suggests that peri-domestic or non-traditional hosts could participate in local transmission cycles. While the epidemiological significance requires further investigation, wildlife surveillance improves understanding of parasite circulation and supports integrated control strategies within a One Health approach.

P-026 Kanamycin Resistance Does Not Necessarily Compromise Virulence in *Salmonella* Typhimurium.

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Background: Antimicrobial resistance (AMR) is a major One Health threat. *Salmonella enterica* is a leading cause of foodborne illness and has developed resistance to antibiotics used in human and veterinary medicine, including kanamycin (KAN). However, it is unclear whether resistance-associated genetic changes compromise virulence remains unclear.

Objectives: This study aimed to determine whether adaptive acquisition of KAN resistance alters virulence in *Salmonella* Typhimurium LT2 (SeT) and to identify genetic changes potentially underlying the observed phenotypes.

Methods: KAN-resistant variants (RVs) were generated by adaptive laboratory evolution (ALE) through stepwise exposure to increasing KAN concentrations, from 0.085× to 40× the parental minimum inhibitory concentration (MIC). Five independent lineages were evolved in parallel. After confirming resistance acquisition, RVs were whole-genome sequenced (Illumina) to identify mutations associated with resistance. Virulence was assessed using a *Galleria mellonella* infection model. Inocula were prepared from standardized cultures and injected into the hemocoel (10 µL per larva) at two doses (10^4 and 10^5 CFU/larva). Larvae were incubated at 37 °C, and survival was determined at 24, 48, and 72 h post-infection. Each condition included three independent experiments (n = 10 larvae per experiment) and a PBS-injected control group.

Results: ALE produced five KAN-RVs. All RVs carried mutations in *fusA* and, except SeT_KAN1, with additional mutations in genes related to heme biosynthesis. In *Galleria*, virulence was attenuated in four RVs, reaching approximately 53–81% of the parental strain (SeT) virulence, whereas SeT_KAN4 maintained parental-level virulence, indicating that KAN resistance can arise without an obligate virulence cost.

Conclusions: KAN resistance acquired through ALE showed lineage-dependent effects on virulence in *S.* Typhimurium. The recurrent involvement of *fusA* and heme-related genes highlights candidate pathways linking antibiotic adaptation and host-pathogen fitness, which should be validated in follow-up functional studies.

P-027 Survival of Listeria monocytogenes and Salmonella Typhimurium in edible insects and impact of microbial interactions in a "one health" perspective.

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Background: In recent years, insect farming has experienced unprecedented growth. Absence of Salmonella spp. and Listeria monocytogenes is mostly reported for reared insects, though high level of natural background microbiota is generally described.

Objectives: This study evaluated pathogens survival in powdered insects, as well as diversity of total microflora, using conventional and molecular microbiology, and mass spectrometry.

Methods: Two matrices, Tenebrio molitor larvae and Hermetia illucens flours, were analyzed for their total flora using conventional enrichment and plating methods, Matrix Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry and metagenomic (DNA extraction and sequencing of bacterial rRNA 16S amplicons). Samples were artificially inoculated with of L. monocytogenes or Salmonella Typhimurium and pathogens survival in flours stored at 5 and 20°C was followed by direct plating on selective agar. Total flora was screened for inhibitory activities toward pathogens using both deferred antagonism and drop tests.

Results: Results highlighted presence of a rich total flora, in particular entomopathogen bacteria, and pathogens for humans. Isolates identified as Paenibacillus thiaminolyticus and Micrococcus luteus exhibited inhibitory activities against *L. monocytogenes* and *Salmonella*. Standardized inactivation kinetics revealed persistence of both pathogens cultivable cells during extended periods of more than two months.

Conclusions: In conclusion, a complex set of interactions may explain rare pathogen detection in edible insect flours, including a combination of low initial contamination levels, decrease of the population in stored flours, and inhibitions due to bacterial interactions.

The combined Maldi-tof and metagenomic approaches gave us a global picture of background microflora, in relation with their impact on human and insect health, in a "one health" perspective. It enabled us to better understand its evolution and possible impact on pathogens behaviour in insect flours. Moreover, the extremely abundant microflora and the presence of entomopathogen bacteria raises questions about farming practices, from an animal welfare perspective.

P-028 Description of a new resistance conferring SXT/R391-like ICE in Vibrio parahaemolyticus.

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Background: This study emphasises the monitoring of antimicrobial resistance (AMR) in Vibrio species to detect the emergence of clinically important AMR. It has been demonstrated that Vibrio species carry AMR of clinical importance, which can be transmitted within the genus and to other bacterial species. Vibrio species are naturally occurring waterborne bacteria, some of which can cause severe disease or outbreaks in animals and humans. As environmental bacteria, they are well-suited as indicators for AMR surveillance in aquatic reservoirs associated with food products.

Objectives: To describe the SXT/R391-like ICE and its possibility of transferring AMR.

Methods: Bacterial typing was conducted using mass spectrometry fingerprinting, determination of the analytical profile index, and PCR-based amplification and analysis of the species-specific toxR and hemolysin genes. Whole-genome sequencing was performed using Illumina and Oxford Nanopore Technologies. Antimicrobial susceptibility testing was conducted using both agar disk diffusion and broth microdilution assays.

Results: During a routine inspection of imported seafood in Germany in 2024/2025, *V. parahaemolyticus* (25-VB00034) was isolated from a shrimp retail sample. WGS revealed various acquired AMR, including $bla_{\text{VIM-71}}$, which was located on chromosome 1. 25-VB00034 has been shown to be resistant to beta-lactams and other antibiotics, but lacks carbapenem resistance. The AMR region resembles ICEValChn1833 that was recently described in *Vibrio alginolyticus*. However, ICEVpaChn25-VB00034 is ~27kb larger. Apart from AMR, genes coding for a type-IV secretion system associated with conjugative transfer were also detected. Filter mating confirmed that this ICE is transmissible to *Escherichia coli*. Phenotypic evaluation of the *E. coli* transconjugants revealed non-wildtype phenotypes against certain antibiotics but still no resistance to the tested carbapenems. Chromosomal integration of ICEVpaChn25-VB00034 was determined in the *prfC* gene. Further interspecies/genus transmission of this MDR-conferring ICE can be expected, potentially contributing to a further spread of AMR.

Conclusions: ICE may substantially contribute to a spread of AMR in *Vibrio* spp.

P-029 Seroprevalence of emerging zoonosis among exposed workers as a tool of One Health surveillance: an occupational medicine perspective.

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Background: Seroprevalence studies of emerging zoonoses among workers with high risk of occupational exposure to animals may provide valuable insights into virus circulation and potential transmission dynamics.

Objectives: To investigate the seroprevalence of the orthomyxovirus influenza D virus (IDV), the arenavirus Lassa virus (LASV) and the protoparvovirus Tusavirus (TuV), among livestock workers in Southern Italy, in 2023-2024, and to compare the results with those of a control group from the same geographical area.

Methods: Serum samples from 140 cattle workers and 60 controls were tested by hemagglutination inhibition and virus neutralization (VN) assays for antibodies against IDV D/660 and D/OK lineages. LASV seroprevalence was screened in 251 livestock workers by ELISA, and positive samples, along with a subset of negative samples, were subsequently evaluated using a pseudovirus-based VN assay. Additionally, 114 livestock workers and 30 controls were analyzed for TuV-specific IgG by ELISA.

Results: Overall, among cattle workers, 43% (60/140) were positive for at least one IDV lineages, with all but one positive result confirmed by the VN assay. The control group was tested only for the D/660 lineage and showed a seroprevalence of 65% (39/60). Five samples were positive for LASV by ELISA but were not confirmed by the VN assay. For TuV, one livestock worker (1%) and two samples from the control group (6.7%) tested positive.

Conclusions: These findings underscore the relevance of indirect diagnostic assays for monitoring workers occupationally exposed to zoonotic risk, as a part of the One Health surveillance approach. As suggested by the IDV results, differences in seroprevalence between exposed workers and the general population might be interpreted as a shift from zoonotic transmission to an acquired capacity for human-to-human transmission, potentially posing a major panzootic threat. In this context, occupational medicine can play a key role in identifying and intercepting these changes.

P-030 Free-living amoebae as environmental reservoirs of carbapenem-resistant bacteria in hospital wastewater.

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Background: Antimicrobial resistance (AMR) is a major global health concern, with carbapenem-resistant bacteria (CRB) posing a critical threat due to limited therapeutic options and high associated mortality. Hospital wastewater (HWW) is an important environmental reservoir of AMR, containing antibiotics, metals, disinfectants, and other contaminants. Free-living amoebae (FLA) can internalize bacteria, facilitating the persistence and dissemination of these microorganisms.

Objectives: This study aimed to investigate the role of FLA as hosts of CRB in hospital wastewater and to characterize FLA populations and its microbiome, and the phenotypic and genotypic antimicrobial resistance profiles of FLA-associated CRB.

Methods: HWW samples were filtered to isolate FLA populations using non-nutrient agar plates. Viable CRB were recovered from the FLA microbiome by plating treated FLA cultures on SuperCarba medium. The diversity of FLA and their associated bacterial communities was assessed by high-throughput 18S and 16S rRNA amplicon sequencing. CRB were isolated and antimicrobial susceptibility testing was performed to determine its resistance phenotypes. Whole genome sequencing (WGS) and analysis was conducted on these CRB isolates to identify antimicrobial resistance genes (ARGs) and other genetic resistance determinants.

Results: Some FLA that were identified are *Vermamoeba vermiformis*, and *Naegleria* spp. Several CRB, including *Pseudomonas* spp. and members of the Enterobacterales, were isolated from within FLA. These isolates exhibited multidrug-resistant phenotypes, with resistance to multiple antibiotic classes. WGS analyses showed a high prevalence of ARGs conferring resistance to β-lactams and aminoglycosides, as well as genes encoding efflux pumps and resistance to metals, particularly mercury and arsenic.

Conclusions: Hospital wastewater hosts FLA carrying CRB with diverse phenotypic AMR profiles. Whole-genome analyses revealed ARGs, efflux pumps, and metal-resistance genes matching observed resistances. Environmental pressures likely promote persistence of these resistant consortia, highlighting the need for amoebae monitoring and targeted control in antimicrobial resistance surveillance.

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P-031 InFlame: Counter-acting the pandemic potential of flaviviruses: addressing virus-host interactions and defence strategies to design new therapeutics against WNV and DENV.

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The InFlaMe project (Grant Agreement No. 101191725) aims to improve preparedness for future flavivirus epidemics, particularly dengue virus (DENV) and West Nile virus (WNV), while enhancing the European Union's leadership in antiviral research and therapeutic innovation through an integrated One Health approach. The emergence and spread of flaviviruses are determined by complex interactions between humans, animals, vectors, and environmental changes. InFlaMe therefore brings together multidisciplinary expertise ranging from virology, immunology, epidemiology, structural biology, genomics, and climate science.

InFlaMe aims to gain new insights into the molecular and immunological determinants of DENV and WNV infection severity and identify potential viral, host genetic, and immune risk factors associated with severe disease. The study and characterization of humoral and cellular immune responses will enable the selection and functional analysis of monoclonal antibodies and T cell signatures relevant to protection and pathogenesis. In addition, interactions between viruses and host proteins will be analyzed in parallel to enable the rational design and synthesis of new host-targeted antiviral inhibitors, accelerating the discovery of therapies through advanced screening and structural methodologies.

One of the main objectives is to establish integrated surveillance between humans, animals, vectors, and the environment in order to obtain an overview of the epidemiological situation for WNV and DENV and the strains circulating among the actors involved. Climate and vector competence analyses will provide data on the role of vectors in virus spread and how environmental changes influence the epidemiology of flaviviruses in Europe.

By bringing together European research communities and infrastructures, InFlaMe will strengthen coordinated preparedness, foster innovation pathways from discovery to application, and promote sustainable One Health surveillance and response systems. Ultimately, the project aims to reduce the burden of flavivirus diseases and position Europe at the forefront of antiviral research and epidemic preparedness.

P-032 CSIC MICROBIOME-HUB: Building an integrated One Health framework through cross-ecosystem microbiome science.

