

# BOOK OF ABSTRACTS



## One Health Nexus

Bridging Human, Animal, and Environmental Health Across Europe

**December 8-11**  
**2025**

**Patras, Greece**



Keynote Speakers, Plenary Sessions, Round Tables, Oral and Poster Presentations, Experts Panel, Creative discussions, Stakeholder Dialogue, Policy Panels, Cultural nights and more!

Conference Info,  
Abstract submission,  
Registrations



<https://www.onebridge.eu/en/oneford25/>

### Day 1:

Monday,  
December 8, 2025  
"Preventing Human  
and Zoonotic Disease  
Transmission: A One  
Health Perspective"

### Day 2:

Tuesday,  
December 9, 2025  
"Combating Antimi-  
crobial Resistance  
through Integrated  
Policies"

### Day 3:

Wednesday,  
December 10, 2025  
"Climate Change and  
Health: An Integrated  
Approach to  
Resilience"

### Day 4:

Thursday,  
December 11, 2025  
"Leveraging Digital  
Innovation to Advance  
One Health"



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**ONE- Bridge project is supported by co-funding from the European Union's EU4Health programme under Grant Agreement Nr 101233407**

The ONE-Bridge project aims to advance the One Health approach by fostering collaboration and addressing the interconnected challenges at the interface of human, animal, and environmental health.

Through a high-level One Health Conference in Patras, Greece, and three workshops in Barcelona, Lille, and Dresden, the project will provide a dynamic platform for stakeholders to engage in interdisciplinary dialogue, exchange knowledge, and co-develop actionable strategies. The four events are organized within the framework of the EU co-funded project titled: 'One Health Nexus: Bridging Human, Animal, and Environmental Health Across Europe.'

## **Objectives**

The project's primary objectives include promoting the One Health approach by raising awareness of the critical interdependencies among human, animal, and environmental health systems and highlighting the importance of integrated policies to combat zoonotic diseases, antimicrobial resistance (AMR), and the health impacts of climate change.

ONE-Bridge also seeks to facilitate cross-sectoral collaboration by bringing together policymakers, scientists, healthcare professionals, veterinarians, environmental experts, and civil society to work on shared health priorities.

The project emphasizes the need to address emerging health challenges, such as pandemics and food system vulnerabilities, by fostering innovative solutions, strengthening resilience, and enhancing preparedness.

## **Key focus**

A key focus of the project is to support policy and governance by aligning discussions with the European Health Union's objectives, promoting effective regulatory frameworks, and generating evidence-based recommendations for integrating the One Health approach into national and EU-level strategies.

Moreover, the initiative will highlight the role of digital innovation in improving health surveillance, diagnostics, and system efficiency, while building capacity among professionals and empowering youth to lead future One Health efforts.

The implementation of the conference and workshops, ONE-Bridge will deliver a comprehensive roadmap for advancing One Health collaboration across Europe, including practical tools, policy recommendations, and dissemination activities to ensure long-term impact.

This project will contribute significantly to the resilience, sustainability, and inclusivity of health systems, strengthening Europe's leadership in addressing complex, cross-sectoral health challenges.

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## ONE-Bridge in Health Conference

European One Health Conference: Bridging Human, Animal, and Environmental Health  
December 8–11, 2025

Conference & Cultural Center of the University of Patras, Greece

### Organizing Committee

Apostolos Vantarakis, Professor of Hygiene, Department of Medicine, University of Patras

Spyros Papaioannou, Postdoc Sociologist

Zoi Anastopoulou, Biologist, MSc, PhD candidate

Rafail Fokas, Agronomist – Food Scientist, MSc, PhD candidate

Athanasia Palaiologou, Physicist, MSc, PhD candidate

### Scientific Board

**Apostolos Vantarakis** Professor of Public Health Laboratory of Public Health, Epidemiology and Quality of Life Medical Department, University of Patras, Greece

**Uli Klümper** Senior Researcher, Department of Hydrobiology Technical University of Dresden (TUD), Germany

**Sara Soto** Head of the Viral and Bacterial Infections Programme Barcelona Institute for Global Health (ISGlobal), Spain

**Yannick Rossez** Research Scientist, Centre National de la Recherche Scientifique (CNRS) University of Lille, France

**Yann Guérardel** Research Director, Structural & Functional Glycobiology Unit Université de Lille, CNRS, France

**Catherine Robbe-Masselot** Research Scientist, Structural & Functional Glycobiology Unit Université de Lille & CNRS, France

**Nikolaos Thomaidis**, Professor of Analytical Chemistry at the Department of Chemistry, NKUA, Greece

**Panagiotis Kalatzis**, Assistant Professor at the University of Copenhagen, Greece

**Vasileios A. Diamantopoulos**, Assistant Professor, Faculty of Public and One Health, University of Thessaly

**Angeliki I. Katsafadou**, Assistant Professor, Faculty of Public and One Health, University of Thessaly, Greece

**Yiannis Kiouvrekis**, Assistant Professor, Faculty of Public and One Health, University of Thessaly, Greece

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DAY 1

## ONE BRIDGE IN HEALTH CONFERENCE AGENDA

Monday December 8, 2025		Preventing Human and Zoonotic Disease Transmission: A One Health Perspective
	Title	Presenters
08:30-09:30	<b>Registrations Opening</b>	
09:00-09:30	<b>Ceremony &amp; Welcome Addresses</b>	<b>C. Bouras</b> , Professor, Rector of University of Patras. <b>G. L. Adonakis</b> , Professor, Chair of Department of Medicine, University of Patras, <b>C. Stathopoulos</b> , Professor, Dean of Dept. of Medicine, <b>A. Mastorakou</b> , Regional Governor for Public Health, Region of Western Greece, <b>C. Peletidis</b> , Mayor of Patras, <b>A. Vantarakis</b> , Professor, Coordinator of One Bridge project
09:30-10:00	<b>HADEA – Funding opportunities in health: EU4Health</b>	<b>Ludmila Nistor-Mihajlova</b> , Project Adviser, HADEA A1
10:00-11:00	<b>Session I1</b>	Chair: <b>Apostolos Vantarakis</b> , Professor of Public Health, Department of Medicine, University of Patras, Coordinator of One Bridge project
10:00-10:30	<b>KEYNOTE:</b> One Health as a Strategic Compass for European Public Health.	<b>Agis Tsouros</b> , International Adviser Health Policy and Strategy - Former Director at World Health Organization - Adjunct Professor, Boston School of Public Health
10:30-11:00	<b>KEYNOTE:</b> Double-Edged Viruses: Bacteriophages as Promising Antibacterials with a Hidden Side".	<b>Panos G. Kalatzis</b> , Assistant Professor, Faculty of Health and Medical Sciences, GLOBE Institute, Section for Evolutionary Hologenomics, University of Copenhagen, Denmark
11:00-11:30	<b>Coffee break</b>	
11:30-13:00	<b>Session I2</b>	Chair: <b>Eleni Jelastopulu</b> , Professor of Public Health, Director of Lab of Public Health, Epidemiology and Quality of Life, Department of Medicine, University of Patras, Greece
11:30-12:00	<b>KEYNOTE:</b> H5N1 Avian Influenza Virus: Evolution, Pandemic Potential and One Health Perspective	<b>Chrysostomos Dovas</b> , Professor of Molecular Microbiology, School of Veterinary Medicine, Aristotle University of Thessaloniki, Greece
12:00-12:30	Managing human and zoonotic disease outbreak: When One Health meets our ethics	<b>Karolina Akinosoglou</b> , Internist-Infectiologist Associate Professor, Department of Medicine, University of Patras, Greece
12:30-13:00	Glycosylation at the frontline: protecting poultry and humans from Salmonella in a One Healthperspective	<b>Yannick Rossez</b> , Researcher, Centre National de la Recherche Scientifique (CNRS), University of Lille, France
13:00-14:00	<b>Lunch</b>	

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	<b>Session I3</b>	Chair: <b>Yann Guérardel</b> , Research Director, Structural & Functional Glycobiology Unit, University of Lille, CNRS, France
14:00-14:30	Preventing bacterial and viral infections by targeting host-microbe glycointeractions	<b>Catherine Robbe Masselot</b> , Prof. Unité de Glycobiologie Structurale et Fonctionnelle, University of Lille/CNRS, France
14:30-15:00	Wastewater-based surveillance from hospital settings to animal farms: a One- Health approach as tool for public health future	<b>Elisabete Valerio</b> , Researcher, Department of Environmental Health, National Institute of Health Dr. Ricardo Jorge Lisbon, Portugal
15:00-15:30	Belgium's SARS-CoV-2 wastewater surveillance: from pandemic achievements to a future One-Health early warning system.	<b>Koenraad Van Hoorde</b> , Researcher, Head of Service, Foodborne Pathogens, Sciensano, Belgium
15:30-16:30	<b>Coffee break</b>	
16:30-17:30	<b>One Bridge Workshops- Presentations and Outcomes</b>	One Bridge team
	<b>Session I4</b>	Chair: <b>Michalis Leotsinidis</b> , Professor Emeritus, Environmental Toxicology and Epidemiology, Medical Department, University of Patras
17:30-19:00	<b>Round Table-Migration and One Health: Interconnected Challenges</b>	<b>Apostolos Veizis</b> , Executive Director of INTERSOS Hellas, <b>Santino Severoni</b> , Director of the Health and Migration at World Health Organization, World Health Organization, Geneva, Switzerland, <b>Kayvan Bozorgmehr</b> , Professor of Public Health, Director of the Department of Population Medicine and Health Services Research, Bielefeld University, Head of the Section of Health Equity Studies and Migration, Heidelberg University Hospital, <b>Teymur Noori</b> , European Centre for Disease Prevention and Control, Sweden, <b>Bernadette Kumar</b> , Professor, President of the Global Society on Migration, Ethnicity, Race and Health
18:00-19:00	<b>Workshop - When One Health Meets our Ethics: Case studies</b>	<b>Karolina Akinosoglou</b> , Internist-Infectiologist Associate Professor, Department of Medicine, University of Patras, <b>Anne-Lise deLastic</b> , Assistant Professor, Laboratory Haematology, Department of Medicine, University of Patras, <b>Katerina Grafanaki</b> , Teaching Staff, Department of Dermatology-Venereology, School of Health Sciences, University Hospital of Patras, <b>Eleni Polyzou</b> , Internal Medicine Resident, Department of Internal Medicine, University General Hospital of Patras, Greece
19:00-20:00	<b>Light Dinner- Welcome Cocktail</b>	

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## **Double-Edged Viruses: Bacteriophages as Promising Antibacterials with a Hidden Side**

*Panos G. Kalatzis<sup>1</sup>*

<sup>1</sup>Centre for Evolutionary Hologenomics, Globe Institute, University of Copenhagen, Denmark

Antimicrobial resistance (AMR) is a rising global threat that hampers the efficacy of life-saving treatments. Excessive and often inappropriate administration of antibiotics has led to a surge of pathogens that are resistant even to last resort antibiotics. Recently, European Commission, through One Health AMR partnership, and World Health Organization (WHO) emphasized the need for innovative research and regionally tailored strategies to combat the rise of antibiotic-resistant pathogens.

Bacteriophages, or phages, are viruses that infect bacteria; they are ubiquitous in nature, highly specific and self-propagating in the presence of their bacterial host. These properties make phages ideal biological agents that can selectively target and remove pathogenic bacteria while leaving the natural microbiota intact. Hence, phage therapy can be a potent strategy against antibiotic-resistant infections, while in line with the One Health approach. Numerous studies have demonstrated promising results in environmental, animal and human sectors, including several lifesaving compassionate phage therapy cases of severely infected patients. However, the therapeutic potential of bacteriophages can be hampered by biological complexities such as dynamic phage-host interactions, development of resistance and horizontal gene transfer. Randomized clinical trials are still needed to validate phage therapy and facilitate the development of an appropriate regulatory framework, which would eventually approve large-scale applications.

Recent advances in bioinformatics, structural biology, and synthetic biology now enable innovative methods to enhance phage-based interventions. By combining predictive modeling, high-throughput experimental validation, and knowledge-driven phage selection, we can have a versatile platform to address key challenges in combating antibiotic-resistant pathogens.

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## **Wastewater-based surveillance from hospital settings to animal farms: a One- Health approach as tool for public health future**

Elisabete Valério<sup>1</sup>

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**Keywords:** Wastewater based surveillance; sentinel system; One Health

Wastewater-based surveillance (WBS) is a powerful One Health tool that can help link human, animal, and environmental health by monitoring pathogens and/or chemical substances in sewage.

Regular wastewater surveillance, combined with other indicators, proved their effectiveness during COVID-19 pandemic management, aiding decision-making, particularly during periods with limited testing. Given this success, some countries have incorporated WBS into their national strategies for different pathogens or/and chemical substances. While the maturity of pathogen detection in wastewater varies globally, ongoing efforts aim to establish a standardized global surveillance system.

Since viruses, bacteria, antimicrobial-resistant (AMR) genes, and even pharmaceuticals are excreted by humans and animals before clinical symptoms appear, wastewater may provide an early warning of emerging health threats. In a One Health context, WBS helps identify zoonotic pathogens circulating across species, track antimicrobial resistance shared between humans and livestock, and assess environmental contamination that may affect both ecosystems and public health. The goal for the future is to be able to integrate data obtained during wastewater, clinical, veterinary, and environmental monitoring, so that decision-makers gain a more complete understanding of disease dynamics and can respond more rapidly to protect from health threats.

**Acknowledgments:** Author thanks the Joint Action EU-WISH (European Union Wastewater Integrated Surveillance for Public Health, GA: 101140460) and also the project SIVIZ - Development of an Integrated Surveillance and Alert System of Zoonosis in Portugal (GA: 101132818 ) both of the EU4Health programme. Also would like to express my acknowledgments to AgIR project - a partnership to characterize the wastewater from some hospitals and the corresponding downstream water treatment, funded by the Environmental Fund.

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DAY 2

## ONE BRIDGE IN HEALTH CONFERENCE AGENDA

Tuesday December 9, 2025

Combating Antimicrobial Resistance through Integrated Policies

	Title	Presenters
08:30-09:00	<b>Registrations</b>	
09:00-11:00	<b>Session II1</b>	Chair: <b>Marina Tarrús</b> , Researcher, ISGlobal
09:00-09:30	<b>Antimicrobial Resistance: Shaping the Future of Health in the EU</b>	<b>Ivan Vazquez, Hannah Sievers, Beatrice Marquez-Garrido</b> European Commission (DG SANTE A1) Directorate-General for Health & Food Safety, European Commission
09:30-10:00	<b>KEYNOTE:</b> Ecological and Evolutionary Drivers of Environmental Antibiotic Resistance	<b>Uli Klumper</b> , Senior Researcher, Institute of Hydrobiology, Technical University of Dresden (TUD), Germany
10:00-10:30	<b>KEYNOTE:</b> AMR as a Silent Pandemic: Global and EU Perspectives	<b>Sara Soto</b> , Head of the Viral and Bacterial Infections Programme, Barcelona Institute for Global Health (ISGlobal), Spain
10:30-11:00	<b>KEYNOTE:</b> Prudent use of veterinary drugs and antibiotics in productive animals. Risk of development of antimicrobial resistance	<b>Christos Zafeiridis</b> , European Commission, Seconded National Expert Directorate-General for Health and Food Safety, Directorate for Crisis Management in Food, Animals and Plants, Directorate for Official Controls, EU Representative, Northern Ireland Liaison Group (UK), Official Veterinarian of the Ministry of Rural Development & Food, MED-OH, Asclepius One Health
11:00-11:30	<b>Coffee break</b>	
11:30-13:00	<b>Session II2</b>	Chair: <b>C. Stathopoulos</b> , Professor, Dean of Dept. of Medicine, University of Patras
11:30-12:00	Effect of Subinhibitory Biocide Exposure on Conjugal Transfer of Antibiotic Resistance Plasmids	<b>Barth F. Smets</b> , Professor, Department of Biological and Chemical Engineering Aarhus University, Denmark
12:00-12:30	The Challenge of Antimicrobial Resistance in Clinical Settings	<b>Tryfinopoulou Kyriaki</b> , Biopathologist-Microbiologist, Assistant Professor of Clinical Microbiology, School of Medicine, University of Crete
12:30-13:00	Combating Antimicrobial Resistance through Integrated One Health Policies: Bridging Gaps between Human, Animal, and Environmental Sectors	<b>Asma Bashir</b> , Assistant Professor, Shaheed Zulfikar Ali Bhutto Institute of Science and Technology, Pakistan
13:00-14:00	<b>Lunch</b>	
14:00-15:30	<b>Session II3</b>	Chair: <b>Uli Klumper</b> , Senior Researcher, Department of Hydrobiology, Technical University of Dresden (TUD), Germany
14:00-14:30	Surveying AMR in wastewater samples: some first results from the application of different methodologies in two WWTPs in Crete, Greece	<b>Dimosthenis Chochlakis</b> , Researcher, School of Medicine, University of Crete, Greece

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14:30-15:00	Tracking antibiotic resistance and pathogens across a Mediterranean city: insights from wastewater surveillance and risk assessment in Larnaca, Cyprus	<b>Popi Karaolia</b> , Researcher, Nireas-International Water Research Center, University of Cyprus
15:00-15:30	Identification and antibiotic resistance profiles of clinically important Salmonella serovars isolated from egg products	<b>Andritsos Nikolaos</b> , Assistant Professor, Department of Food Science and Technology, University of Patras
15:30-16:00	<b>Coffee break</b>	
16:00-18:00	<b>Session II4</b> Oral Presentations	Chair: <b>Karol Delgado</b> , Researcher, ISGlobal, Spain
16:00-16:20	Like Parent, Like Metabolite: Do antibiotics and their transformation products exert comparable selective pressures?	<b>Pooja Lakhey</b> , Queensland Alliance for Environmental Health Sciences, Australia
16:20-16:40	An overlooked risk: The role of Mycobacterium avium subsp. paratuberculosis in antimicrobial resistance across the One Health spectrum.	<b>Antonia Mataragka</b> , Post Doctoral Researcher in Animal Science, Department of Animal Science, Agricultural University of Athens, Greece
16:40-17:00	Impact of manure fertilization on soil: fate of manure-introduced and indigenous taxa and genes	<b>Marios Valmas</b> , PhD candidate, Department of Biochemistry and Biotechnology University of Thessaly, Greece
17:00-17:20	A One Health Approach to Quantifying the Mobility Potential of Antibiotic Resistance Genes via Linkage-Based ddPCR	<b>Magali de la Cruz Barrón</b> , Researcher, Department of Hydrobiology, Technical University of Dresden (TUD), Germany
17:20-17:40	Fragile inhibition: AZT suppresses plasmid transfer but is easily undermined by resistance and metabolic rescue	<b>Eda Deniz Erdem</b> , Researcher, Institute of Hydrobiology, Technical University of Dresden (TUD), Germany
17:40-18:00	A Cycle of Contamination and Recovery: How Combined Sewer Overflows Increase Antimicrobial Resistance in an Urban Stream	<b>Diala Konyali</b> , Researcher, Institute of Hydrobiology, Technical University of Dresden (TUD), Germany
18:00-19:00	<b>Session II5</b>	
18:00-19:00	<b>Workshop:</b> Bridging One Health and Lifestyle Medicine: An interconnected path	<b>A. Chatziantoniou</b> , PhD candidate, Department of Medicine, University of Patras and <b>K.Vagias</b> , Biologist (BSc)-Nutritionist, Medical Student-University of Crete, Lifestyle Medicine Health Advisor-European Lifestyle Medicine Organisation (ELMO)

# BOOK OF ABSTRACTS

## **Prudent use of veterinary drugs and antibiotics in productive animals. Risk of development of antimicrobial resistance**

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**Keywords:** Antimicrobial resistance, prudent use, livestock, One Health, EU policy.