Moreno-Arribas, M.V.; Logares, R., CSIC MICROBIOME-HUB

The One Health paradigm recognizes the interdependence between human, animal, plant, and environmental health and calls for integrated, cross-sectoral approaches to address global challenges such as infectious diseases, antimicrobial resistance, food security, and environmental change. Microbiomes are increasingly recognized as key biological connectors across these domains. They are major reservoirs of biodiversity and biomass in soils, oceans, plants, animals, and humans, and they support essential functions including nutrient cycling, carbon sequestration, ecosystem resilience, host physiology, immune regulation, pathogen resistance, and metabolic balance. These interconnected microbial systems can be understood as part of a broader “One Health microbiome,” shaped by ecological interactions, shared microbial taxa, and cross-domain transmission processes. However, despite this integrative role, microbiomes remain insufficiently incorporated into coordinated One Health research strategies, governance frameworks, and infrastructure planning.

To address this gap, **Conexión-MICROBIOMA CSIC (CSIC MICROBIOME-HUB)** has been established as a coordination initiative designed to align microbiome research with a systemic One Health perspective. The initiative promotes integration across human, animal, plant, food, and environmental microbiomes, fostering collaboration between disciplines, institutions, and sectors. Its main objective is to create a shared scientific and infrastructural ecosystem that enables microbiome research to contribute more effectively to prevention, surveillance, and intervention strategies.

A central component of the initiative is the **MICROBIOME Catalogue**, designed to map and connect resources across ecosystems. This catalogue integrates information on research groups, datasets, biobanks, repositories, experimental platforms, technological infrastructures, and analytical capabilities, providing a structured overview of available resources and gaps. By linking knowledge generation, infrastructure, and data governance, the catalogue aims to support coordinated research, enhance interoperability, strengthen training and capacity building, and facilitate translational applications in health, food systems, and the environment.

By linking science, infrastructure, and policy, Conexión-MICROBIOMA provides a framework for advancing microbiome research from fragmented disciplinary efforts toward a more integrated One Health approach.

P-033 The Hunt One Health pathfinder -an animal metagenomic cohort for One Health research.

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Background: Human and animal health are closely linked, and microorganisms circulate between species through direct contact or indirect via the environment. While harmless in one host, it may cause disease in another. Understanding faecal material is key to understand these interactions. The Hunt One Health project aimed to initiate One Health-focused studies on companion and production animals in Norway.

Objectives:

- Establish a large-scale fecal sample and metadata collection from animals owned by HUNT4 participants
- Develop and validate pipelines for high-quality DNA extraction and deep shotgun metagenomic sequencing of fecal card samples
- Generate a reusable sample biobank and a metagenomic data repository
- Enable integrative analyses by linking animal metagenomic data with HUNT4 human health and demographic data
- Establish guidelines and principles for active sharing of samples and biodata

Methods: A citizen-science–based sampling strategy enabled collection of >3000 fecal card samples from dogs, cattle, sheep, horses and pigs. A short survey captured metadata. Pilot studies were conducted to identify the best suitable DNA-extraction protocol(s) that provided the highest sequence quality and data reusability from these samples. All samples were processed and subjected to deep shotgun next-generation sequencing. Resulting datasets and metadata were curated and incorporated into a project repository for controlled sharing with research groups.

Results: Pilot testing identified a robust extraction workflow for fecal card samples. Biological samples are stored in the NVI Biobank. The resulting mNGS datasets exhibit sequencing depth and technical consistency to support microbial, functional, and pathogen-focused analyses.

Conclusions: The HUNT One Health project represents one of Norway's most comprehensive fecal metagenomic repositories for companion and production animal. By combining large-scale citizen-science sampling and metagenomic sequencing, it provides a unique infrastructure for cross-species microbiome research. Geographic overlap with the HUNT4 human cohort enhances potential for integrative One Health research, including microbial exchange, shared exposures, and antimicrobial resistance across humans and animals.

P-034 Enhancing diagnostic capacities for Crimean-Congo hemorrhagic fever virus: results of an external quality assessment in veterinary laboratories.

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Background: Crimean-Congo hemorrhagic fever virus (CCHFV) is the most widely distributed tick-borne pathogen in the world and represents a major threat for public health. Effective surveillance in animals and ticks is essential for disease prevention and control. The MediLabSecure (MLS) and OneHealthSecure (OHS) projects, funded by the European Commission, aim to strengthen One Health preparedness and response capacities against vector-borne diseases in 22 countries across the Mediterranean, Black Sea and Sahel regions. A training program was implemented in 2022-2023 to reinforce CCHFV diagnostic capacities of beneficiary laboratories combining hands-on diagnostic training with a subsequent external quality assessment (EQA) exercise.

Objectives: To evaluate the molecular CCHFV diagnostic capacities in veterinary laboratories belonging to the MLS/OHS network.

Methods: Nineteen veterinary laboratories from 18 non-EU countries participated in the EQA. The evaluation panel consisted of eight blind samples spiked with different dilutions of inactivated CCHFV. To simulate routine testing conditions, several matrices commonly processed in veterinary laboratories, including sheep blood, liver tissue and tick homogenates, were used. Laboratories were provided with extraction and PCR positive controls, as well as reagents and kits to perform the recommended real-time RT-PCR protocol (https://doi.org/10.1089/vbz.2011.0770).

Results: All the laboratories successfully applied the requested PCR protocol and submitted their results within the established deadline. In addition, three laboratories analysed the panel using their own protocols. Overall performance was highly satisfactory since 89.5% of the laboratories correctly identified 100% of the samples.

Conclusions: This study represents the first CCHFV proficiency test specifically targeting veterinary laboratories. Only one previous EQA had been conducted in 2011 but it was limited to human diagnostic laboratories. The results demonstrate that most veterinary laboratories of the network possess the infrastructure and technical expertise required for reliable detection of CCHFV genome. Furthermore, the training strategy implemented proved to be highly effective in enhancing CCHFV diagnostic capacities of participant labs.

P-035 Occupational Health Surveillance of Tick-Borne Diseases within a One Health Perspective.

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Background: Tick-borne diseases (TBDs) represent an emerging concern within the One Health framework. Health surveillance of workers occupationally exposed to tick-borne pathogens (TBPs) could serve as a tool for the early and prompt diagnosis of TBDs with subacute or chronic manifestations and for monitoring the local circulation of TBPs within a One Health perspective.

Objectives: To assess the contribution of occupational health surveillance in identifying subacute or chronic infections caused by *Borrelia burgdorferi* sensu lato (s.l.) and *Coxiella burnetii* among workers with a potential occupational exposure to tick bites.

Methods: University workers, including veterinarians, agronomists, and geologists, with potential exposure to tick bites, were enrolled in 2023–2024 in the occupational health surveillance programme. Serum samples were collected and tested for anti-*Borrelia burgdorferi* IgG by enzyme-linked immunosorbent assay (ELISA), with confirmation by immunoblot, and for anti-phase I IgG and anti-phase II IgM and IgG against *Coxiella burnetii* by indirect immunofluorescence assay (IFAT). Seropositive workers underwent a second-level evaluation including a neurological examination and echocardiography.

Results: Out of 63 enrolled workers (median age 49.0 years; median job seniority 14.0 years), 16 reported previous tick bites (25.4%) and 13 reported having found ticks on their clothes (20.6%) during working activities. Overall, 4 workers (6.3%) were immunoblot-positive for *Borrelia burgdorferi* s.l., whereas 2 (3.2%) were IgG-positive for *Coxiella burnetii*, with antibody titres consistent with past infection. Second-level diagnostic evaluations were negative.

Conclusions: The occupational health surveillance protocol appears to be effective in intercepting hidden cases of *Borrelia burgdorferi* s.l. and *Coxiella burnetii* infections, providing insights into the circulation of these pathogens and potentially representing a crucial component of a broader One Health approach. Future results of the monitoring programme are also expected to highlight the usefulness of occupational health surveillance to detect subacute or chronic cases of Lyme disease and Q fever.

P-036 Twenty-five years of Danish antimicrobial resistance surveillance: linking indicator E. coli and zoonotic bacteria from broilers and cattle.

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Background: The Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP) celebrates its 30-year jubilee in 2026. DANMAP was established to monitor antimicrobial use (AMU) and antimicrobial resistance (AMR) in bacteria from human and domestic-animal populations. The programme has monitored AMR in three major categories of microorganisms: i) human and animal pathogens, ii) zoonotic bacteria, and iii) indicator bacteria from animals. The latter are ubiquitous in their reservoirs and can develop AMR in response to selective pressure and participate in events of horizontal transfer of resistance genes. *Escherichia coli* is commonly the indicator organism of choice, and the occurrence of AMR in *E. coli* from healthy food-producing animals at slaughter has been reported in DANMAP since its beginning. Similarly, AMR levels in the zoonotic bacteria *Salmonella enterica*, *Campylobacter jejuni* and *Campylobacter coli* recovered from the same animal populations have been part of DANMAP since its inception.

Objectives: This study aimed to assess if and how the AMR profiles of indicator *E. coli* reflect over time shifts in AMR occurring in zoonotic bacteria within an animal population.

Methods: In this study, we characterized the phenotypic resistance profiles of both indicator and zoonotic bacteria monitored in the Danish domestic populations of cattle and broilers at slaughter between 2000 and 2025. The analysis included indicator *E. coli*, *C. jejuni* and *C. coli*, and was performed separately for broilers and cattle.

Results: The findings illustrate the relationship between AMR trends in indicator and in zoonotic bacteria in broilers and cattle, highlighting both the instances where *E. coli* represented a valid indicator and those where the trends were unmatched, suggesting that alternative indicators should be considered in the future of AMR monitoring.

Conclusions: We have illustrated the value of *E. coli* as an AMR-indicator organism in the context of One Health AMR surveillance.

P-037 Zoonotic tuberculosis in Spain: first integrative study at national level.

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Background: Zoonotic tuberculosis (zTB) is a form of human tuberculosis acquired from an animal source, mainly caused by *Mycobacterium bovis* and *M. caprae*. In Europe, zTB is relatively rare with 171 notified cases in 2024, being Spain the country that reported the most zTB cases and is the second highest bovine tuberculosis prevalence within the EU countries. However, it has never studied at national level whether zTB cases are related to the animal TB outbreaks.

Objectives: To improve the surveillance and control of zoonotic tuberculosis in Spain through a One Health approach.

Methods: The first step of the project was to conduct a retrospective study (2018-2022) using different sources and databases with human and animal TB information in order to map the cases of zTB. Statistics for qualitative and quantitative variables (cases, sex, age, location of lesion, etc.) were used and temporal and geographic patterns were evaluated.

Results: Data analysis showed that only 32.3% (n=6,098) of all autochthonous human TB cases were reported at mycobacterium species level. Of these, 4.3% (n=249) were caused by *M. bovis* and *M. caprae*. Patients were mostly Spanish, median aged >55, with a strong male predominance and over 50% extrapulmonary cases.

Geographically, *M. bovis* zTB predominated in N/NW Spain, even though these areas are officially declared as bovine TB free and were historically milk-producing regions. Conversely, *M. caprae* cases in Central/SW Spain and Barcelona overlapped with the higher prevalence of bovine TB and goat population density.

Conclusions: The reported zTB rate in Spain is higher than previous reports and likely underestimated. While its association with current bovine TB prevalence remains unclear, the median age of patients points toward ancient infections. Upcoming genomic studies will further investigate potential transmission chains. Finally, the study's success relies on the collaboration between public and animal health institutions, and the national and regional authorities.

P-038 Superbugs in a One Health perspective: Similar resistance patterns and sporadic interspecies clustering among human and animal isolates from Suriname.

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Background: Antimicrobial resistance (AMR) is a public health threat, with humans and animals serving as reservoirs. Transmission between these domains poses risks, however, in Suriname there is limited data on AMR which makes the extent of spread unclear.

Objective: Comparison of antimicrobial susceptibility patterns of indicator *E. coli* and molecular relatedness of resistant *E. coli*, *K. pneumoniae* and methicillin-resistant *Staphylococcus aureus* (MRSA) isolates from hospitalised patients, and non-hospitalised patients (n-hp) and animals.

Methods: We collected 289 indicator *E. coli* isolates from non-hospitalised patients and 323 from cattle, pigs and poultry, using non-selective culture. Antimicrobial susceptibility was determined by broth microdilution. Additionally, 233 resistant isolates (carbapenemase- and/or ESBL-producing *K. pneumoniae* and *E. coli*, and MRSA) obtained via selective culture from hospitalised patients, non-hospitalised patients and animals were analysed by cgMLST.