Antimicrobial resistance (AMR) constitutes a major global public health challenge that transcends the boundaries of human medicine, veterinary practice, and environmental management. In food-producing animals, veterinary antimicrobials play an essential role in disease treatment and animal welfare; however, improper or excessive use accelerates the development and dissemination of resistant microorganisms. This presentation outlines the key drivers of AMR in livestock production systems and examines the consequences for animal health, farm productivity, and public health, including the transmission of resistant zoonotic pathogens such as *Salmonella*, *Campylobacter* and *Escherichia coli*. Current European Union policies and regulatory initiatives are reviewed, including the prohibition of antimicrobial agents for growth promotion, enhanced surveillance programs, strengthened risk-management measures, and the promotion of microbiological diagnosis to support evidence-based prescribing. Emphasis is placed on the prudent use of antimicrobials—correct indication, dosing, treatment duration, and the reduction of critically important antibiotics—as well as on preventive strategies encompassing improved biosecurity, vaccination, hygiene, and good agricultural practices. These actions align with the One Health approach, recognizing the interconnectedness of human, animal, and environmental health. The abstract highlights the need for sustained collaboration among veterinarians, farmers, policymakers, and industry stakeholders to safeguard antimicrobial efficacy and ensure the long-term sustainability of food-animal production systems.

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## Effect of Subinhibitory Biocide Exposure on Conjugal Transfer of Antibiotic Resistance Plasmids

Zhiming He<sup>1</sup>, Lars Jelsbak<sup>1</sup>, Yong-Guan Zhu<sup>2</sup>, Arnaud Dechesne<sup>1</sup>, Barth F. Smets<sup>3</sup>

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**Keywords:** ARG, biocide, conjugation, selection, plasmids

Clinically relevant ARGs are often plasmid-borne, and their metabolic burden may select against their hosts. However, many such plasmids are conjugal, and dissemination to other microbiome members may ensure their survival in the environment. Previous studies have documented biocides stimulating conjugation. Those studies primarily focused on the IncP1 $\alpha$ /MOBP plasmid RP4 as model system; we sought to examine the generalizability of these observations. We developed unbiased conjugation assays and conducted inter and intrageneric matings to investigate the effects of a wide variety of biocides, using *E. coli* and *P. putida* donor strains and plasmids of the IncP/MOBP, IncH/MOBH, and IncF/MOBF families. Biocide exposure more often inhibited than stimulated conjugative transfer of the tested plasmids. CuSO<sub>4</sub>, known as a ROS generator, was the only biocide capable of stimulating conjugation during intrageneric transfer of IncP/MOBP plasmids among *E. coli*. Biocide exposure inhibited RP4 transfer between *P. putida* cells as well as R27 and R1 transfer between *E. coli* cells. ROS levels varied significantly between strains/species, suggesting differences in ROS detoxification and tolerance mechanisms. Using the *recA*-KO mutant *E. coli* donor, we found that RecA can be essential for both + and - modulation of conjugation under biocide exposure. Overall, we underscore the importance of testing a diverse range of biocides, plasmids, and bacterial strains to establish patterns across plasmid and strain combinations. Such insights can ultimately allow us to predict the impact of biocides on dissemination of antibiotic resistance genes, supporting effective environmental management strategies within a One Health context.

**Reference:** He, Z., A. Dechesne, F. Schreiber, D. G. J. Larsson, B. F. Smets. 2024 Understanding stimulation of conjugal gene transfer by nonantibiotic compounds: How far are we? *Environ. Scie. Technol.* doi:10.1021/acs.est.3c06060

# BOOK OF ABSTRACTS

## Combating Antimicrobial Resistance through Integrated One Health Policies: Bridging Gaps between Human, Animal, and Environmental Sectors

Asma Bashir<sup>1</sup>, Neha Farid<sup>1</sup> and Kashif Ali<sup>1</sup>

<sup>1</sup>Shaheed Zulfiqar Ali Bhutto Institute of Science and Technology University, Pakistan

**Keywords:** Antimicrobial resistance, One Health, Policy integration, Surveillance, Stewardship, Intersectoral collaboration

This study aims to investigate the effectiveness of integrated One Health policies in combating antimicrobial resistance (AMR) across human, animal, and environmental sectors, in the context of escalating global AMR threats and fragmented governance systems. Utilizing a mixed-methods approach combining policy analysis, stakeholder surveys, and microbiological data review, data were collected from healthcare facilities, veterinary settings, and environmental monitoring programs to assess antimicrobial use patterns, resistance trends, and intersectoral coordination mechanisms. The analysis revealed that inconsistent policy enforcement, limited data sharing, and lack of cross-sectoral communication are major barriers to AMR mitigation. However, regions implementing joint surveillance programs and harmonized stewardship frameworks demonstrated significant reductions in resistant isolates and improved antimicrobial stewardship compliance. These findings indicate that sustainable progress against AMR requires cohesive policy integration, resource alignment, and multisectoral collaboration under the One Health paradigm. This research contributes to global AMR containment strategies by providing evidence-based recommendations for developing inclusive, cross-sectoral policies that safeguard public and environmental health.

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# BOOK OF ABSTRACTS

## Identification and antibiotic resistance profiles of clinically important *Salmonella* serovars isolated from egg products

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**Keywords:** antibiotic, antimicrobial resistance, egg, multiplex PCR, *Salmonella*, serovar

*Salmonella* is a pathogen of major concern that can be detected in foods, with nontyphoidal salmonellosis cases each year ranking globally among the top three of foodborne diseases caused by bacterial pathogens. This study aimed to investigate the distribution and the antimicrobial resistance (AMR) of three of the most commonly detected foodborne clinical serovars of *Salmonella enterica* (i.e., *S. Enteritidis*, *S. Typhimurium*, *S. Thompson*), isolated from egg products. Ten salmonellae strains were recovered from an equal number of pasteurized egg products and a raw egg. Strains were biochemically and serologically confirmed as *Salmonella* spp., according to the ISO 6579-1 protocol. Following their confirmation, isolates were serotyped through multiplex PCR and screened for AMR against a panel of eight antibiotics (ampicillin, tetracycline, meropenem, norfloxacin, gentamicin, ciprofloxacin, ceftazidime, cefotaxime). Serotyping of the isolates revealed that *S. Enteritidis* was most prevalent (40%), whereas *S. Thompson*, *S. Typhimurium* and *Salmonella* spp. accounted for 30, 20 and 10% of the isolates, respectively, indicating that egg products can be contaminated with epidemiologically significant *Salmonella* serovars. All but two strains (AAL 10119, AAL 10127) were susceptible to all antibiotics tested. *S. Typhimurium* strain AAL 10119 isolated from pasteurized egg yolk showed intermediate resistance to ciprofloxacin, but it was finally deemed susceptible after the determination of its minimum inhibitory concentration (MIC), according to EUCAST (MIC = 0.125 µg/mL < 0.25 µg/mL). However, AMR against ampicillin (MIC > 256 µg/mL), tetracycline (MIC = 64 µg/mL) and cefotaxime (MIC = 24 µg/mL) was recorded for *S. Thompson* strain AAL 10127 isolated from pasteurized egg white, which was finally deemed resistant in three classes of antibiotics (penicillins, tetracyclines, cephalosporines) and thus was classified as multidrug resistant (MDR) strain. These findings highlight the presence of MDR and clinically important *Salmonella* serovars in egg products, contributing to the possible dissemination of foodborne pathogens with increased AMR across the food chain as per the One Health approach.

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# BOOK OF ABSTRACTS

## Like Parent, Like Metabolite: Do antibiotics and their transformation products exert comparable selective pressures?

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**Keywords:** Antimicrobial resistance, selection pressure, wastewater treatment plants

While the selective pressure of antibiotics on microbial communities is well-documented, their transformation products (TPs), frequently detected in wastewater and natural aquatic systems, remain an overlooked factor in antimicrobial resistance (AMR) development. Given their persistence at comparable or even higher concentrations than their parent compounds, TPs may play a significant role in the maintenance and dissemination of AMR. This study investigates whether antibiotic TPs exert selective pressure on bacterial communities and how their effects compare to those of their parent compounds, providing key insights into the broader implications of antibiotic pollution on resistance dynamics. To assess this, the SELECT assay was used to determine the selective effect concentrations. Based on this data, a seven-day bacterial selection experiment using wastewater-derived microbial communities was conducted. Cultures were exposed to environmentally relevant concentration (250 µg/L) of antibiotics from three widely detected antibiotic classes—fluoroquinolones, sulfonamides, and MLS—and their respective TPs. This was followed by qPCR analysis to quantify *intI1* (class 1 integron integrase gene) relative to 16S rRNA gene abundance, serving as a proxy for resistance selection. . Our findings demonstrate that both parent antibiotics and their TPs drive AMR selection, with varying degrees of selective pressure. Notably, some TPs exhibited selection pressure comparable to or even exceeding that of their parent compounds. For example, desmethylene ofloxacin (a ofloxacin TP) led to a significant increase in *intI1* abundance, suggesting that TPs can contribute to the persistence of AMR in wastewater-impacted environments. To our knowledge, this is one of the first studies demonstrating that antibiotic TPs can exert selective pressure on AMR at environmentally relevant concentrations, with implications for environmental risk assessments and regulatory policies.

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# BOOK OF ABSTRACTS

## **An overlooked risk: The role of *Mycobacterium avium* subsp. *paratuberculosis* in antimicrobial resistance across the One Health spectrum**

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**Keywords:** *Mycobacterium avium* subsp. *paratuberculosis*, antimicrobial resistance, One Health, zoonoses, public health

**Background:** *Mycobacterium avium* subsp. *paratuberculosis* (MAP) causes Johne's disease in ruminants and has been implicated in human diseases such as Crohn's disease. While MAP's presence in livestock, food, and environments is established, its role in antimicrobial resistance (AMR) and zoonotic transmission is underexamined. **Aim:** To systematically assess the evidence for AMR in MAP including genetic, phenotypic, and ecological data, and to explore the implications for human health and One Health policy. **Methods:** A narrative and semi-systematic literature review (2015–2025) was conducted, sourcing articles reporting phenotypic susceptibility testing, whole-genome identification of AMR genes, and surveillance data from animal, food, and environmental sources. **Key Findings:** MAP isolates carry multiple AMR-associated genes (e.g. efflux pumps, resistance-gene homologs). Phenotypic studies show reduced efficacy of antimicrobials under anaerobic/persister states. Evidence of viable MAP in milk and meat suggests routes of exposure. Antimicrobial use in livestock and environmental persistence emerge as driving factors for resistance development. **Implications:** These findings indicate MAP is a potential zoonotic AMR risk. There is a critical need for standardized AMR testing protocols for MAP, inclusion of MAP in AMR surveillance programs, and One Health policy frameworks that consider animal, food, and environmental dimensions. **Conclusion:** MAP's antimicrobial resistance potential is a "hidden" public health threat. Recognizing and acting on this now can prevent downstream clinical and food safety challenges.