Results: Indicator *E. coli* from animals and non-hospitalised patients showed highest level of resistance to the same six antimicrobials. The cattle *E. coli* population showed the highest susceptibility (97%), followed by pigs (61%) and poultry (42%).

cgMLST analysis of resistant *K. pneumoniae* identified three interspecies clusters: Two small clusters (both one non-hospitalised patient/animal carrier) and one large, hospital-dominated cluster with single animal and non-hospitalised patient isolates. For *E. coli*, two small interspecies clusters involved poultry and non-hospitalised patients, while one large cluster comprised 13 animal isolates and one non-hospitalised patient. MRSA isolates from non-hospitalised patients and animals were unrelated.

Conclusions: The antimicrobial susceptibility of indicator *E. coli* populations from non-hospitalised patients and animals is similar. Albeit, the molecular comparison of the resistant isolates from hospitalised patients, non-hospitalised patients and animals only showed sporadic similarities and source-dominated clusters, suggesting no regular transmission or shared sources of bacteria or their genes/plasmids. These findings indicate minimal molecular overlap between patients, non-hospitalised patients and animals, suggesting that prevention efforts should mainly focus on human-to-human transmission, especially in health care settings.

P-039 **Neuraminidase-based cross protection against H5N1 in Humans.** Iván Sanz-Muñoz[1], Carlos J. Ciria-Gil[2], Alejandro Martín-Toribio[1], Marina Toquero-Asensio[1], Javier Sánchez-Martínez[1], Carla Rodríguez-Crespo[1], Marta Hernandez[1], Ahmed Mostafa[3], Jose M. Eiros[1], Luis Martinez-Sobrido[3], Aitor Nogales[2,4*].

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Background: The global situation surrounding the highly pathogenic avian influenza (HPAI) H5N1 virus is increasingly concerning, marked by widespread outbreaks across wild birds, poultry, and various mammalian species. Moreover, HPAI H5N1 strains exhibiting genetic markers associated with mammalian adaptation have been identified, raising significant public health and pandemic preparedness implications. Neuraminidase (NA) is a key surface antigen of the influenza virus that, despite its relevance, has historically received less attention than hemagglutinin (HA) in serological studies and vaccine design.

Objectives: We analyzed the presence and magnitude of NA-specific antibodies (Abs) in human sera collected over ten influenza seasons, before and after the 2009 pandemic, using three representative genotypes (B.3.13, D1.1, and EA) of the circulating H5N1 clade 2.3.4.4b. *Our aim was to characterize baseline anti-NA and anti-HA cross-reactive Ab levels, and evaluate the effect of seasonal vaccination in the induction of these Abs.*

Methods: A retrospective study was performed evaluating the presence of Abs inhibiting NA activity in 749 paired serum samples (total 1498 samples), collected either prior to vaccination (T1) or 28 days post-vaccination (T2) with the seasonal inactivated influenza vaccine, using the Enzyme-Linked Lectin Assay (ELLA). In parallel, we assessed the humoral response to HA using hemagglutination inhibition (HAI), ELISA, and luciferase-based microneutralization (MN) assays.

Results: Anti-NA Abs were detected across all three genotypes analyzed. Moreover, seasonal vaccination elicited a modest yet consistent increase in anti-NA Ab levels, particularly from the 2009–2010 season onward, coinciding with the introduction of the A(H1N1)pdm09 pandemic strain. HAI titers were generally low or undetectable in most serum samples. Nevertheless, ELISA confirmed the presence of HA-reactive Abs, although it remains unclear whether these Abs target conserved HA epitopes.

Conclusions: Our findings reinforce the evidence that NA contributes significantly to influenza immunity and that its assessment should be systematically integrated into vaccine effectiveness studies. The induction of anti-NA Abs, even in the presence of limited HA responses, could has implications for the design of broader and longer-lasting vaccines.

P-040 From Field to Facility: A Practical Solution for Advancing One Health Rabies Surveillance.

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Background: Rabies is a fatal zoonotic disease of significant challenge at the human-animal-environment interface. Widespread under-reporting with surveillance deficits and low testing rates generate uncertainty around case numbers, especially in high-risk areas. To address this issue diagnostic approaches that are robust and operationally feasible within diverse settings are required. Pre-analytical specimen handling is a notable critical limiting factor restricting diagnostic accessibility particularly in low-resource and remote areas.

Objectives: The objective of this study was to evaluate the ability of PrimeStore® Molecular Transport Medium (PS-MTM) to inactivate rabies viruses as a practical solution to bridge the methodological gap between rabies field sampling and implementation of modern diagnostic tools.

Methods: Brain tissue inoculated with CVS-11 rabies virus (RABV) was incubated with PS-MTM for different times and at various buffer concentrations to evaluate the effect on virus infectivity using a cell culture assay. In parallel, preservation of viral RNA and compatibility with downstream molecular diagnostics were evaluated using a RT-qPCR.

Results: All samples treated with PS-MTM demonstrated complete loss of virus infectivity with sample-to-buffer ratios as low as 1:1 after at least 3 minutes. Detection of RABV RNA was unaffected, with minimal impact on cycle threshold values compared to untreated controls confirming consistent analytical performance and RNA stability suitable for downstream molecular testing. Extraction platform comparison showed earlier amplification with mean Ct values of 2-3 cycles lower with Maxwell® extracted samples.

Conclusions: The use of transport media with demonstrable RABV inactivation capabilities represents a practical pathway to strengthen integrated surveillance by enhancing occupational health protections from field to laboratory. The removal of biosafety barriers expands specimen referral pathways by enabling decentralized testing in molecular laboratories lacking high-containment infrastructure. Improved rabies diagnostic capacity across networks will facilitate timely data sharing across sectors, more reliable epidemiological data and accelerate progress toward global rabies elimination goals.

P-041 Occupational Exposure to Tick-Borne and Zoonotic Pathogens: Implications for One Health Surveillance and Prevention in Southern Italy.

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Background: Tick-borne diseases (TBDs) represent an emerging public health concern, particularly among outdoor workers exposed to rural and peri-urban environments. Occupational exposure to ticks and zoonotic pathogens is influenced by environmental, climatic, and work-related factors, highlighting the relevance of a One Health approach.

Objectives: This study aimed to assess the seroprevalence of tick-borne pathogens (TBPs) in outdoor workers in Apulia (southern Italy), identify occupational risk factors, and investigate the presence and distribution of ticks in working environments

Methods: A total of 232 outdoor workers were enrolled. Serum samples were tested for antibodies against *Coxiella burnetii* by indirect immunofluorescence assay (IFAT), and against *Borrelia burgdorferi* sensu lato, *Rickettsia conorii*, and *Francisella tularensis* using chemiluminescent immunoassays (CLIA), with immunoblot confirmation for *B. burgdorferi*. Environmental tick sampling was performed using dragging and flagging techniques, followed by morphological identification and molecular analysis for pathogen DNA detection.

Results: Overall, 53% (123/232) of workers were seropositive for at least one TBP. IgG antibodies against *C. burnetii* were detected in 45.2% of subjects, with 2.16% also IgM-positive; one case showed IgG titres >1:1024, suggestive of chronic Q fever. Seroprevalence was 16.8% for *R. conorii*, 3.4% for *F. tularensis*, and 0.86% for *B. burgdorferi*. Tick bites were significantly associated with seropositivity ($p<0.001$). Compared with a control group, workers showed a significantly higher seroprevalence for *C. burnetii* ($p<0.001$). Among 217 collected ticks, DNA of *Rickettsia* spp. and *Ehrlichia* spp. was detected, while *C. burnetii* was not identified.

Conclusions: Outdoor workers in southern Italy show high exposure to zoonotic pathogens, particularly *C. burnetii*, likely driven by occupational and environmental factors. Environmental investigations indicate that pathogen circulation is shaped by local ecological conditions and work-related practices, while the absence of *C. burnetii* in ticks suggests alternative transmission pathways that should be considered in risk assessment frameworks.

P-042

An environmental surveillance network for zoonotic pathogens in surface water: A case study on Avian Influenza. Nikki Thie[1], Daisy Spoelman[1], Sean Visser[1], Leonie Ran[1], Robert-Jan ten Hove[1], Marieke de Cock[1]

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Background: The health of humans, animals, and the environment are closely interconnected. Changes in these relationships—such as through ecosystem alterations, urbanization, or climate change—increase the risk of (emerging) zoonotic pathogens. While current surveillance systems mainly focus on human and animal disease cases, a broader One Health approach is essential for monitoring emerging infectious risks. Environmental surveillance, particularly in surface water, is a valuable addition, as pathogens can persist and remain infectious in water. An effective surface water monitoring network will enable the early detection of zoonotic pathogens and provides insight into their circulation and transmission routes, supporting timely preventive measures. As a first step in developing such a network, we have conducted a case study with monthly detection of highly pathogenic avian influenza viruses (HPAIV) in various surface waters in the Netherlands.

Objectives: Enhancing the detection and monitoring of (emerging) zoonotic pathogens by implementing and improving surface water surveillance for HPAIV as a part of a One Health strategy.

Methods: During fall and winter of 2025-26, we deployed passive samplers and collected 0.5L grab samples on a monthly basis from eight selected surface water sites. Samples were screened for avian influenza as well as specifically the H5-subtype using PCR. PCR-positive samples were then sequenced to further identify the detected subtype(s).

Results: We regularly detected avian influenza in the collected surface water samples, however the prevalence and frequency of detected was highly dependent on the specific sites and sampling method. H5-specific AIV was rarely detected by PCR, likely due to the diverse mix of AIV-subtypes present in surface water, as was revealed by genetic sequencing.

Conclusion: Surface water surveillance for zoonotic pathogens, such as AIV, offers valuable insights into the prevalence, diversity, and temporal dynamics of the virus.

P-043 Protective and redox modulation induced by low and high molecular weight chitosan in *Apis mellifera* larvae against *Paenibacillus larvae.*

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Background:

Honey bees are essential for biodiversity and crop production. American foulbrood (AFB), caused by *Paenibacillus larvae*, threatens bee health worldwide. Antibiotic restrictions and resistance require sustainable control strategies. Chitosan, derived from chitin recovered from seafood waste, supports circular economy principles. Sustainable AFB control protects bee health, sustaining pollination services that ensure food crop quality and quantity, linking environmental, animal, and human health within a One Health framework.

Objectives:

Characterization of antimicrobial, redox, and developmental responses to low (30 kDa) and high (1250 kDa) molecular weight (MW) chitosan in *Apis mellifera* larvae, and evaluation of its protective efficacy against *Paenibacillus larvae*.

Methods:

Antimicrobial activity of chitosan against *P. larvae* was assessed by microdilution in MYT broth at concentrations ranging from 100 to 1500 ppm. In vitro-reared L7 *A. mellifera* larvae were fed diets supplemented with each chitosan type (100–1500 ppm), and antioxidant enzyme activity (CAT, GST), larval survival and development were evaluated. For infection assays, larvae were inoculated with *P. larvae* spores at half the LD50 dose and treated with chitosan at 500 ppm.

Results:

Chitosan at 30 kDa and 1250 kDa inhibited *P. larvae* growth at concentrations ≥250 ppm. Concentrations ranging from 100 to 500 ppm of both low and high MW chitosan allowed larvae to reach pupation and were suitable for larval diet supplementation. Notably, high MW chitosan at ≤250 ppm reduced larval mortality. Both high and low MW chitosan activated CAT and GST enzymatic activities, suggesting modulation of the antioxidant defense system. A protective effect against *P. larvae* infection was observed, as feeding with 500 ppm of 1250 kDa chitosan significantly increased survival of infected larvae, restoring survival curves to control levels.

Conclusions:

These findings support chitosan as a sustainable strategy for honey bee health management within a One Health framework.

POSTERS· THEME 3: INNOVATIVE SOLUTIONS FOR ONE HEALTH CHALLENGES

P-044 Strengthening laboratory diagnostic capacities in the Mediterranean region to reinforce surveillance of zoonotic arboviruses through a One Health collaborative action.