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## Impact of manure fertilization on soil: fate of manure-introduced and indigenous taxa and genes

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**Keywords:** microbial coalescence, manure fertilization, pathogens, antimicrobial resistance

Manuring promotes sustainable agriculture but also induces pathogen and antimicrobial resistance (AMR) dispersal contrasting One Health incentives [1]. Having observed manure taxa disappearing in soil in 25 days [2], we attempted to model the impact of pig manure input employing soil microcosms, including treatments with antibiotics. The microbial mass, marker genes (qPCR) and microbial diversity (amplicon sequencing) were monitored at five timepoints (0, 0.5, 1, 4 and 25 days). Shotgun sequencing was also conducted for key samples, alongside Nanopore sequencing for class 1 integrons. Manure taxa comprised 6-34% of the total soil community right after amendment, with some prokaryotes being persistent (e.g. clostridia), whereas others dissipated relatively quickly ( $\leq 4$  days) (e.g. lactobacilli), or slower ( $> 4$  days) (e.g. mycobacteria), with several following exponential decay. Most manure-introduced resistance genes (ARGs) were also exponentially decayed. In exponential decay responses, antibiotic application increased taxon or gene persistence, according to estimated dissipation time values. Interestingly, *intl1* and specific soil taxa (e.g. streptomycota) were manure-boosted. Finally, manure-introduced ARG loci and integron cassettes included well-structured variants, with some persisting up to 25 days. Fragmented and structurally poorer variants were derived from soil, with some being manure-boosted. Overall, we observed an apparent immediate overall manure microbiome-related risk reduction, yet several introduced enteric taxa (including putative pathogens) and ARGs persisted, while indigenous soil taxa, horizontal markers (e.g. *intl1* cassettes) and ARG abundances were stimulated. This study deepens our understanding about the impact of manure agricultural inputs from the One Health perspective for zero tolerance to pathogen and AMR dispersal.

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# BOOK OF ABSTRACTS

## A One Health Approach to Quantifying the Mobility Potential of Antibiotic Resistance Genes via Linkage-Based ddPCR

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**Keywords:** antibiotic resistance; droplet digital PCR; mobile genetic elements; mobility potential

The spread of antibiotic resistance is a core One Health challenge, driven by the horizontal transfer of resistance genes (ARGs) among bacteria that move between humans, animals, and the environment<sup>1</sup>. Current surveillance primarily tracks ARG abundance, which fails to capture their mobilization potential via mobile genetic elements (MGEs) and complicates risk assessment 2-6. To address this limitation, we have developed a novel, sequencing-independent method for quantifying the mobility potential of ARGs. This innovative approach relies on droplet digital PCR (ddPCR) technology, distinguished by the random dispersion of individual DNA molecules among numerous droplets, each serving as an independent PCR reaction vessel. Through statistical analysis of the proportion of droplets wherein both ARG and MGE marker genes coexist, it is feasible to quantify their physical linkage within the same DNA molecule. Notably, a low linkage between an ARG and an MGE suggests a weaker association, making it less likely for the gene to be transferred between bacteria. We validated our linkage-ddPCR assay using engineered plasmid mixtures containing the sulfonamide resistance gene *sul1* and the class 1 integron-integrase gene *int1* in both linked and unlinked configurations. The method remained robust with natural occurring plasmids and increasing genetic distances, confirming its broader applicability. Our findings establish a rapid, quantitative tool for surveilling ARG mobility potential that could be applied across diverse One Health settings, from wastewater and soil to clinical samples. Consequently, it provides a critical new metric for antimicrobial resistance risk assessment and targeted interventions at the human-animal-environment sectors.

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# BOOK OF ABSTRACTS

## **Fragile inhibition: AZT suppresses plasmid transfer but is easily undermined by resistance and metabolic rescue**

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**Keywords:** conjugation blockers, zidovudine resistance, thymidine metabolism, antibiotic resistance spread

The rise of AMR is not only driven by antibiotic use but also efficient spread of resistance genes through horizontal gene transfer (HGT). Compounds that can limit plasmid-mediated HGT are urgently needed. The nucleoside analogue zidovudine (3'-azido-3'-deoxythymidine, AZT), historically used for antiretroviral therapy, has gained attention for inhibiting plasmid transfer in Gram-negative bacteria. However, AZT-resistance emerging rapidly through point mutations in the thymidine kinase (TK) gene may compromise its effectiveness. Here, we aimed to test whether AZT can reliably function as a conjugation inhibitor and to determine if resistance in one or both mating partners is sufficient to eliminate its effect. Using *Escherichia coli* and generated AZT-resistant recipient and donor strains carrying plasmid pKJK5, we examined how susceptibility of each partner shapes AZT's impact on conjugation. AZT resistant strains displayed no detectable fitness cost in monoculture. In liquid matings AZT reduced plasmid transfer in a concentration-dependent manner for both susceptible partners. The presence of an AZT-resistant mutant in either or both mating partners abolished this inhibition entirely, indicating that effective transfer suppression requires susceptibility in both partners. Unexpectedly, in AZT absence, conjugation frequencies between pairs of susceptible and resistant strains were markedly reduced. Supplementation with dTMP, a downstream metabolite in the thymidine pathway unaffected by TK mutations, restored transfer, revealing an underlying metabolic mechanism. Thus, AZT can suppress plasmid transfer but resistance emerging in either partner nullifies this potential. Understanding metabolic dependencies is essential for evaluating AZT and related compounds as tools to restrict HGT and limit AMR spread across One-Health settings.

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## **A Cycle of Contamination and Recovery: How Combined Sewer Overflows Increase Antimicrobial Resistance in an Urban Stream**

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**Keywords:** AMR, MGE, Combined sewer overflow, Urban stream, Environmental Surveillance

Combined sewer systems convey wastewater and stormwater in one pipe and are designed to overflow during heavy rainfall to prevent flooding. These combined sewer overflows (CSOs) release untreated wastewater into receiving waters, introducing pathogens, antimicrobial resistance genes (ARGs), and mobile genetic elements (MGEs), which pose risks to environmental and public health. This study examined how CSOs alter microbial and resistome dynamics in an urban stream and assessed the system's capacity to recover following these events. We studied an urban stream (Lockwitzbach, Dresden, Germany) that has multiple CSO outlets releasing wastewater during heavy rainstorms. Water was sampled at two monitoring stations differing in distance to CSO outlets. We tracked 25 ARGs, 4 MGEs, bacterial abundance, pathogens, and community structure using high-throughput qPCR and 16S rRNA gene sequencing bi-weekly and at high-time resolution during two CSO events. CSO events caused a pronounced shift in the stream microbiome by increasing total bacterial and pathogen abundance and enriching diverse ARGs and MGEs by over two orders of magnitude. Following the CSO events, the river displayed marked resilience. The abundance of ARGs, bacteria and fecal pathogen, along with the microbial structure returned to baseline, pre-storm state levels within 2 weeks. This provides quantitative evidence that CSOs, acting as recurring sources of AMR in urban streams, are short-term, pulse disturbances and can be overcome by the river's natural microbiota. This highlights the need to integrate temporally resolved AMR risks into urban water management and to evaluate the long-term consequences of repeated contamination recovery cycles.

# BOOK OF ABSTRACTS

## Bridging One Health and Lifestyle Medicine: Pathways to Sustainable Well-Being

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<sup>3</sup> Medical School, University of Crete, Greece

**Keywords:** One Health, Lifestyle Medicine, Planetary Health, Sustainable Well-being, Systems Thinking, Behavioral Change

In the face of chronic disease burdens, sustainability challenges, and global environmental change, the interdependence of human, animal, and environmental health has become increasingly evident. To promote sustainable well-being at individual, community, and global levels, this session explores the conceptual and practical integration of the One Health approach with Lifestyle Medicine [1]. The workshop introduces the eight evidence-based pillars of Lifestyle Medicine (nutrition, physical activity, sleep, stress management, social connection, substance avoidance, environmental and planetary health, and sexual health and fertility), highlighting how lifestyle choices directly affect planetary health [2]. Through real-world examples, participants will see how adopting healthy habits enhances both personal well-being [3] and environmental sustainability. Participants will examine reciprocal links between lifestyle determinants and planetary outcomes such as biodiversity, climate impact, and resource use. In this interactive workshop, each participant will select one high-impact habit that benefits both personal and planetary health. Through guided reflection and group collaboration, participants will co-design practical, evidence-based interventions and develop individualized plans for sustainable behavior change. By the end of the session, participants will understand the deep connections between One Health and Lifestyle Medicine, identify lifestyle choices with dual human and environmental benefits, and commit to concrete actions that advance planetary well-being. Aligned with the One Health framework, this workshop emphasizes empowerment, collaboration, and systems thinking, positioning lifestyle change as a vital lever for global sustainability and long-term health.

### References

1. Oliveira, C. J. B., & Gebreyes, W. A. (2022). One Health: Connecting environmental, social and corporate governance (ESG) practices for a better world. *One health* (Amsterdam, Netherlands), 15, 100435. <https://doi.org/10.1016/j.onehlt.2022.100435>
2. Pathak, N., Pollard, K. J., & McKinney, A. (2022). Lifestyle Medicine Interventions for Personal and Planetary Health: The Urgent Need for Action. *American journal of lifestyle medicine*, 16(5), 589–593. <https://doi.org/10.1177/15598276221090887>
3. Li, Y., He, P., Shan, Y. et al. Reducing climate change impacts from the global food system through diet shifts. *Nat. Clim. Chang.* 14, 943–953 (2024). <https://doi.org/10.1038/s41558-024-02084-1>

# BOOK OF ABSTRACTS

DAY **3**

## ONE BRIDGE IN HEALTH CONFERENCE AGENDA

Wednesday December 10, 2025 **Climate Crisis, Public and Environmental Health: An Integrated Approach to Resilience**

	Title	Presenters
08:30- 09:30	<b>Registrations</b>	
09:30-11:00	<b>Session III1</b>	Chair: <b>Apostolos Vantarakis</b> , Professor of Public Health, Department of Medicine, University of Patras, Coordinator of One Bridge project
09:30-10:00	<b>KEYNOTE:</b> Health at the Crossroads of Climate Crisis and Migration	<b>Bernadette Kumar</b> , Professor, President of the Global Society on Migration, Ethnicity, Race and Health
10:00-10:45	<b>KEYNOTE:</b> The hidden pollution: The role and impact of disasters on ecosystems and human exposure	<b>Thomaidis Nikolaos</b> , Professor of Analytical Chemistry, Department of Chemistry, NKUA, Greece, Adjunct Professor at Yale University, School of Public Health, Visiting Professor, East China University of Science and Technology (ECUST), Shanghai
10:45-11:00	<b>Students discussing climate crisis</b> - Experimental Lower Secondary School of the University of Patras	Supervised by <b>Ioannis Chiotelis</b> , PhD, Mathematician, Principal of the School and <b>Constantina Marazioti</b> , PhD, Biologist
11:00-11:30	<b>Coffee break</b>	
11:30-13:00	<b>Session III2</b>	Chair: <b>Yannick Rossez</b> , Researcher, (CNRS), University of Lille, France
11:30-12:00	From Climate Stress to Food Insecurity: Nutritional implications	<b>Emmanuella Magriplis</b> , Professor, Agricultural University of Athens, Greece
12:00-12:30	Early warning systems for climate-sensitive vector borne diseases.	<b>Ioannis Kioutsioukis</b> , Professor, Laboratory of Atmospheric Physics, Department of Physics, University of Patras
12:30-13:00	Latest Epidemiological Evidence on the Association Between Short- and Long-Term Heat Exposure and Adverse Birth Outcomes	<b>Michalis Koureas</b> , Environmental Engineer, Researcher, University of Thessaly, Greece
13:00-14:00	<b>Lunch</b>	
14:00-15:30	<b>Session III3</b>	Chair: <b>Ioannis Kioutsioukis</b> , Professor, Laboratory of Atmospheric Physics, Department of Physics, University of Patras

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14:00-14:45	<b>KEYNOTE:</b> The changing landscape of fungal diseases and antifungal resistance through the lens of climate variability and change	<b>Aristea Velegraki</b> , Professor Emeritus of General Microbiology, School of Medicine, National and Kapodistrian University of Athens, Greece
14:45-15:05	Integrating Oxidative and Endocrine Biomarkers to Assess PFAS-Induced Stress in Freshwater Fish	<b>Sophia Schumann</b> , Researcher, TUD Dresden University of Technology, Germany
15:05-15:30	Climate-Driven Health Threats: The Next Frontier of One Health	<b>Eleni Sazakli</b> , Assistant Professor, Department of Medicine, University of Patras, Greece
15:30-16:00	<b>Coffee break</b>	
16:00-18:30	<b>Session III4</b>	Chair: <b>Apostolos Vantarakis</b> , Professor of Public Health, Department of Medicine, University of Patras, Coordinator of One Bridge project
16:00-16:30	<b>KEYNOTE:</b> The One Health Approach One Health-One Planet: a resilience approach	<b>Zacharoula Andreopoulou</b> , Professor Forest Informatics & Technologies for Green Regional Policy Director, MED-OHC
16:30-17:00	Climate Change, Health of Ecosystems and of People	<b>Panayotis Dimopoulos</b> , Professor in Ecology, Chair in the Biology Department, University of Patras, Greece
17:00-17:30	The Region of Thessaly facing Climate Crisis	<b>Dimitris Kouretas</b> , Professor of Animal Physiology- Toxicology, Department of Biochemistry and Biotechnology, University of Thessaly, Governor of the Region of Thessaly, Greece
17:30-19:30	<b>Policy Panel: Society's Response to the Climate Crisis</b>	Moderator: <b>A. Mastorakou</b> , Deputy Regional Governor for Public Health, Region of Western Greece <b>Sinaia Netanyahu</b> , WHO Regional Office for Europe, European Centre for Environment and Health, <b>Thanos Myloneros</b> , Public Health Officer WHO Athens Quality of Care & Patient Safety Office, <b>Tony Holohan</b> , Director, WHO Collaborating Centre for One Health, Adjunct Full Professor of Public Health, University College Dublin, <b>D. Kouretas</b> , Professor, Governor of the Region of Thessaly, <b>P. Dimopoulos</b> , Department of Biology, University of Patras

# BOOK OF ABSTRACTS

## Integrating Oxidative and Endocrine Biomarkers to Assess PFAS-Induced Stress in Freshwater Fish

Sophia Schumann<sup>1</sup>, Elisabetta Piva<sup>2</sup>, Sara Pacchini<sup>2</sup>, Daniela Bertotto<sup>3</sup>, Gianfranco Santovito<sup>2</sup>

<sup>1</sup>Institute of Hydrobiology, Technische Universität Dresden, Germany,

<sup>2</sup>Department of Biology, University of Padova, Italy,

<sup>3</sup>Department of Comparative Biomedicine and Food Science, University of Padova, Italy

**Keywords:** PFAS, oxidative stress, cortisol, antioxidant enzymes, fish physiology

Per- and polyfluoroalkyl substances (PFAS) are persistent anthropogenic contaminants that interfere with endocrine and metabolic pathways, challenging the resilience of aquatic organisms and the ecosystems they inhabit. This study investigates the physiological responses of two freshwater fish species chronically exposed to PFAS in rivers of the Veneto Region, Italy. In a biomonitoring approach, *Squalius cephalus* and *Padogobius bonelli* were sampled across three sites differing in PFAS concentrations. Endocrine responses were quantified through radioimmunoassay, analysing cortisol levels in plasma, fin and scales. Oxidative stress was assessed by measuring the activity and gene expression of catalase (CAT) and selenium-dependent glutathione peroxidases (GPx1 and GPx4) in the liver, the primary organ for PFAS accumulation and detoxification. Complementary histological evaluation of hepatic tissue was performed to identify structural alterations associated with pollutant exposure. The results revealed species-specific patterns: *S. cephalus* displayed elevated cortisol concentrations associated with higher PFAS loads, whereas *P. bonelli* exhibited pronounced antioxidant activation and histological evidence of lipid vacuolisation, suggesting distinct physiological strategies for coping with long-term chemical stress. These findings underscore the importance of integrating endocrine and oxidative biomarkers to distinguish between acute stress activation and chronic adaptive responses. This approach advances One Health-based environmental assessment by linking organismal physiology with ecosystem resilience under conditions of persistent contamination.

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## Climate Change, Health of Ecosystems and of People

<sup>1</sup>Panayotis Dion. Dimopoulos

<sup>1</sup> Department of Biology, University of Patras, University Campus, 26504 Rio, Greece

**Keywords:** biodiversity, climate, health, crisis, mitigation, adaptation

Climate variability (fluctuations around stable means) differs from climate change (long-term shifts in averages like temperature and precipitation), that is driven by fossil fuels, agriculture, and deforestation amplifying the greenhouse effect. Rapid global warming has been recorded since the industrial era, with CO<sub>2</sub> levels up 150% from 1750.

Climate change impacts include intensified droughts, floods, heatwaves, and wildfires, threatening biodiversity and ecosystems. Climate change exacerbates existing threats, causing increased summer heatwave mortality (60,000 deaths in Europe in 2022 alone, with 37% attributable to human activity), while slightly reducing winter cold deaths. Projections indicate 250,000 additional global deaths annually by 2030-2050 from heat stress, malnutrition, malaria, and diarrhea. It worsens cardio-respiratory diseases, strokes, infectious outbreaks, cancer, and mental health issues like anxiety, depression, suicide, and aggression. Urban areas are particularly vulnerable, with compact cities showing higher mortality. Solutions emphasize resilient health systems, green urban planning, active transport, and emission reductions. Urban heat islands amplify premature mortality, alongside shifts in allergens, vector-borne diseases (e.g., zoonoses), air quality hazards, and psychosocial distress. In Greece, a 1.5°C rise could boost wildfires by 41% and heatwaves by 173%.

Climate, biodiversity, and health crises are interlinked, thus urging for interconnected actions for sustainability, such as: a) prioritize mitigation through greenhouse gas reductions as primary prevention, b) adaptation measures through building resilient health systems via investments in crisis preparation, early-warning systems, and infrastructure, c) promotion of urban greening (e.g., 30m<sup>2</sup> green space per inhabitant), active transport (bike lanes to avert 10,000 premature deaths in Europe), reduced car dependency, and health impact assessments in all policies.

COP28's Declaration urges climate action for health co-benefits, synthesizing evidence for stakeholders and translating benefits economically to enhance resilience.