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Background: The OneHealthSecure project (OHS, formerly MediLabSecure) is a One Health network dedicated to the prevention of vector-borne diseases (VBDs) in 23 countries of the Mediterranean, Black Sea and Sahel regions. One of its priorities is to strengthen preparedness and response capacities for VBDs by enhancing laboratory diagnostic performance. Over eleven years, OHS has developed and implemented a series of training programs aligned with the One Health approach, integrating human and animal virology, and entomology laboratories to promote interdisciplinary collaboration.

Objectives: To describe the OHS training methodology designed to improve diagnostic capacity for zoonotic arboviruses and to promote technology transfer. To achieve excellence in arbovirus diagnosis while fostering harmonization of diagnostic practices among participating laboratories.

Methods and results: Each training program follows a similar structure. Initially, on-site workshops focused on serological and molecular detection of selected arboviruses are organized, combining lectures with hands-on laboratory sessions and transfer of standard operating procedures. This is followed by external quality assessment exercises for virus/antibodies detection in different sample matrices, aimed at evaluating the diagnostic skills of the laboratories. Individualized feedback reports are provided, highlighting performance indicators, strengths and areas for improvement. Finally, a follow-up meeting is organized to collectively review results, discuss challenges and share best practices. Through this methodology, OHS has significantly strengthened laboratory capacities for West Nile, Rift Valley fever, and Crimean-Congo haemorrhagic fever diagnosis. Innovative technologies are also being incorporated into the laboratory diagnostic portfolio, mainly to support pathogen genomic surveillance, with special focus on bioinformatic data analysis. These technologies have been, and will continue to be, transferred to network laboratories over the coming months.

Conclusions: As early detection and characterization of emerging pathogens are critical to minimize animal and human health consequences, the OHS laboratory network is a successful collaborative instrument to update and reinforce the surveillance tools across Mediterranean, Black Sea and Sahel countries.

P-045 RePlas-GT: A novel workflow combining bioinformatic approaches to horizontal gene transfer detection and pathogenicity in prokaryotes.

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Background: Horizontal gene transfer (HGT) allows bacteria to rapidly adapt to new environments by acquiring novel genes, contributing to the spread of antimicrobial resistance (AMR) and virulence genes. Interactions between human bacterial pathogens and AMR bacteria in the environment or animal microbiome can transfer resistance genes to these pathogens, affecting human health. Understanding HGT is therefore critical to develop effective mitigation against AMR.

Objectives: To investigate whether AMR genes present in bacterial genomes are associated with HGT we are developing a workflow for detecting HGT in bacterial isolates, contextualized by their AMR and virulence profile. Our workflow combines established tools to process whole genome short-read sequences, isolate plasmid assemblies, identify resistances and detect HGT.

Methods: Short-read Illumina sequences from *Salmonella* Typhi and *S*. Typhimurium L2 isolates with known plasmids were downloaded from GenBank, trimmed using fastp and asssembled with SPAdes. Downstream analysis was performed using our Snakemake workflow RePlas-GT. Using CheckM2 to assess assembly quality; genomes with <5% contamination were retained. AMR and virulence genes were identified with Abricate using Resfinder and VFDB databases. Plasmid assemblies were identified and extracted using GplasCC. Chromosomal HGT events were detected across samples using Gubbins. Associations between AMR and HGT were determined by overlaying the positions of AMR genes and HGT events.

Results: RePlas-GT identified and reconstructed the IncFII/IncHI2 plasmid in 63% of positive control samples(n=39), and identified *dfrA*1,*sul*1,*sul*2 and *bla*TEM genes in the isolated plasmid assemblies, in agreement with the literature. Two misclassifications occurred in the negative control(n=83). No association was observed between chromosomal HGT events and chromosomal AMR genes in this dataset.

Conclusions: RePlas-GT demonstrated a low false-positive rate for plasmid detection, though sensitivity could be improved. Future work will extend the pipeline to detect HGT within plasmids using SHIP, applying the workflow to investigate associations between HGT, AMR, virulence, and plasmids in *Salmonella* outbreaks in Ireland.

P-046 Innovative One Health Competence-Based Education Using the Bovilis Cryptium ® Vaccine Against *Cryptosporidium parvum*: An Interdisciplinary ULab Project.

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Background: Interdisciplinary competences are essential to address parasitic zoonoses within a One Health framework. *Cryptosporidium parvum*, a major zoonotic protozoan with cattle as the main reservoir, presents an excellent context for integrated training. The recent introduction of the Bovilis Cryptium® vaccine for bovine neonates offers a real One Health scenario that links animal-health interventions with public-health relevance. This U-Lab project represents a teaching innovation integrating Veterinary and Biomedical Sciences students through competence-based active learning.

Objectives: To evaluate the effectiveness of this interdisciplinary educational innovation in enhancing disciplinary, procedural, integrative and transversal competences; to quantify student participation by degree; and to identify significant pre–post improvements while assessing soft-skill development.

Methods: Mixed teams from both degrees worked across four Agile–Scrum sprints to produce posters, videos, and podcasts. The project was designed within the academic setting. MSD Animal Health served exclusively as an external evaluator. Pre–post questionnaires assessed C1 (knowledge), C2 (procedures) and C3 (integration). Paired-sample t-tests ($\alpha=0.05$) were applied to matched responses.

Results: A total of 204 students completed the initial questionnaire and 156 the final one, yielding 96 paired responses (Biomedical: 31; Veterinary: 65). Significant improvements were detected in knowledge competences (C1) in both degrees: Biomedical +1.70 (95% CI [+1.00, +2.40], t=4.967, p<0.001); Veterinary +0.96 (95% CI [+0.32, +1.60], p=0.004). Procedural competences (C2) increased significantly in Biomedical Sciences (mean +10.0; 95% CI [+7.6, +12.3], p<0.001; small n), while Veterinary students showed a significant decrease (mean –2.1; 95% CI [–2.8, –1.4], $p\approx4.2\times10^{-7}$), attributed to greater cognitive complexity in the final item. Integrative competences (C3, post-only) were high (Biomedical: 9.99; Veterinary: 7.15). Teamwork, communication and problem-solving also improved.

Conclusions: This innovation strengthened disciplinary, procedural, integrative and transversal competences. Using a novel vaccine as a real-world challenge increased engagement, interdisciplinary collaboration, and professional readiness, providing a scalable model aligned with One Health principles.

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P-047 Innovative surveillance for marine brucellosis: integrating diagnostics and genomics for epidemiological resolution.

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Background: Marine ecosystems are a critical yet underdeveloped frontier for operational One Health surveillance. Zoonotic pathogens in marine mammals, such as *Brucella ceti*, challenge conventional diagnostic frameworks and require integrated, field-adapted approaches connecting marine ecology, veterinary medicine, and public health.

Objectives: To develop and evaluate a robust, multi-layered surveillance strategy for marine brucellosis that integrates innovative diagnostic and genomic tools for One Health implementation.

Methods: Stranded dolphins along the Western Mediterranean coast (Spain) were analyzed using bacteriological isolation, genus-specific qPCR, serology, whole-genome sequencing (WGS) and pathological assessment. A blocking ELISA was validated using panels of culture-confirmed positive and brucellosis-free reference sera, to refine cut-off thresholds. WGS was applied to identify sequence types (STs) and SNP variation within and between hosts.

Results: Minor diagnostic discrepancies were observed between culture and qPCR, supporting qPCR as a practical screening tool, while proper bacteriological culture methods remain essential for definitive diagnosis. Validation of indirect diagnostics demonstrated improved reliability, comparability, and operational interpretability when used in combination.

By validating a blocking ELISA for use in cetaceans, this study addressed an important gap in marine brucellosis surveillance, where serological assays remain insufficiently validated to support robust interpretation.

WGS identified two sequence types (ST26 and ST49) and showed minimal intra-host SNP variation, supporting genomic stability during systemic infection. Some strains from animals stranded months or years apart differed by only 2–5 SNPs, suggesting persistence or circulation of closely related lineages, whereas others exhibited up to 144 SNPs, reflecting broader phylogenetic divergence. These findings provide an operational genomic framework to support outbreak reconstruction, lineage tracking, and transboundary risk assessment.

Conclusions: These advances position marine brucellosis as a scalable One Health surveillance model that bridges research and field implementation, underscoring the strategic value of integrating marine ecosystems within global health monitoring networks.

P-048 Investigating the beehive microbiome to inform and develop one health probiotics.

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Background: Microbiome One Health is a holistic approach that aims to protect and improve the health and well-being of animals and humans through microbiome-based innovative strategies that promote a global healthy ecosystem (https://doi.org/10.1016/j.soh.2024.10006). This revolutionary ecology-focused is exemplified by the so-called **one health probiotics** (https://doi.org/10.1002/imo2.30), a promising sustainable agrifood solution at the human-animal-agricultural interface.

Objectives: Very recently we have discovered that **honey contains potentially beneficial bacteria** such as lactic and acetic acid bacteria (LAB-AAB) (https://doi.org/10.1186/s40793-023-00460-6). LAB-AAB have previously been associated with plant heath https://doi.org/10.3389/fpls.2022.1047945). Whether they protect beehives and ultimately contribute to the health of animals and humans is an unresolved question.

The **aim of this project** is to investigate and characterize the microbial communities of the beehive as a model to inform and develop one-health probiotics.

Methods & Results: To achieve our main goal we are carrying out the following specific objectives:

(1) **Evaluate the protective role of LAB-ABB in the beehive** following a geno- and pheno-typic characterization of strains that we have already isolated from beehives. Their ability to antagonize bee pathogens and ferment sugars will be determined.

(2) **Determine the immunomodulatory properties of LAB-ABB**. Upon microbial exposure we are monitoring the activation of innate immune responses in our recently developed macrophage model (https://doi.org/10.1080/19490976.2019.1707015). Through transcriptomics and proteomics we will identify potential immunomodulatory markers.

(3) **Develop probiotics for animal and human consumption**. We are planning to design and manufacture probiotic formulations using LAB-ABB strains related to specific biological and physiological traits such as pest-repellent and antioxidant activities.

Conclusions: Microorganisms play a critical role in the closely linked and inter-dependent health of humans, animals and plants. Our project will support this new paradigm by providing new data informing of the tangible possibility of using the microbes that we share with animals (honeybee) and the environment as one health probiotics.

P-049 Integrated Management of West Nile Disease: The "One Health" Model of ASP Ragusa.

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Background: In October 2025, an outbreak of West Nile Disease (WND) was recorded in an equine in Contrada Zinna Fondo, Province of Ragusa. The event occurred during a late autumn period characterized by exceptionally high average temperatures, necessitating the immediate activation of emergency protocols.

Objectives: To analyze the effectiveness of the ASP Ragusa organizational model in managing the outbreak and to define proactive strategies for 2026 in response to climate change.

Methods: Following confirmation by IZS, the Department of Prevention activated its integrated organizational model. The UOC SIAV coordinated targeted pest control using adulticide and larvicide treatments. Simultaneously, through official note, a collective response was requested from all Mayors of the Province for widespread disinfection in urban centers. Entomological surveillance was also strengthened at strategic sites, such as the Port of Pozzallo and wetlands.

Results: 100% of the Municipalities responded with urgent ordinances, ensuring systematic environmental remediation. The synergy between veterinarians, local authorities, and livestock stakeholders significantly reduced the density of the *Culex pipiens* vector, preventing human spillover despite climatic conditions favoring the virus.

Conclusions: This case demonstrates that One Health participatory governance is the only effective defense against emerging arboviruses. For 2026, ASP Ragusa will transition from emergency response to permanent, digitalized prevention, shifting remediation activities to early spring to proactively mitigate the impact of seasonal thermal anomalies.

P-050 Development and validation of a multi-species double antigen ELISA to detect anti-H5 HPAIV antibodies in human and mammalian sera.

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Background: The global spread of Highly Pathogenic Avian Influenza Virus (HPAIV) H5N1 clade 2.3.4.4b requires a One Health approach, having already infected over 50 mammalian species. Recent emergence in dairy cattle and human cases have significantly heightened zoonotic concerns. Antigenic differences between H5 of LPAI and HPAI viruses can influence the sensitivity of currently available serological assays, underscoring the need for ELISAs specifically designed to detect antibodies against H5 viruses of clade 2.3.4.4b.