# BOOK OF ABSTRACTS

## **WHO's approach to Health and Environment within the framework of the One Health approach**

Sinaia Netanyahu, PhD, Senior Advisor, Nature and Health,

WHO European Center for Environment Climate Change and Health

Environmental change is reshaping both communicable and noncommunicable disease (NCD) patterns, underscoring the need for a One Health approach that integrates human, animal, and ecosystem health. Traditional One Health priorities—zoonotic spillover, vector-borne diseases, food safety, and antimicrobial resistance (AMR)—are intensified by land-use change, biodiversity loss, and climate warming, which expand vector ranges, alter wildlife–livestock–human contact, and accelerate the spread of resistant pathogens. At the same time, these same environmental drivers underpin major NCD burdens. Air and chemical pollution from fossil fuels, industry, and agriculture accumulate in crops and animal tissues, entering the food chain and contributing to diseases. Degraded ecosystems and unsustainable food systems reduce nutritional quality and limit access to nature, affecting metabolic and mental health. Climate change acts as a threat multiplier across both domains. A One Health lens enables integrated policies that simultaneously reduce infectious disease risks, AMR, and environmentally mediated NCDs while strengthening climate and ecosystem resilience. At the policy level, the Global Quadripartite (WHO, FAO, UNEP and WOA) One Health Joint Plan of Action integrates environmental integrity into One Health by embedding biodiversity, pollution, land-use and climate data into surveillance and policy. It calls for strengthening the environmental-sector capacity, promoting ecosystem protection and sustainable resource use, and aligning multisectoral action to reduce environmental drivers of health risks and enhance long-term resilience. Supplement to this global policy is the WHO Europe's One Health Adaptation Guide that addresses regional priorities such as governance, preparedness, inclusion, evidence, financing, and workforce competencies to advance coordinated, sustainable, multisectoral health action across the Region.

# BOOK OF ABSTRACTS

DAY 4

## ONE BRIDGE IN HEALTH CONFERENCE AGENDA

Thursday December 11, 2025

Leveraging Digital Innovation to Advance One Health

	Title	Presenters
08:30-09:30	<b>Registrations</b>	
09:30-11:00	<b>Session IV1</b>	Chair: <b>Kiouvrekis Ioannis</b> , Assistant Professor, Department of Public and One Health, University of Thessaly, Greece
09:30-10:00	<b>KEYNOTE:</b> Harnessing Big Data and AI for Real-Time Health Surveillance" The Artificial Intelligence of Things in Health: smart sensors and wearables for screening respiratory symptoms and diseases	<b>Sotiris Nikolettseas</b> , Professor and Founding Director of the Internet of Things Laboratory (IoT-Lab) at the Computer Engineering and Informatics Department of Patras University, Greece
10:00-10:30	<b>KEYNOTE:</b> Using Machine Learning Models to anticipate the spread of Respiratory Diseases	<b>Mario Munoz Organero</b> , Associate Professor, Department of Telematics Engineering, Universidad Carlos III de Madrid, Spain
10:30-11:00	Innovative evidence synthesis methodologies within One Health data ecosystems	<b>Evangelia Ntzani</b> , Associate Professor and Head, Department of Hygiene & Epidemiology, School of Medicine, University of Ioannina, Greece
11:00-11:30	<b>Coffee break</b>	
11:30-13:00	<b>Session IV2</b>	Chair: <b>Sotiris Nikolettseas</b> , Professor and Founding Director of the Internet of Things Laboratory (IoT-Lab) at the Computer Engineering and Informatics Department of Patras University, Greece
11:30-12:00	<b>KEYNOTE:</b> Integrating Spatial Geometry and Control Charts for Public Health Event Monitoring	<b>Economou Polychronis</b> , Associate Professor, Department of Civil Engineering, University of Patras, Greece
12:00-12:30	AI and Risk Analysis in One Health approach	<b>Athanasia Palaiologou</b> , PhD candidate, Department of Medicine, University of Patras, Greece
12:30-13:00	<b>KEYNOTE:</b> Estimating the relationship between wastewater viral load and clinical markers during a long period of Omicron subvariants: Evidence of a stable decline in the death ratio.	<b>Dimitrios Paraskevis</b> , Professor, Medical Department, NKUA, Member of the Public Health Expert Committee of NPHO, Greece
13:00-14:00	<b>Lunch</b>	

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14:00-16:00	<b>Session IV3</b>	Chair: <b>Economou Polychronis</b> , Associate Professor, Department of Civil Engineering, University of Patras, Greece
14:00-15:00	<b>Round Table:</b> Artificial General Intelligence for Strategic Planning and Decision Support	<b>Vasilis A. Diamantopoulos</b> , Assistant Professor, <b>Katsafadou Angeliki</b> , Associate Professor, <b>Kiouvrekis Ioannis</b> , Assistant Professor, Department of Public and One Health, University of Thessaly, Greece
15:00-15:30	<b>KEYNOTE:</b> Hybrid and Self-Adaptive SPOCU-Based Neural Networks in Health Strategies	<b>Milan Stehlik</b> , Professor, Department of Statistics, Universidad de Valparaíso, Valparaíso, Chile
15:30-16:00	<b>KEYNOTE:</b> AI and surveillance of AMR in the One Health context	<b>Adrian Egli</b> , Professor of Medical Microbiology and Director, Institute of Medical Microbiology, University of Zurich, Switzerland
16:00-16:30	<b>Coffee break</b>	
16:30-19:00	<b>Session IV4</b>	Chair: <b>Eleni Sazakli</b> , Assistant Professor, Department of Medicine, University of Patras, Greece
16:30-17:30	<b>Workshop:</b> Artificial Intelligence in Practice: Selecting and Evaluating the Optimal Model	<b>Kiouvrekis Ioannis</b> , Assistant Professor, Department of Public and One Health, University of Thessaly, Greece
17:30-18:00	Empowering Youth for One Health in the Digital Era	<b>Kyriakos Giallourakis</b> , President of One Health Students Greece
18:00-18:30	<b>Closing summary:</b> "Shaping the Future of One Health in Europe"	<b>Apostolos Vantarakis</b> , Professor of Public Health, Department of Medicine, University of Patras, Coordinator of One Bridge project



# BOOK OF ABSTRACTS

## Integrating Spatial Geometry and Control Charts for Public Health Event Monitoring

Economou Polychronis<sup>1</sup>, Sachlas Athanasios<sup>2</sup>, Bersimis Sotirios<sup>3</sup>

<sup>1</sup>Department of Civil Engineering, University of Patras, Greece,

<sup>2</sup>Department of Computer Science and Biomedical Informatics, University of Thessaly, Greece,

<sup>3</sup>Department of Business Administration, University of Piraeus, Greece.

**Keywords:** Public health surveillance, Spatio-temporal monitoring,

Early warning systems This study aims propose a new, general monitoring framework to detect unusual public health and emergency events, in the context of early-warning and surveillance systems. Utilizing a combination of convex hull geometry and control chart techniques, the methodology provides a flexible and widely applicable tool for tracking both the temporal dynamics and spatial distribution of events. To illustrate its practical value, data from Emergency Medical Services (EMS) calls in three municipalities of Montgomery County, Pennsylvania were analyzed as a case study. The dataset, comprising 17,516 unique calls between December 2015 and April 2020, was aggregated into three-day intervals. The analysis revealed that the framework effectively identifies both temporal fluctuations and localized clustering, demonstrating its capacity to provide timely and interpretable signals. These findings highlight the method's potential for broad use in public health, emergency management, and environmental monitoring, while the EMS application underscores its real-world relevance.

### Reference:

Bersimis, S., Sachlas, A., & Economou, P., (2023). Public health monitoring using control charts based on convex hull. *Research in Statistics*, 1(1).

# BOOK OF ABSTRACTS

## POSTER PRESENTATIONS

Authors	Department	Title
Anna Bilida <sup>1</sup> , Alexandra A. Ioannidi <sup>1,2*</sup> , Dionissios Mantzavinos <sup>1</sup> , Maria Antonopoulou <sup>1</sup>	<sup>1</sup> Department of Sustainable Agriculture, University of Patras, 30131 Agrinio, Greece, <sup>2</sup> Department of Chemical Engineering, University of Patras, Caratheodory <sup>1</sup> , University Campus, GR-26504 Patras, Greece	Advanced Oxidation Approaches for the Remediation of Antibiotics Contaminated Aquaculture Effluents.
Soraya Alfonsi <sup>1</sup> , Pohl Milon <sup>2</sup> Dezemona Petrelli <sup>1</sup> , Roberto Spurio <sup>1</sup>	<sup>1</sup> School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy; <sup>2</sup> Biomolecules Laboratory, School of Biology, Faculty of Health Sciences, Universidad Peruana de Ciencias Aplicadas, Lima, Peru.	Bacteria-based army tank crew: plastic bits as vehicles for transporting pathogens and their repertoire of resistance genes.
Lamprini Chani, Anastasios Kyriazis, George Aggelis, Alexandra Lianou*	Department of Biology, University of Patras	Assessment of the antimicrobial activity of pomegranate residues' extract in selected food products.
K.A. Koukouvini <sup>1</sup> , R. Fokas <sup>1</sup> , Z. Anastopoulou <sup>1</sup> , A. Chatziantoniou <sup>1</sup> , D. Fiteli <sup>2</sup> , C. N. Karamperi <sup>3</sup> , G. S. Gorgogetas <sup>3</sup> , A. Khan <sup>4</sup> , A. Vantarakis <sup>1</sup>	<sup>1</sup> Department of Public Health, Medical School, University of Patras, 26504 Patras, Greece. <sup>2</sup> Thrasio General Hospital, Dimokratias Street, Magoula 19018, Elefsina, Attica, Greece. <sup>3</sup> E-TRIKALA, Department of Research & Communication 6, Valkanou str, 421 32 Trikala, GR. <sup>4</sup> Atmospheric Chemistry Research Group, School of Chemistry, University of Bristol, Bristol, UK.	Molecular Surveillance of Airborne Respiratory Viruses in Healthcare Settings in Greece and the UK Under Post-Pandemic Conditions.
Erofilii-Vagia Gkogkou, Alkistis Kanteraki, Ekavi Aikaterini Isari, Eleni Grilla, Ioannis Kalavrouziotis, Petros Kokkinos	Hellenic Open University, Greece	Biochar from Sewage Sludge: A Circular Strategy Enhancing Water and Health Resilience under Climate Stress.
Levan Tsitskishvili <sup>1</sup> , Tengiz Kurashvili <sup>2</sup> , Levan Makaradze <sup>2</sup> , Irma Geguchadze <sup>1</sup> , Gogi Jikia <sup>2</sup> , Tea Museliani <sup>2</sup>	<sup>1</sup> Scientific-Research Center of Agriculture, Georgia, <sup>2</sup> Ivane Beritashvili Center of Experimental Biomedicine, Georgia	Genetic Diversity and Zoonotic Relevance of Mycobacterium bovis in Georgian Livestock: A One Health Surveillance Framework.
Diana Patricia Calixto Morales	Universidad Pedagógica y Tecnológica de Colombia (UPTC), Colombia	Antimicrobial Resistance Linked to the Meat Chain in Boyacá (Colombia): Consumption in Vulnerable Contexts and Persistence of Illegal Slaughter Under the One Health Approach.

# BOOK OF ABSTRACTS

<p>Bellou Zoi Stamatia<sup>1</sup>, Lazou Thomai<sup>2</sup>, Pexara Andreana<sup>1</sup>, Skambardonis Vasileios<sup>3</sup>, Solomakos Nikolaos<sup>1</sup></p>	<p><sup>1</sup>Laboratory of Hygiene of Foods of Animal Origin, Faculty of Veterinary Science, School of Health Sciences, University of Thessaly, Karditsa, Greece</p> <p><sup>2</sup>Laboratory of Animal Food Products Hygiene-Veterinary Public Health, School of Veterinary Medicine, Aristotle University of Thessaloniki, Thessaloniki, Greece</p> <p><sup>3</sup>Laboratory of Epidemiology, Biostatistics and Animal Health Economics, Faculty of Veterinary Science, School of Health Sciences, University of Thessaly, Karditsa, Greece</p>	<p>Hepatitis E Virus in Wild Boars as A One Health Challenge: Preliminary Results from A Study in Greece.</p>
<p>Perruchon Chiara<sup>1</sup>, Tagkalidou Niki<sup>1</sup>, Katsivelou Eleni<sup>1</sup>, Karas A Panagiotis<sup>1</sup>, Kalogiouri Natasa<sup>2</sup>, Menkisoglou Ourania<sup>2</sup>, Vasileiadis Sotirios<sup>*1</sup>, Karpouzas G Dimitrios<sup>1</sup></p>	<p><sup>1</sup>Department of Biochemistry and Biotechnology, University of Thessaly, 41500, Larissa, Greece;</p> <p><sup>2</sup>Laboratory of Analytical Chemistry, Department of Chemistry, Faculty of Sciences, Aristotle University of Thessaloniki, 54124 Thessaloniki, Greece;</p> <p><sup>3</sup>Department of Agricultural Sciences, Aristotle University of Thessaloniki, 541 24, Thessaloniki, Greece</p>	<p>Isolation and characterization of a Sphingomonas antibiotroph able to degrade the pleuromutilin antibiotic tiamulin.</p>

# BOOK OF ABSTRACTS

## Advanced Oxidation Approaches for the Remediation of Antibiotics Contaminated Aquaculture Effluents

Anna Bilida<sup>1</sup>, Alexandra A. Ioannidi<sup>1,2</sup>, Dionissios Mantzavinos<sup>2</sup>, Maria Antonopoulou<sup>1</sup>

<sup>1</sup>Department of Sustainable Agriculture, University of Patras, 30131 Agrinio, Greece,

<sup>2</sup>Department of Chemical Engineering, University of Patras, Caratheodory 1, University Campus, GR-26504 Patras, Greece

**Keywords:** Aquaculture, Advanced Oxidation Processes; Antibiotics, UVC, H<sub>2</sub>O<sub>2</sub>, Ecotoxicity

Aquaculture frequently utilizes antibiotics as sulfamethoxazole (SMX), sulfamethazine (SMZ), and trimethoprim (TMP), whose persistence raises ecological and antimicrobial-resistance concerns [1]. This study examined the simultaneous removal of SMX–TMP and SMZ–TMP mixtures using a UVC/H<sub>2</sub>O<sub>2</sub> process tested in a controlled UVC immersion setup and a top-illuminated reactor open to the atmosphere. HPLC monitored antibiotic concentrations. Aquaculture waters were spiked with environmentally relevant levels of SMX-TMP, and SMZ-TMP, and the selected H<sub>2</sub>O<sub>2</sub> dose. With 15 ppm H<sub>2</sub>O<sub>2</sub>, ~90% removal was achieved across matrices for all antibiotics, with SMX and SMZ degrading faster.

**Acknowledgements:** The research project is implemented in the framework of H.F.R.I call "3rd Call for H.F.R.I.'s Research Projects to Support Faculty Members & Researchers" (H.F.R.I. Project Number: 26141).

### Reference:

[1] Cherian, T., Ragavendran, C., Vijayan, S., Kurien, S., Peijnenburg, W.J.G.M. A review on fate, human health and environmental impacts, as well as regulation of antibiotics used in aquaculture. *Environmental Advances* 2023; 13:100411. <https://doi.org/10.1016/j.envadv.2023.100411>

# BOOK OF ABSTRACTS

## **Bacteria-based army tank crew: plastic bits as vehicles for transporting pathogens and their repertoire of resistance genes.**

Soraya Alfonsi<sup>1</sup>, Pohl Milon<sup>2</sup>, Dezemona Petrelli<sup>1</sup>, Roberto Spurio<sup>1</sup>

<sup>1</sup>School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, Italy; <sup>2</sup>Biomolecules Laboratory, School of Biology, Faculty of Health Sciences, Universidad Peruana de Ciencias Aplicadas, Lima, Peru.

**Keywords:** Plastisphere, Microplastics, Antimicrobial Resistance, Biofilm, Riverine ecosystem, Resistome.

In this study, we have analysed plastic substrates placed in a river of central Italy to investigate the associated biofilm and their role as carrier of antibiotic resistance genes (ARGs). Plastics derived from industrial processes and plastic degradation and fragmentation, represents an emerging health threat in aquatic environments. By providing a suitable surface for bacterial adhesion, plastic bits promote biofilm formation, and can act, even over a long distance, as means of transport of pathogens and ARGs. Polypropylene and polyethylene fragments (1 cm x 1 cm) were placed within nylon filter cages on three sites of the river, during the 3-weeks experiment, while river water samples were simultaneously collected. The off-site analysis of plastic fragments included sonication for cells detachment, cultivation in selective agar medium supplemented with cefotaxime (1mg/L), identification of resistant strains, antimicrobial susceptibility test of isolates, and metagenomic analysis. High proportions of multidrug-resistant (MDR) isolates (72% from plastics, 84% from water), were detected, including extended-spectrum  $\beta$ -lactamase (ESBL) producers (80% and 56%, respectively). Notably, three carbapenemase-producing *K. pneumoniae* strains belonged to sequence type ST1519, reported here for the first time in a natural aquatic environment in Italy. Metagenomic analysis revealed a diverse plastisphere dominated by Comamonadaceae, Sphaerotilaceae, and Flavobacteriaceae. In a One Health perspective, this study highlights the role of plastic debris, “armed” with potential weapons, in the spread of the environmental resistome, which may be a source of genetic determinants conveyed by bacterial strains enriched in clinically relevant ARGs.

# BOOK OF ABSTRACTS

## **Assessment of the antimicrobial activity of pomegranate residues' extract in selected food products**

Lamprini Chani<sup>1</sup>, Anastasios Kyriazis<sup>1</sup>, George Aggelis<sup>1</sup>, Alexandra Lianou<sup>1</sup>

<sup>1</sup>Department of Biology, University of Patras

**Keywords:** Agro-industrial residues, natural antimicrobials, food preservation

The objective of this study was the in situ investigation of the antimicrobial activity of an ethanolic extract derived from pomegranate residues (PRs) against foodborne spoilage and pathogenic bacteria, namely *Bacillus subtilis* and *Listeria monocytogenes*. The activity of the PRs extract at various concentrations was assessed at 15°C in plant-based milk alternatives (rice and almond milks) and at 4°C in turkey deli meat homogenate for *B. subtilis* and *L. monocytogenes*, respectively. In plant based milk alternatives, the PRs extract demonstrated a dose-dependent effect [with regard to its content in total phenolic compounds (TPC) expressed as gallic acid equivalent in mg/L] against *B. subtilis* growth, which was more evident in almond milk compared to rice milk. Specifically, in almond milk, the extract induced an 8-h lag phase at TPC of 480 and 960 mg/L. At 480 mg/L, bacterial populations eventually aligned with the control (ca. 8 log CFU/mL) after 96 h of storage at 15°C, while at 960 mg/L a stronger inhibitory effect was recorded, yielding a lower final population (7.4 log CFU/mL). In turkey deli meat homogenate, *L. monocytogenes* exhibited prolific growth in the control (approaching ca. 9 log CFU/mL within 25 days of storage at 4°C), whereas the extract-treated sample (TPC of 575 mg/L) induced an 8-day lag phase and resulted in considerably lower concentrations of the pathogen for up to 30 days of refrigerated storage. These findings indicate that PRs extracts hold promising antimicrobial potential, contributing to One Health by supporting sustainable, circular, and eco-friendly food preservation strategies.

# BOOK OF ABSTRACTS

## **Molecular Surveillance of Airborne Respiratory Viruses in Healthcare Settings in Greece and the UK Under Post-Pandemic Conditions**

K.A. Koukouvini<sup>1</sup>, R. Fokas<sup>1</sup>, Z. Anastopoulou<sup>1</sup>, A. Chatziantoniou<sup>1</sup>, D. Fiteli<sup>2</sup>, C. N. Karamperi<sup>3</sup>, G. S. Gorgogetas<sup>3</sup>, A. Khan<sup>4</sup>, A. Vantarakis<sup>1</sup>

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Respiratory viruses remain a major public health concern, especially in healthcare settings where close contact and confined spaces promote airborne transmission. Despite lessons from the COVID-19 pandemic, few studies have examined the presence and dynamics of airborne respiratory viruses under routine, post-pandemic conditions across diverse healthcare environments. This study aimed to detect and quantify airborne respiratory viruses, including SARS-CoV-2, Adenovirus, Rhinovirus, Influenza A, and RSV A/B, in selected healthcare facilities in Greece and the United Kingdom, and to examine how environmental and spatial parameters, such as ventilation, occupancy, and human activity, influence viral presence. Air sampling was conducted between January 2024 and November 2024 in an elderly care facility and a general hospital in Thriassio (Greece), and in a large teaching hospital in Bristol (UK). High-volume air samplers (2000 L per sample) were used to collect bioaerosols, and viral RNA was extracted and analyzed via RT-qPCR. Results were evaluated both qualitatively (presence/absence) and quantitatively (Ct values, genome copies per 2000 L of air). Environmental monitoring of indoor air in healthcare facilities from Greece and the UK revealed heterogeneous viral detection patterns. SARS-CoV-2 and Adenovirus were the most prevalent (both 50%), whereas Influenza A was detected in 25% of samples and RSV was not detected in any case. These findings underscore the importance of international environmental surveillance to track respiratory virus circulation and identify risk factors like poor ventilation. They also emphasize the need for continuous airborne pathogen monitoring and targeted control measures in healthcare settings.