Objectives: The aim of this study was to develop and validate a safe, versatile, standardized, and specific multi-species double-antigen ELISA (DA-ELISA) based on the recombinant hemagglutinin (HA) 1 domain (rHA1) of H5N1 viruses (H5N1V), clade 2.3.4.4b, useful to monitor AIV H5 exposure in various domestic and wild mammalian populations within an integrated One Health surveillance framework.

Methods: The HA1 domain of an H5N1V clade 2.3.4.4b isolate was expressed in mammalian cells, purified, and used as both the coating antigen and the horseradish peroxidase-conjugated detection antigen. The assay was validated using a panel of 1,204 sera from different species, including humans, wild and domestic animals, previously analyzed through HI and MN. The diagnostic performance was evaluated through ROC analysis to determine the optimal S/P ratio cut-off.

Results: The DA-ELISA demonstrated excellent diagnostic accuracy with an area under the curve (AUC) of 0.998. Using an optimal S/P cut-off of 0.1, the assay achieved diagnostic sensitivity and specificity of 97.1% and 99.5% respectively. Furthermore, the test showed high analytical specificity, with no cross-reactivity observed against a panel of sera positive for other influenza A subtypes (H1N1, H1N2, H3N1, and H3N2).

Conclusions: The rHA1-based DA-ELISA is a robust, sensitive, and, specific tool for detecting anti-H5 antibodies. Its ability to identify infections across multiple species makes it invaluable for large-scale surveillance and rapid outbreak response.

P-051 Detection of autoinducing peptides for the diagnosis *Staphylococcus aureus* infections.

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Background: *Staphylococcus aureus* is a human and animal pathogen responsible for a wide range of infections, capable of disseminating antimicrobial resistance worldwide. Its virulence is modulated by the *agr* quorum sensing system, which produces four types of autoinducing peptides (AIPs 1-4), that could act as diagnostic biomarkers. This work is based on an innovative proprietary approach for which a patent application has been filed.

Objectives: Generation of antibodies targeting native AIPs and their derivative linear forms, and establishment of immunochemical assays for assessing their potential as biomarkers of infection.

Methods:
Haptens mimicking linear AIPs 1-4 were synthetized and conjugated to proteins to be used as immunogens and as ELISA regents. Antibodies were produced for the development of specific competitive indirect ELISAs of 1h 30min. The assays were characterized in terms of assay detectability, specificity, accuracy, reproducibility, precision and robustness.

Results: The developed conjugation method was successful for the immunization and production of antibodies. An ELISA was developed for the detection of linear AIP3 in bacterial medium diluted in PBST (TSB ½) with a LOD of 0.11 ± 0.04 nM and IC_{50} of 6.95 ± 4.49 nM. The cross-reactivity with other AIPs was <0.05%. *S. aureus* bacterial isolates obtained from human respiratory tracts were grown in TSB until a concentration equivalent to $2x10^9$ CFU/mL. AIP3 were detected in bacterial cultures of *agr* III isolates, while no presence of AIP was detected in negative control strains, bringing to light the specificity of this diagnostic method. Significant differences (p=0.0073) were seen between infection and colonization group samples.

Conclusions: The ELISAs developed revealed the potential of linear AIPs as biomarkers of *S. aureus* infections, which can be implemented in rapid and reliable diagnosis in point-of-care devices. The applicability of this method in biological samples could noticeably ameliorate the management and treatment of the disease, reducing the burden of AMR.

P-052 Building Veterinary Capacity in Bosnia and Herzegovina.

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Background: Veterinary capacity building is an essential component of effective One Health systems, particularly where free-roaming dog populations pose zoonotic disease risks. In Bosnia and Herzegovina (BIH), advanced training in veterinary medicine is delivered through anaesthesia and surgery programmes for veterinarians and veterinary technicians. The Veterinary Training Programme (VTP) is delivered as theoretical and practical training at the Veterinary Faculty, bringing together academic and international mentors.

Objectives: To assess the role of a standardised VTP in establishing consistent veterinary practice across BIH, supporting infection prevention and One Health integration.

Methods: This abstract is based on a structured assessment of the VTP implemented between 2012 and 2023, delivered as part of a broader programme combining humane dog population management with veterinary and public education in BIH.

During training, VTP candidates sterilised a high number of free-roaming dogs in the Sarajevo region under supervised operational conditions. Each animal was vaccinated against rabies, registered in a centralised database, and treated in accordance with strict asepsis and antisepsis standards. Following training, participants applied the same standardised clinical procedures in routine veterinary work.

Results: A total of 83 VTP trainings were delivered, including surgical training for 239 veterinarians and anaesthesia training for 252 veterinary technicians, with participants from across the country. Standardised infection control practices improved surgical safety and reduced risks associated with zoonotic pathogen transmission. Integration of rabies vaccination following sterilisation directly strengthened rabies prevention within the wider One Health system - rabies postexposure prophylaxis centre (Sarajevo Canton) reports no rabies cases for 15 years.

Conclusions: The VTP represents an effective One Health solution - by standardising clinical practices across BIH and integrating zoonotic disease prevention into routine veterinary care, the programme strengthened veterinary capacity, supported rabies control, and contributed to public health risk reduction.

P-053 Dog Population Management as a One Health Intervention to Reduce Zoonotic and Public Health Risks. Mia Čeifović Baltić

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Background: Free-roaming dog populations represent a persistent One Health challenge, contributing to uncontrolled reproduction, zoonotic disease transmission, dog bite injuries, and environmental contamination. In Bosnia and Herzegovina, a coordinated, large-scale Dog Population Management (DPM) programme was implemented between 2012 and 2023, initially in Sarajevo and subsequently expanded to approximately 80% of the country. This long-term programme provides an opportunity to demonstrate multisectoral impacts of dog population management on public and dog health within a One Health framework.

Objectives: To assess the long-term impact of a sterilisation-led DPM model on free-roaming dog density and public health risks, demonstrating the role of veterinary services and multisectoral collaboration in sustainable One Health systems.

Methods: The DPM programme combined large-scale Catch-Neuter-Vaccinate-Return (CNVR), sterilisation of free-roaming dogs, rabies vaccination in line with national legislation, routine endoparasite treatment, and systematic data recording. An 11-year longitudinal dataset was analysed, including free-roaming dog population trends, reported dog bite incidents, surgical complication rates, and rabies surveillance indicators.

Results: Between 2012 and 2023, free-roaming dog numbers declined by 85% in Sarajevo City and 70% in the wider canton, corresponding to an average annual reduction of 16-18%. This decline paralleled a reduction in reported dog bite incidents. Data from the Sarajevo Emergency Medical Centre show a decrease in dog bite cases from 948 in 2013 and 947 in 2014 to 240 cases in 2023, representing a 75% reduction over ten years. More than 100,000 dogs were sterilised, with surgical complication rates below 1%. High rabies vaccination coverage was achieved, with no reported rabies cases in the main intervention areas for over a decade.

Conclusions: This evaluation demonstrates that sustained, sterilisation-led DPM delivered through multisectoral collaboration can reduce free-roaming dog populations and associated public health risks while strengthening veterinary capacity. The findings position DPM as a scalable, evidence-based One Health intervention.

P-054 X-ray imaging to assess climate change impacts on coral ecosystems.

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Background: Corals are highly sensitive to environmental stressors and are valuable indicators of climate change. The Columbretes Islands (NW Mediterranean) represent a sentinel site for climate change, where coral populations have been monitored over the last two decades. The Marine Global Change and Conservation group at the Instituto de IATS, led by Dr. Diego K. Kersting, has expertise in marine ecology and coral research, with a focus on long-term monitoring and the effects of environmental change on Mediterranean coral species. I3M develops advanced imaging instrumentation, particularly X-ray-based systems. X-ray imaging has proven to be a powerful non-destructive tool for investigating coral skeletal architecture, growth dynamics, and density variations, providing information to study climate change impacts.

Objectives: This work develops a dedicated computed tomography (CT) system for coral imaging. By integrating advanced imaging with ecological research, the collaboration seeks to obtain quantitative information on coral structure and condition, allowing long-term reconstruction of their response and resilience to environmental change in the context of climate change.

Methods: The first prototype of a CT system has been developed. The setup includes an X-ray source operating up to 75 kV, a high-resolution flat-panel detector, and a motorized rotation stage capable of handling coral samples of varying sizes.

Results: First scans have been obtained using the prototype. The images reveal internal skeletal structures in high detail and enable assessments of structural organization, density distribution, and morphological characteristics. Analyses based on these datasets are in progress and will be presented at the conference.

Conclusions: This work represents an initial step toward establishing a multidisciplinary platform for coral research. The combined expertise of both institutions offers new perspectives on coral research, including their response to climate change and reconstruction of information archived in their skeletons, allowing these responses to be contextualized through time.

P-055 Presenting the Catalogue of Solutions of the AMRHubCSIC: A Multi-disciplinary Resource to Combat Antimicrobial Resistance.

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Background: Antimicrobial resistance (AMR) is a global health challenge that undermines the effectiveness of existing therapies and threatens human, animal, and environmental wellbeing. Addressing AMR requires integrated research efforts across disciplines and effective translation of scientific knowledge into practical solutions within a One Health framework.

Objectives: To present the Catalogue of Solutions developed by the AMRHub of the Spanish National Research Council (CSIC) as a strategic tool to identify, organize, and disseminate research-based solutions targeting antimicrobial resistance.

Methods: The catalogue compiles structured contributions from research groups within the AMRHubCSIC network. Solutions are categorized according to their application domain and stage of development, covering key areas such as prevention, surveillance, diagnosis, and treatment. Each entry includes a concise description of the technology or approach, its scope of application (human, animal, or environmental health), and contact information to facilitate collaboration and knowledge transfer.

Results /Key Content: At present, the catalogue includes solutions spanning prevention, surveillance, diagnostics, and therapeutic innovation. Examples include rapid molecular diagnostic tools for detecting resistant pathogens in clinical and veterinary settings; genomic and informatic platforms for AMR surveillance and resistome analysis; strategies for infection prevention and antimicrobial stewardship; and the development of alternative therapeutic approaches such as novel antimicrobial compounds or bacteriophage-based treatments. These solutions reflect the multidisciplinary expertise of the network and demonstrate its capacity to address AMR from molecular mechanisms to applied interventions across sectors.

Conclusions: The AMRHubCSIC Catalogue of Solutions serves as a dynamic platform to enhance visibility, foster interdisciplinary collaboration, and accelerate the translation of research into practical applications. By structuring and showcasing concrete solutions, it contributes to coordinated and evidence-based responses to antimicrobial resistance at national and international levels.

P-056 Microbial emissions from manure processing: Towards a monitoring framework to protect public health.

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Background: With an increase in manure processing and uncertain risks of microbial emissions for residents, the question arises how to efficiently monitor microbial emissions from manure processing.
Objectives: This study aims to provide initial steps to monitor microbial emissions from pig farms with manure processing in order to assess potential risks to public health.

Methods: Intestinal enterococci (IE) and spores of sulfite-reducing Clostridia (SSRC) were selected to indicate the possible presence of manure-borne pathogens in air surrounding manure processing. Besides sampling manure and air at varying distances upwind and downwind from the manure processing plant, the atmospheric dispersion of IE and SSRC was predicted up to 2000 m by applying a Gaussian plume model.

Results: IE and SSRC were detected in raw manure and in all processed manure samples, except for the fraction treated with a membrane bioreactor. Also in air, IE and SSRC were found in varying concentrations. The modelled indicator concentrations in the air decreased at greater distances from the manure processing plant.

Conclusions: Since IE and SSRC were detected in raw and processed manure as well as in air, it may be concluded that IE and SSRC are suitable indicators for monitoring microbial emissions from manure processing. The Gaussian plume model was used to estimate the emission strength and predict the dispersion of indicators over greater distances. Uncertainties in the estimated emission strength and the predicted concentrations were due to the limited number of measurements, differences in and restrictions of the study locations, and possible influence of farm emissions on the measured indicator concentrations. Model uncertainties can be improved by further research at centralized manure processing plants with a single emission source. These initial steps provide insights into the dispersion of microbial emissions of manure processing and can provide input for a monitoring framework.

P-057 **Data-driven analysis of fine-scale badger movement in the UK.**

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Background: Understanding animal movements at different spatial scales presents a significant challenge as patterns can vary widely from daily foraging behaviours to seasonal migration or territorial movements. This challenge is of general interest because it impacts the ability to manage wildlife populations effectively.

Objectives: The objective of this study, where we focused on European badgers (*Meles meles*), a social species whose movements are important for understanding behaviour and risk of bovine TB in UK cattle, was to explore how badger movement patterns vary both from day to day and over longer periods.

Methods: In this study, we conduct diffusion analysis based on badger movement data obtained from three different regions in the UK (Gloucestershire, Cornwall, and Northern Ireland) and fit a generalised linear mixed-effects model to examine the relationship between variables. We also used a novel application of *extended dynamic mode decomposition* (EDMD) to uncover patterns relating to badger social organisation. By applying our approach to these different populations, we were able to assess its performance across a range of badger densities.

Results: A key result was that in some areas, EDMD clusters matched observed group home ranges, whilst in others, discrepancies likely arose because of population management interventions, such as badger culling.

Conclusions: The methods presented offer a promising approach for studying territoriality and the impacts of management strategies on animal movement behaviour, which in turn may inform wildlife management and policy in conservation and disease control.

P-058 From Science to Policy: Co-developing a Real-Time One Health Early Warning System for Avian Influenza.

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Background: The unprecedented evolution of highly pathogenic avian influenza (HPAI) since 2020 has challenged traditional surveillance systems. Changes in seasonality, geographic spread, and spillover into mammals have highlighted the urgent need for integrated One Health monitoring tools capable of supporting rapid policy decisions.

Objectives: To present the joint experience of a research institute and a national ministry in the co-design, transfer, and operational use of DiFLUsion, a real-time early warning system for avian influenza introduction into Spain.

Methods: DiFLUsion was developed through continuous dialogue between CISA-INIA-CSIC and the Ministry of Agriculture. The system integrates European outbreak notifications, wild bird migratory connectivity data from over 100 risk species, and environmental parameters influencing viral survival. A spatial-temporal risk model generates weekly alerts predicting the probability of virus introduction into specific areas of Spain. The tool operates in real time and provides structured reports and interactive visualization for decision-makers.

Results: Since its implementation in 2021, the system has generated approximately 25,000–30,000 risk alerts per year, providing continuous nationwide coverage. Retrospective validation showed a sensitivity of 85.4% for high-risk alert categories and a specificity of 74.5% at the highest alert level. The system has consistently identified recurrent high-risk areas and atypical seasonal patterns. DiFLUsion is currently used by MAPA as an operational decision-support tool to reinforce surveillance, prioritize control measures, and guide risk-based biosecurity recommendations.

Conclusions: This joint presentation will take the form of a short dialogue between science and policy, illustrating how sustained institutional collaboration can transform epidemiological modeling into an operational One Health decision-support system. DiFLUsion demonstrates that when research and administration co-create tools from the outset, innovation becomes actionable, transferable, and policy-relevant.

P-059 The Spanish Network of High Biosafety Level Laboratories (RLASB) as a Pillar for One Health Preparedness.

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Background: The Spanish Network of High Biosafety Level Laboratories (RLASB) is a Unique Scientific and Technical Infrastructure (ICTS) that integrates two high-containment nodes: CISA-INIA-CSIC and IRTA-CReSA. RLASB strengthens Spain's capacity to detect, confirm, and respond to high-risk biological agents affecting humans, animals and environment. Aligned with the One Health approach, RLASB promotes interdisciplinary collaboration and coordinated responses to emerging health threats. In addition, it contributes to scientific training, innovation in diagnostics and vaccines, and preparedness for biological emergencies.

Objectives: This presentation aims to showcase the two nodes of RLASB. We describe its core functions, operational structure, and recent developments, highlighting its strategic contribution to biosurveillance, emergency preparedness, and rapid response to biological threats.

Methods: We conducted a descriptive overview of organization and operational workflows, including diagnostic capabilities and available facilities through competitive open access. Recent activation events and preparedness exercises were reviewed to assess RLASB's performance and added value.

Results: RLASB provides advanced biosecurity facilities for research, surveillance, and technological development with capacities ranging from BSL-3 to BSL-4 (according to the World Organisation for Animal Health). It supports national and international users by offering specialized services, experimental platforms, and access to high-level biocontainment infrastructures. RLASB has played a key role in early detection and response during recent public health events such as COVID19, supporting national surveillance systems and providing confirmatory testing for pathogens of human, veterinary, and environmental relevance. As an ICTS infrastructure, RLASB develops cutting-edge, high-quality research and acts as a hub for knowledge exchange, technology transfer, and innovation while maintaining a strong One Health perspective.

Conclusions: RLASB represents a robust national infrastructure supporting One Health surveillance and biological emergency preparedness. Its multisectoral structure enhances Spain's capacity to prevent, detect, and respond to high-impact biological risks. All interested entities are encouraged to apply to RLASB's competitive open-access calls.

P-060 IRIDA-ARIES One Health platform for the genomic surveillance of infectious diseases in Italy.

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Background: Public health agencies worldwide are ever more adopting pathogen genomics applied to disease surveillance through its integration in research and infectious disease outbreak control. Real-time production and collection of genomic typing data of samples isolated from cases of infection, food, animals and environment offer the most comprehensive means for monitoring pathogenic populations in circulation.

Objectives: The IRIDA-ARIES project aims to deliver a versatile Information System for the collection of genomic and epidemiological data to enable genomics-based surveillance of infectious disease epidemics, foodborne outbreaks and diseases at the animal-human interface. The system was expected to be intuitive and present results directly to the variety of domain experts involved in surveillance, overcoming information silos.

Methods: IRIDA-ARIES is a combination of two open-source software packages: a personalised IRIDA instance providing a web-based user interface, utilising a Galaxy cluster as a workflow engine for the bioinformatic analyses. Upon upload of genomic reads, a pathogen-specific analysis pipeline is launched automatically, performing a series of typing and clustering operations raising alerts in case of matching genomic profiles. Automation and scaling of the data collection are made possible by use of batch uploads.

Results: IRIDA-ARIES has been well-accepted by all types of users and currently hosts surveillance systems developed for *Listeria monocytogenes*, Shiga toxin-producing *Escherichia coli* (STEC), *Salmonella* and pathogenic *Yersinia enterocolitica*. The platform is used in Italy on a nation-wide scale, connecting independent regional public health systems. Furthermore, upload of sequences from European outbreaks originating from both human (ECDC) and animal/food/feed (EFSA) samples for comparison with national data, allows for integration within an international One Health perspective.

Conclusions: IRIDA-ARIES provides the territory with an instrument of aggregation for systemic risk monitoring, capable of triggering alarms on possible critical situations that might go unnoticed otherwise. The system architecture has proven to be readily scalable and adaptable for a multiplicity of pathogens.

P-061 Ecological risk prioritization of wild birds for HPAI H5N1 surveillance in Panama.

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Background: Highly Pathogenic Avian Influenza (HPAI) H5N1 continues to expand globally, affecting wild birds, poultry, and mammals across the Americas. Panama represents a strategic ecological corridor between North and South America, hosting diverse aquatic and migratory bird assemblages that may contribute to viral maintenance and dissemination. Structured ecological prioritization of wild bird species is essential to optimize surveillance and early detection.

Objectives: To develop a transferable ecological risk framework for prioritizing wild bird groups for HPAI surveillance in Panama, integrating global outbreak evidence, ecological traits, and local spatiotemporal patterns.

Methods: Wild bird taxonomic groups were classified into ecological risk categories based on published evidence of HPAI involvement, viral prevalence, and ecological role in transmission dynamics. A semi-quantitative ecological scoring system was applied (3= primary reservoirs; 2.5= frequent involvement; 2= occasional involvement; 1.5= limited involvement; 1= low involvement). Family-level H5N1 HPAI notification data and eBird observation records were integrated to contextualize ecological relevance and abundance in Panama. Monthly phenological profiles were analyzed to identify seasonal peaks in high-risk groups. Spatial clustering was assessed using Kernel Density Estimation and Getis-Ord Gi* hotspot analysis, while spatio-temporal clusters were identified using SatScan space-time permutation models.

Results: Anatidae and Laridae were classified as high and high-medium ecological risk groups, respectively, consistent with their role as reservoirs and amplifiers. Phenological analysis revealed marked seasonal concentration of high-risk groups during migration and coastal aggregation periods. Kernel Density analysis identified higher densities of high-risk bird observations in coastal areas, particularly around Panama Bay. Getis-Ord analysis highlighted coastal and wetland districts with significant clustering, while preliminary SatScan analyses suggested spatio-temporal patterns consistent with phenological peaks.

Conclusions: Integrating ecological scoring, citizen science data and spatial-spatio-temporal modeling provides a robust framework for risk-based HPAI surveillance in Panama, strengthening early warning capacity in a key biogeographic corridor and supporting One Health preparedness strategies.

P-062 RADAR-PPI: Identifying antimicrobial resistance needs and innovative solutions across animal and environmental sectors.

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Background: Antimicrobial resistance (AMR) is a naturally occurring phenomenon by which microbes no longer respond to antimicrobials mainly due to horizontal gene transfer. The misuse and overuse of antimicrobials across human, animal and agri-food settings have promoted the worldwide emergence and spread of AMR. The additional lack of sustainable antibiotic innovation pipelines and rapid AMR diagnostics preventing broad-spectrum antibiotic usage aggravates the issue, resulting in infections becoming harder to treat. According to UNGA Declaration 2024, AMR is an international public health concern needing a One Health approach.

Objectives: In the framework of the EU-funded RADAR project on value-based cross-border innovation procurement of AMR diagnostics, identify the currently available AMR solutions and understand the feasibility and challenges of adopting AMR innovation across One Health sectors in Europe.

Methods: A grey literature review was performed to identify AMR unmet needs and available solutions across animal and environmental sectors, mainly including global action plans, research agendas and policy briefs. Secondly, an EU survey on animal health and AMR innovation is currently launched and disseminated across relevant stakeholders mapping clinical unmet needs, available solutions, barriers and enablers. All these results will be summarized in a policy brief later this year.

Results: The grey literature review identified common and specific research needs and innovative solutions in the areas of transmission, surveillance, interventions, diagnostics, treatment and risk assessment across food-producing animals, food safety, plant health and the environment. Other areas of unmaterial innovation were found, namely capacity building, data management, communication and awareness raising. While most of these research needs and innovative technologies are better characterized in the animal health domain, regulatory bottlenecks and innovation death valleys may impede their successful uptake.

Conclusions: Further attention and scientific evidence by European institutions and public health initiatives is urgently required to identify AMR innovation needs in the environment through a One Health approach.

P-063 Developing an Early Warning System for Canine Leishmaniasis in Iberia: The PLANET4HEALTH Case Study.

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Background: Zoonotic leishmaniasis, caused by *Leishmania infantum* and transmitted by phlebotomine sand flies, remains endemic in the Mediterranean region, where dogs serve as primary hosts and reservoirs for human infection. In the Iberian Peninsula, canine leishmaniasis (CanL) seroprevalence varies widely, reflecting heterogeneous transmission dynamics. Climate and environmental changes, together with human and animal movements, are expected to expand vector distribution and increase transmission potential.

Objectives: This study aims to co-develop, with veterinarians and other stakeholders, an Early Warning System (EWS) for CanL to support early detection and prevention strategies, protecting both animal and human health.

Methods: The EWS integrates high-resolution hydrometeorological (temperature, humidity, precipitation, soil moisture), environmental, entomological predictors, and CanL data using statistical and machine learning models to identify sand fly seasonality and transmission risk, generating spatial risk maps, short-term forecasts, and projections.

Results: The first operational prototype combines near real-time climate and epidemiological data to create dynamic risk assessments, improving understanding of spatiotemporal CanL risk across the Iberian Peninsula as a scalable, data-driven EWS demonstration. Stakeholder validation is underway to evaluate forecasting accuracy, improve features, and enhance user experience.

Conclusions: This case study, focused on the Iberian Peninsula, advances integrated disease monitoring and proactive leishmaniasis prevention in animals and humans supported by a collaborative One Health approach, with potential for future replication in other endemic regions to support veterinary surveillance and preventive decision-making.

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P-064 Phlebotomine sand fly surveillance, pathogen transmission, and canine sentinels across Europe & Neighbours: the CLIMOS project.