# BOOK OF ABSTRACTS

## Biochar from Sewage Sludge: A Circular Strategy Enhancing Water and Health Resilience under Climate Stress

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**Keywords:** Biochar, sewage sludge, pyrolysis, adsorption, wastewater treatment, circular economy

The urgent need for sustainable, low-cost and circular solutions capable of addressing critical environmental challenges has been well recognized. This study aims to investigate the potential of sewage sludge-derived biochar (BCxSS) as a material for wastewater treatment, environmental and public health protection [1]. Biochar produced through pyrolysis of sewage sludge represents a promising resource that aligns with circular economy principles while addressing various environmental and public health risks [2,3]. By applying a structured PRISMA-based methodology, 150 studies were examined to evaluate how BCxSS contributes to robust pollutant removal and microbial inactivation [4]. Pyrolysis of sewage sludge produces a porous, carbon-rich material with strong sorption capacity. Pyrolysis conditions shape critical physicochemical properties of biochar — such as yield, ash content, pH, specific surface area and functional groups — which ultimately determine its sorptive performance [5]. Findings show strong removal efficiencies for organic micropollutants, dyes and heavy metals [6]. In addition, the study indicates that BCxSS can adsorb bacterial indicators, inactivate different pathogens, and reduce antibiotic resistance genes, supporting its relevance to environmental and public health protection [4,7,8]. Under climate-change-driven pressures -including increasing water scarcity, the growing need for safe and clean water, as well as for effective wastewater treatment, and the protection of valuable water resources- BCxSS can serve as a cornerstone technology in the transition to a CE, fostering sustainable resource management at the intersection of urban sanitation, agriculture, and environmental protection. These findings contribute to the One Health agenda by highlighting the role of circular wastewater-derived materials in reducing cross sectoral risks.

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# BOOK OF ABSTRACTS

## Genetic Diversity and Zoonotic Relevance of *Mycobacterium bovis* in Georgian Livestock: A One Health Surveillance Framework

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**Keywords:** *Mycobacterium bovis*, zoonotic tuberculosis, livestock, Georgia, One Health, molecular epidemiology

The research established Georgia's integrated framework for detecting, monitoring, and analyzing zoonotic tuberculosis caused by *Mycobacterium bovis* and other members of the *Mycobacterium tuberculosis* complex (MTBC). Phase 1 focused on livestock as the primary reservoir, forming a scientific basis for future investigations at the human-animal interface. Fieldwork was conducted in collaboration with 17 slaughterhouses across Georgia. In total, 591 cattle carcasses were examined, of which 184 exhibited tuberculosis-like lesions. Geographic coordinates were recorded for geospatial mapping and risk visualization. Laboratory diagnostics included histopathology, culture on LJ pyruvate and Coletsos media, and real-time PCR targeting IS6110. Optimized decontamination protocols improved culture viability. Eleven isolates were microbiologically confirmed as *M. bovis*, and three were PCR-positive. Whole-genome sequencing of one isolate yielded over five million reads and 926 SNPs, classifying it within the European 1 clonal complex - genetically distinct from vaccine strains - indicating circulation of wild-type field strains. GIS-based mapping revealed localized clusters of bovine TB, while statistical analysis showed a strong correlation between cattle TB and human pulmonary TB (Pearson  $R = 0.72$ ;  $p = 0.043$ ), suggesting a potential zoonotic link. The research established a robust framework for characterizing bovine TB dynamics in Georgia. The findings confirm the presence of circulating wild-type *M. bovis* strains and spatial overlap with human TB cases, underscoring the importance of sustained One Health collaboration. These outcomes provide a durable foundation for evidence-based zoonotic TB surveillance and control in Georgia and the broader Caucasus region. The work was supported by Shota Rustaveli National Scientific-Research Foundation of Georgia (SRNSFG) [Grant Number FR-22-6780]

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# BOOK OF ABSTRACTS

## **Antimicrobial Resistance Linked to the Meat Chain in Boyacá (Colombia): Consumption in Vulnerable Contexts and Persistence of Illegal Slaughter Under the One Health Approach**

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**Keywords:** Antimicrobial resistance, meat chain, illegal slaughter, public health, One Health, food safety Antimicrobial resistance in animals affects you, your community and your food system. In Boyacá the meat chain has large informal activity. Many municipalities do not have legal slaughter services. Illegal sites process animals without inspection. This meat reaches childcare centers, school feeding programs, prisons and local markets. These sites serve groups with higher health risks. Reports from the Health Secretariat of Boyacá and Hospital San Rafael describe frequent seizures of meat with signs of contamination. News reports also describe animals in poor health, lack of refrigeration and direct contact with waste. These practices increase exposure to bacteria with resistance traits. Work from national and international studies shows the presence of ESBL producing *Escherichia coli*, methicillin resistant *Staphylococcus aureus* and non susceptible *Salmonella* in meat from informal slaughter. I organized this study with three steps. First, I reviewed ten years of official records across the region. Second, I analyzed scientific evidence on resistance trends in cattle and pigs. Third, I built a "One Health Nexus: Bridging Human, Animal, and Environmental Health Across Europe" One Health model that links farm drug use, slaughter practices, water quality and community exposure. The findings show a stable pattern. Illegal slaughter continues even after closures. Enforcement alone does not solve the problem. There is no regional system for routine microbiology testing. There is no tracking system for meat that enters vulnerable settings. This study supports the need for a local One Health plan. The plan should include constant monitoring, safe slaughter routes and clear protection rules for high risk groups.

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# BOOK OF ABSTRACTS

## Isolation and characterization of a *Sphingomonas* antibiotroph able to degrade the pleuromutilin antibiotic tiamulin.

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**Keywords:** tiamulin, *Sphingomonas*, antibiotrophy, biotransformation, multi-omics

Tiamulin (TIA) is commonly used in veterinary practice. It is persistent in the animal digestive system, its excreta and receiving environments, posing environmental and public health concerns due to potential selection for microbial TIA resistance. Antibiotrophy could be exploited for the reduction of antibiotic pressure in environmental settings. We isolated a TIA-degrading bacterium with such prospect<sup>1</sup>. Our isolate biotransformed TIA in very short time-periods (1-10 days depending on TIA dose and rest conditions), even at concentrations of up to 100 mg ml<sup>-1</sup> of TIA, at a range of pH values between 5.5 and 9, and at cool (16 °C) and warm (25 °C) temperatures. Phylogenomic analysis deemed the isolate to be a new *Sphingomonas* species (83.87 % ANI with *S. laterariae*, ≤ 95 %), which was named *Candidatus Sphingomonas perruchoniana*. Genomics and transcriptomics revealed the TIA mediated induction of features conducive with the antibiotrophic character for the microbial isolate, including (i) ABC-F transporters and efflux pumps able to protect the ribosome and microbial cells from TIA, and (ii) oxygenases (e.g. P450 cytochrome) and hydrolases (e.g. alpha/beta-hydrolases and amidohydrolases) possibly contributing to its degradation. LC-MS/MS analysis detected putative transformation products of TIA, involving a primary oxidation of the tricyclic moiety of TIA to a mono-hydroxylated derivative (OH-TIA), potentially mediated by the highly upregulated monooxygenases, which was either further oxidized to di-OH-TIA or hydrolysed, by the upregulated hydrolase or amidohydrolases, to 2-diethylamino-ethyl-thio acetic acid, both not degrading further. This study delves in the prospects of antibiotrophy in the race against antibiotic resistance.

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# BOOK OF ABSTRACTS

## Hepatitis E Virus in Wild Boars as A One Health Challenge: Preliminary Results from A Study in Greece.

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**Keywords:** Hepatitis E Virus (HEV), Wild Boars, One Health

**Introduction:** Hepatitis E virus (HEV) is an emerging public health concern and a leading cause of acute viral hepatitis. Transmission occurs via contaminated food or water (Song, 2010; Kamar et al., 2014), while direct human-to-human spread remains rare. Domestic pigs and wild boars serve as important reservoirs (Schlosser et al., 2014), yet the links between animals, humans, and the environment suggest a wider transmission context. A One Health framework becomes crucial for understanding risk and guiding prevention. This study examines HEV prevalence in Greek wild boars to support cross-sector surveillance and enhance public health preparedness. **Materials and Methods:** A total of 113 tissue samples were analyzed: liver (n=83) and muscle (n=30: heart n=18, diaphragm n=12), collected between September 2024–January 2025 and September–November 2025 from seven Greek regions with high wild boar populations. Hunters were trained in tissue sampling. Samples were stored frozen until analysis. RNA was extracted using fine quartz grains, and HEV detection was performed by RT-PCR targeting the ORF3 region using the Eurobio Scientific HEV kit. Samples with Ct <40 were considered positive. **Results:** HEV RNA was detected in 9/113 samples (8%), including 7 liver (8.4%) and 2 muscle (6.7%; heart 5.6%, diaphragm 8.3%) samples, from nine wild boars. Mean Ct value was 34.4. **Conclusion:** Preliminary results indicate notable HEV prevalence in Greek wild boars and its detection in edible tissues. Further research is essential to support comprehensive One Health efforts and accurately assess public health potential impacts across relevant human exposure pathways.

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