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Background: In Mediterranean countries, phlebotomine sand flies are vectors of *Leishmania infantum* (causative agent of zoonotic visceral leishmaniasis; dogs as main reservoir for humans) and several phleboviruses. Their distributions are expanding due to climate and human-mediated environmental changes.

Objectives: One aim of the CLIMOS project (https://climos-project.eu/) is to characterize climatic and environmental factors driving sand fly presence, abundance, and pathogen transmission across Europe and neighbouring countries, supporting policies to mitigate sand fly-borne diseases (SFBDs) and protect One Health.

Methods: Standardized fieldwork in 2023–2024 across 12 endemic/emerging countries collected data on sand fly distribution, seasonality, feeding habits, and tested vectors and hosts (2023-2025) for *Leishmania* and phleboviruses.

Results: Sand flies were collected in all surveyed countries except the Czech Republic, yielding >66,000 specimens (>35,000 in 2023; >31,000 in 2024) from *Phlebotomus* and *Sergentomyia* genera, dominated by *Larroussius* subgenus. Of 12,369 sand fly pools, 109 tested positive for pan-phleboviruses and 328 for *Leishmania* spp. Blood meal analysis of fed females revealed opportunistic feeding on diverse vertebrates. Of 4,043 canine sera, none were *Leishmania*-seropositive in Istria, northern Spain, or several Israeli districts, but seroprevalence exceeded 30% in Sicily and various Turkish/Spanish provinces; Toscana virus was generally <5%, and Sandfly Fever Sicilian virus exposure was focal (mainly Israel, Portugal, Türkiye).

Conclusions: These findings confirm variable sand fly seasonal patterns and diverse co-circulating *Leishmania* spp. and phleboviruses across sites, with dog infections showing marked Mediterranean clustering and reinforcing their role as One Health sentinels. These entomological, pathogen screening, and serological data will feed predictive epidemiological-climatic models to develop the CLIMOS Early Warning System. This innovative framework will enhance surveillance, risk mapping, and timely, targeted control interventions for SFBDs across Europe and neighbouring regions.

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P-065

OH4Surveillance – Setting Up a Coordinated Surveillance Under the One Health Approach in a Belgian Context.

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Background: OH4Surveillance (One Health for Surveillance) is a 3-year EU4Health-funded initiative aimed at strengthening zoonotic disease surveillance under a One Health approach. Since 2024, Belgium has participated in the 11-country consortium, coordinated by Denmark.

Objectives: To enhance surveillance, early warning, and coordinated responses to emerging zoonotic threats across Europe.

Methods: In Belgium, the project targets three zoonotic pathogens: Highly Pathogenic Avian Influenza (HPAI), West Nile Virus (WNV), and Q fever. Existing HPAI surveillance is expanded with serosurveillance in wild birds, rodents, and foxes, combined with active and environmental virosurveillance. WNV surveillance combines active and passive monitoring of wild birds. Q fever surveillance includes air and dust sampling and rodent investigations in nondairy farms.

Results: During the first two years, efforts focused on capacity building, protocol development, and implementation of surveillance.

For HPAI, one virological infection was detected in 297 healthy wild birds. Serology indicated prior exposure in 1/4 actively sampled and 11/38 passively sampled birds. All 246 passive rodent samples tested viro-negative. In foxes, 33/164 were seropositive and 1/250 viro-positive. Environmental testing was positive in 3/226 fecal and 1/17 dust samples, while feathers, air and water were negative.

In year one, all wild birds tested PCR-negative for WNV; however, Usutu virus was detected in 2/452 actively sampled and 44/201 passively sampled birds. In year two, the **first autochthonous WNV cases ever reported in Belgium** were detected (7/644), and 7/644 birds also tested positive for Usutu virus.

For Q fever, 15/138 air and dust samples from 30 locations tested positive, identifying previously undetected positive farms. Rodent testing confirmed pathogen circulation, with 73/192 spleen samples and 104/319 serological samples testing positive.

Conclusions: The project strengthened zoonotic surveillance in Belgium and improved EU preparedness, demonstrating the value of a coordinated One Health approach for early detection and risk assessment of emerging threats.

P-066 Exploring an alternative non-invasive method for surveillance of carbapenemase-producing bacteria based on OXA-48 detection on swine feces.

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Background: Carbapenems are HPCIA β-lactam antibiotics used in humans for multidrug-resistant infections treatments. Circulation of carbapenemase-producing Enterobacterales (CPE) is becoming an emerging concern on global health. Decision (EU) 2020/1729 compels the monitorization of CP-*Escherichia coli* being frequently performed by bacteriological approaches which may result time and resource demanding. Assessment of complementary tools for OXA-48 harboring-bacteria detection may be of interest in a surveillance framework.

Objectives: This study aims to assess the analytical sensitivity of molecular $bla_{\text{OXA-48}}$ detection on spiked environmental samples and determine its detection performance on field samples (in the framework of the project PID2024-159558OB-I00 funded by MICIU/AEI /10.13039/501100011033 and FEDER, UE).

Methods: A panel of spiked environmental samples were prepared using a serial tenfold dilution of CPE DNA (original concentration: 1x10^7 CFU/mL ≈ 2x10^6 copies/100 µL of extraction). DNA was extracted using DNeasy Blood & Tissue Kit (Qiagen) and a PCR (according to Taalin et al. 2021) was implemented in our laboratory. A total of 227 frozen/refrigerated swine feces (collected in the framework of the Spanish Antibiotic-Resistance Surveillance Program) preserved on surfactant liquid was subjected to $bla_{\text{OXA-48}}$ detection.

Results: Implemented PCR was able to detect 10 copies of $bla_{\text{OXA-48}}$ gene/reaction (12/12 replicates, Ct mean= 36.55) on spiked samples. Molecular detection of $bla_{\text{OXA-48}}$ on swine feces preserved on surfactant liquid was possible in 7 out 227 samples (3,08%).

Conclusions: Our results suggested this molecular detection on environmental samples stored on surfactant liquid could be considered a promising approach for OXA-48 surveillance at farm level, although this method may detect any OXA-48-bacteria, not exclusively *E. coli*. Stability, easier-handling and less-demanding storage conditions are provided for this approach which could facilitate its implementation in surveillance programs as complementary tool. Further studies in different epidemiological scenarios are necessary to determine its sensitivity and specificity in field conditions.

P-067 **Sustainable Algal Polysaccharides for Immune Support in Aquaculture: High-Yield Sonication as an Innovative One Health Tool.**

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Background: Aquaculture urgently needs sustainable strategies to enhance fish health and reduce reliance on antibiotics, in line with One Health principles linking environmental, animal and human well-being. Algal polysaccharides, particularly from seaweeds, are emerging as natural immunomodulators capable of strengthening host defences and improving resistance to infections.

Objectives: This work aimed to develop a green, water-based sonication methodology to obtain polysaccharide-enriched extracts from marine macroalgae and microalgae and to characterize their physicochemical, biocompatibility and antioxidant features as a first step towards their use as immunomodulatory additives in aquafeeds.

Methods: Freeze-dried biomass of *Saccharina latissima* and *Laminaria ochroleuca* (macroalgaes), and *Chlorella vulgaris* and *Dunaliella salina* (microalgaes), was extracted using a probe sonicator with water as solvent at 5 g L^{-1} biomass concentration. Triplicate extractions were performed for each species. Carbohydrate content was quantified using a sulfuric acid–UV spectrophotometric method, antioxidant capacity was evaluated by ABTS and FRAP assays, functional groups were assessed by ATR-FTIR spectroscopy and biocompatibility in primary European seabass isolated leukocytes by mitochondrial activity assay.

Results: The sonication protocol yielded more than 50 of soluble extract from all algal species, with macroalgal extracts reaching carbohydrate contents of approximately 50 mg mL^{-1}, indicating efficient polysaccharide enrichment. All extracts showed promising antioxidant capacity in both ABTS and FRAP assays. ATR-FTIR spectra presented characteristic glycosidic linkage bands for all samples, while macroalgal extracts additionally displayed a peak compatible with β-glucans, suggesting the presence of structures associated with immunomodulatory activity. European seabass isolated leukocytes tolerate well the glucan-enriched extracts.

Conclusions: Water-only sonication proved to be an easy, fast and environmentally friendly extraction strategy for obtaining polysaccharide-rich algal extracts with relevant antioxidant and structural features. These extracts hold strong potential as sustainable antioxidant ingredients in aquaculture, supporting reduced antibiotic use and contributing to One Health-oriented aquatic food systems.

P-068 Bacterial Food Safety – Towards a Holistic Metagenomics Approach.

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Background: Ensuring bacterial food safety across the food chain requires analytical approaches capable of capturing the full microbial landscape. Metagenomic sequencing has promise to be a powerful strategy enabling broad detection of bacteria. Yet, challenges remain in achieving sufficient detection limits, differentiating bacterial DNA from the matrix DNA, identifying cell viability, and dealing with complex background microbiota that vary widely across food production environments. Applying metagenomics methods across One Health domains will expose details on transmission routes, shared reservoirs, and interconnected risks essential for control of foodborne pathogens.

Objectives: We aim to develop a robust and reliable metagenomic workflow that provides broad detection of bacterial hazards across key stages of the food chain, supporting One Health approaches for foodborne disease prevention and management.

Methods: We focus on modification and optimization of critical methodological parameters of both wet lab and dry lab methodology. Pre-sequencing optimizations include efficient and low-bias DNA-extraction, matrix DNA depletion and enrichment of bacterial DNA. Post-sequencing methods seek to identify low-abundant species, to detect the presence of mixtures of strains, and to track strains across multiple samples.

Results: Different methods are being tested, leading to a standardized protocol that can be used for different reservoirs of the food production chain. These reservoirs include samples from primary production, production environment and food, with a high degree of diversity. For matrix DNA depletion and enriching bacterial DNA different techniques were tested, and promising results were obtained with regards to detection limits. Bioinformatics methods studied show the possibility of identification of the same strain through multiple samples.

Conclusions: As analytical pipelines improve, metagenomics has the potential to provide earlier hazard detection, more comprehensive risk assessment, and a holistic understanding of bacterial transmission routes across interconnected ecosystems. This positions metagenomics as a key technology in advancing future-ready, integrated food safety management.

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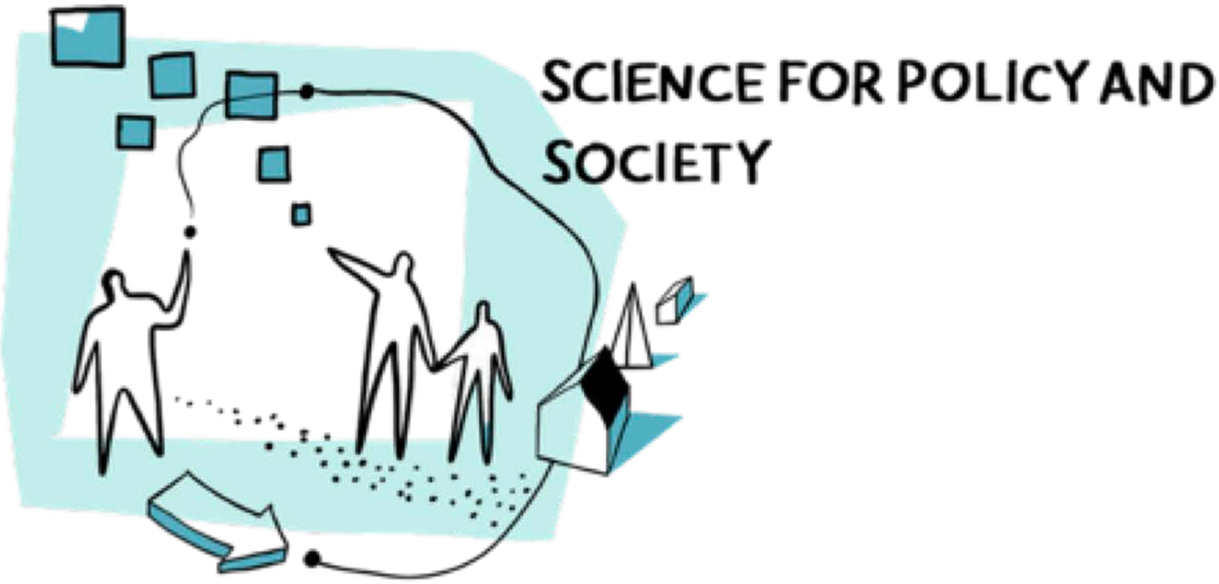

P-069 Epidemiology and economic impact of bovine trypanosomosis in Jawi District, Northwest Ethiopia.

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Background: Bovine trypanosomosis remains one of the most important vector-borne livestock diseases in sub-Saharan Africa, causing substantial production losses and threatening rural livelihoods. In Ethiopia, despite ongoing tsetse control programs, the disease persists and continues to impose significant economic burdens on smallholder farmers, with indirect implications for food security and public health within a One Health framework.

Objectives: This study aimed to determine the epidemiology and economic impact of bovine trypanosomosis in Jawi District, Northwest Ethiopia, and to generate evidence to inform integrated disease control strategies.

Methods: A cross-sectional study design was employed involving parasitological examination of cattle using the buffy coat technique and packed cell volume (PCV) measurement. Structured questionnaires were administered to cattle owners to assess disease-associated production losses and control costs. Descriptive statistics and logistic regression analyses were used to identify epidemiological patterns, while partial budget analysis was applied to estimate economic losses at herd level.

Results: The study revealed an important prevalence of bovine trypanosomosis, with *Trypanosoma congolense* identified as the dominant species. Infection was significantly associated with poor body condition and reduced PCV values, indicating anemia. Economically, the disease resulted in considerable losses due to decreased milk yield, draft power reduction, mortality, and repeated treatment costs, imposing a substantial financial burden on livestock-dependent households.

Conclusions: Bovine trypanosomosis continues to be a major constraint to livestock productivity and rural livelihoods in Jawi District. The findings implicates the need for strengthened, integrated One Health interventions that combine vector control, improved veterinary service delivery, and evidence-based policy support to reduce the disease burden and its wider socio-economic consequences.

P-070 The One Health societal challenges: the case of pesticides use in vineyards.

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Background: Producers in a viticultural area of Northeastern Italy, covering approximately 16,000 ha, aim to qualify food production processes as having low pesticide use through the adoption of a shared masterplan. Pesticide use in this context represents a significant health, economic, social, and environmental concern.

Objectives: To address these societal challenges by framing the proposed masterplan within a "One Health" perspective.

Methods: A SWOT analysis to assess the human, technical, and instrumental resources available within the territory for monitoring pesticide use, evaluating its effects on biota and human health, and generating robust, integrated data to support the masterplan from a One Health standpoint.

Results: Strengths: Identified several institutional actors and data sources relevant to pesticide monitoring: These includes ARPA Veneto (environmental monitoring of water bodies in agricultural areas and tracking pesticide sales and use); the Ministry of Agriculture’s competent bodies (controls within the organic farming framework); the Zooprophylactic Institute (monitoring pesticide residues in livestock, feed, and food, as well as census beehives and honeybee health and welfare as sentinel species); Local Public Health Services for Occupational Prevention and Epidemiology (worker protection and training activities). Weakness: Although monitoring plans are regularly implemented and reported on annual basis, they are not systematically interconnected at the territorial level.

Conclusions: Highlighted both the existing assets and critical gaps in operationalizing a truly integrated One Health approach to pesticide governance within the agri-food sector. Opportunities: demands related to territorial qualification and the sustainability of food products, wine in particular, are fostering a bottom-up adoption of One Health practices. There is a clear need to integrate environmental, animal/food, and human monitoring systems, currently regulated through separate, vertical frameworks. Threats: Official monitoring is not harmonized, transparent, and shared with the local community. Consequently, risk perceived as disconnected from societal needs, thereby undermining trust and weakening institutional accountability.

P-071 A Blueprint for Fostering a One Health Culture: The ICBAS Model of Science Communication and Public Engagement.

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The School of Medicine and Biomedical Sciences (ICBAS), University of Porto (Portugal), has been a pioneer in integrating the One Health approach into academia and society. Since its foundation in 1975, ICBAS has brought together the three pillars of One Health — human, animal, and environmental health — in both education and research, long before the concept was formally established. Nevertheless, despite this longstanding connection, awareness of the full relevance and potential of the concept has not always been straightforwardly accepted by the academic community. This recognition led to the foundation of the **One Health Office** in 2021, with a dual mission: to strengthen the One Health culture within ICBAS, and to promote literacy and engagement across wider society.

The Office, formed by Professors and researchers from medicine, veterinary, and environmental sciences has since developed a **comprehensive communication strategy** combining scientific dissemination, education, and creative outreach. Within the institution, initiatives such as the monthly **"One Health Talks"** and the annual **"One Health PhD Forum"** foster interdisciplinary dialogue and reflection among staff and students, respectively, helping to embed the One Health approach in the academic practice.

Externally, public engagement activities aim to increase societal understanding of the interconnections between humans, animals, and the environment. The **One Health Day celebrations** such as the **Expo One Health**, bring together researchers, policymakers, students, and citizens through interactive exhibits, workshops, and debates. Other relevant initiatives include the **One Health in Schools** program, which introduces younger audiences to One Health principles through hands-on learning at their school, as well as cultural activities as photography exhibitions and film screenings. In 2024, the book publication *One Health: A Contribution from the University* was release, alongside a version for children.

ICBAS demonstrates how universities can cultivate a One Health culture by combining education, participation, and creativity**. This approach bridges** academia and society, offering a **replicable model for promoting interdisciplinary awareness and collaboration.**

P-072 Risk assessment of dredging-induced turbidity on farmed mussel populations in the Gulf of Olbia (Italy) according to One Health approach.

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Background: The Gulf of Olbia (Italy) is characterized by limited hydrodynamic exchange (water renewal time: 8–14 days). It hosts 18 shellfish farms, 10 depuration centers, and 50 ha for clam farming. In 2024, a dredging project involving ~707,626 m^3 of sediments was proposed.

Objectives: To conduct a Health Impact Assessment (HIA) following a One Health approach on potential implications at the ecosystem level and along the food chain.

Methods: Chemical (metals, PAHs, PCBs, organotin compounds) and ecotoxicological data were examined together with hydrodynamic modeling and mapping of sensitive receptors. Exposure pathways of total suspended solids (TSS), light attenuation (Kd), variability in dissolved oxygen (DO) were evaluated.

Results: Sediment analyses revealed the presence of organotin compounds (TBT/DBT/MBT), especially in areas with low circulation. Although toxicity was found to be negligible, TSS peaks associated with dredging may exceed background levels by 2 -4 times during operational phases. Repeated turbidity pulses may accumulate over time, prolonging exposure for benthic communities and aquaculture facilities. Increases in suspended solids of 30–50% can enhance light attenuation (20–40%), reduce the depth of the photic zone, and, under seasonal stratification's conditions, contribute to reductions in DO approaching ecological stress thresholds (<4 mg L^{-1}). The limited water exchange increases the residence time of particles and associated contaminants, raising the likelihood of bioaccumulation in filter feeding mussels and extending exposure along trophic levels.

Conclusions: In low exchange basins, supporting intensive aquaculture, dredging induced turbidity, combined with prolonged residence times, represents the main determinant of environmental health. The HIA highlighted the risks associated with the proposed method. In fact, the monitoring activities might not ensure compliance with environmental parameters and might have negative impacts on production activities and food safety. These critical issues were forwarded to the Health and Environment unit.

P-073 Exploring residents' risk perception of manure treatment.

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Background: Residents living nearby manure treatment plants (MTPs) have communicated odor annoyance and health worries to local health authorities.

Objectives: This cross-sectional study aimed to explore the risk perception of manure treatment by nearby residents.

Methods: A survey was conducted among 15000 people living in the Netherlands. Additionally, 3500 residents living close to MTPs were questioned about manure treatment. Multiple linear and logistic regression analyses were performed.

Results: The response rates were 41% and 34%, respectively. Among residents aware of living close to a MTP, 40% were very or extremely worried about manure treatment. In contrast, in the general residents and in residents unaware of the proximity of a MTP, worries about manure treatment were limited. Besides, odor sensitivity and odor annoyance were correlated with higher levels of worries, but not the distance to the MTP. Perceived control over health risks from the environment was associated with a lower score on worries. Having a say during the installation of a MTP positively affected worries about manure treatment. No differences in self-reported stress levels could be observed among resident groups. A higher frequency of annoyance due to MTPs was actually correlated with fewer stress symptoms. No significant association between distance and self-assessed symptoms of infections was found.

Conclusions: Although only few nearby residents were extremely worried about manure treatment, they should be specifically targeted in risk communication and participation. Since odor annoyance was associated with more worries about manure treatment, we recommend efforts towards the reduction of odor from livestock production and manure treatment.

P-074 JuniorHUB: Fostering Scientific Knowledge and Collaboration through Digital Media and Dynamic Training Platforms.

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Background: The BCBHub is a collaborative network within the Spanish National Research Council (CSIC) designed to foster communication, knowledge exchange, and synergy among its diverse research groups. Within this broader framework, early-career researchers require tailored spaces for continuous training and peer-to-peer interaction. To address this need, the JuniorHUB was established as the dedicated early-career section of the BCBHub. It promotes dynamic initiatives aimed at creating interactive and accessible channels for capacity building and collaboration among emerging professionals.

Objectives: To introduce JuniorHUB's core initiatives aimed at democratizing scientific knowledge and providing dynamic educational resources tailored to the specific, evolving needs of early-career researchers within the BCBHub network.

Methods: The JuniorHUB promotes various initiatives to support its community. Among these, two primary and complementary tools are currently highlighted. First, a video series hosted on the Conexion BCB YouTube channel, featuring periodic, short-format content where researchers concisely explain their work, methodologies, or practical skills, ensuring broad accessibility. Second, a dynamic course catalog hosted on the Conexion BCB website. Unlike static educational repositories, this catalog operates as a "living" platform, continuously updated and expanded based on direct feedback and the emerging needs identified by the users.

Results: These initiatives establish a growing digital library of accessible, peer-to-peer scientific content and an adaptable training framework. The YouTube series fosters community engagement and cross-disciplinary understanding among different CSIC groups, while the Conexion BCB catalog ensures that the training offered remains highly relevant and directly responds to real-time educational demands.

Conclusions: JuniorHUB provides an innovative, engaging, and flexible approach to continuous learning and science communication. By combining accessible video content with a user-driven course catalog, the initiative strengthens the network of early-career professionals within the BCBHub, equipping them with the knowledge and tools necessary to collaborate and tackle current scientific challenges.

P-075 *Salmonella* surveillance in raw pet food and dogs in Great Britain, 2013-2022.

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Background: The rising popularity of raw meat pet food for dogs in Great Britain has prompted concerns about its potential role in transmitting zoonotic pathogens, particularly *Salmonella*.

Objectives: To investigate correlations between *Salmonella* isolated from dog food (both raw and heat-treated) and from dogs, using historical passive surveillance data from manufacturing plants and clinical samples.

Methods: Data collected by the Animal and Plant Health Agency from 2013 to 2022 (phenotypically-determined *Salmonella* serovars plus their phage types and disc-diffusion antimicrobial resistance profiles) were compared between dog food and canine clinical sources.

Results: Over time both the number and serovar diversity of *Salmonella* isolations from raw meat pet food increased, from 4 isolates of 4 serovars in 2013 to 606 isolates of 39 serovars in 2022, in parallel with a five-fold increase in the number of raw meat pet food plants operating in Great Britain. Between 2021 and 2022, following the implementation of statutory *Salmonella* reporting in dogs, considerable overlaps in serovar distributions were observed between raw meat pet food and dog samples, with serovars of significant public health importance such as *S*. Typhimurium, monophasic *S*. Typhimurium and *S*. Infantis among the top ten most frequently isolated from both sources. Some clinically relevant serovars, such as *S*. Typhimurium and *S*. Dublin, were over twice as frequent among dog isolates. Antimicrobial resistance patterns revealed some correlations between sources for certain serovars, such as *S*. Typhimurium, while for others resistance patterns were unique to the dog isolates. Resistances to cefotaxime, ceftazidime or ciprofloxacin were rare.

Conclusions: Despite limitations for establishing direct transmission pathways, the findings highlight raw meat pet food as a potential vector for *Salmonella* transmission, emphasising the risks to both animal and public health and underlining the need for vigilant monitoring and hygiene practices.

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