EcotoxicoMic YR 2025

Third International Webinar of Young Microbial Ecology Researchers

Program & Abstract Book

Online Event

October 13, 20, 27 & November 3rd

24 Oral Presentations • 12 Posters

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Acknowledgements

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Keynote Speakers

Prof. Dr. Tamara Tal

Affiliation: Helmholtz Center for Environmental Research, Leipzig, Germany

Presentation Title: *Exploring chemical microbiome interactions in zebrafish*

Biography:

Prof. Dr. Tamara Tal heads the Molecular Toxicology Group at UFZ, Leipzig and holds a professorship in Integrated Systems Toxicology at the University of Leipzig. Her research focuses on developmental neurotoxicity, chemical-microbiome interactions, and the use of zebrafish models to study chemical exposure effects. Prior to joining UFZ in 2019, she was a Principal Investigator at the U.S. Environmental Protection Agency. Prof. Tal has received multiple awards, including the 2020 Paper of the Year Award from the Society of Toxicology.

Dr. Clémence Thiour Mauprivez

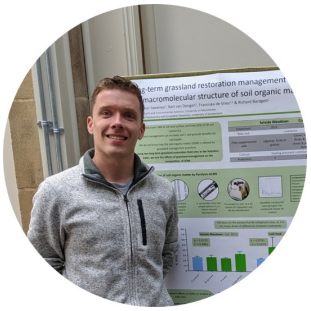
Affiliation: Université Bourgogne Europe, UMR Agroécologie (INRAe BFC), France

Presentation Title: *Effects of microplastics on bacterial communities in agricultural soils*

Biography:

Dr. Clémence Thiour Mauprivez is a microbial ecotoxicologist and assistant professor at Université Bourgogne Europe. Her research at the UMR Agroécologie (INRAe BFC) focuses on the impact of agricultural practices and contaminants (pesticides, microplastics and antibiotics) on soil microbial communities.

Dr. Christopher Sweeney



Affiliation: Syngenta, United Kingdom

Presentation Title: *Better, not just newer: A case study of soil microbial pesticide risk assessment*

Biography:

Dr. Christopher J. Sweeney's research focuses on the environmental risk assessment of plant protection products, particularly their impact on soil microbiomes and invertebrates. His work aims to enhance the ecological relevance and regulatory frameworks of pesticide evaluations. He has co-authored several publications on topics such as the influence of soil organic matter on pesticide toxicity and the inclusion of metabarcoding data in risk assessments.

Dr. Edward Topp

Affiliation: INRAE, Senior Chair on Antimicrobial Resistance, France

Presentation Title: *Impacts of humans on the environmental resistome and mobilome*

Biography:

Dr. Ed Topp is an environmental microbiologist, internationally recognized for his work on the environmental dimensions of antimicrobial resistance (AMR), particularly in agricultural systems. His research focuses on how antibiotics and resistance genes move through soil, water, and manure, contributing to the spread of AMR. Previously based in Canada, he has led major interdisciplinary projects promoting One Health approaches to AMR. At INRAE, he advances science-based strategies to monitor and mitigate AMR risks at the intersection of environment, agriculture, and public health.

Program

Day 1 - Monday, October 13th, 2025

October 13, 2025

13:30 - 13:45 : Opening of EcotoxicoMic YR 2025 webinar

Marine Suchet & Nicolas Gallois

13:45 - 14:30 : **KEYNOTE** - *Exploring chemical-microbiome interactions in zebrafish*

Prof. Dr. Tamara Tal

14:30 - 15:15 : **SESSION** - Microbiome host interactions - Part 1

Chair: Lauris Evariste

- (O01) **Marine Suchet** - “Impacts of chronic exposure to sodium fluoride or tebuconazole on the branchial, intestinal and epidermal microbiota of juvenile rainbow trout”
- (O02) **Chloe Wray** - “Chemical-Microbiome Interactions in Larval Zebrafish: Microbiome-Dependent Effects of Azoxystrobin on Neurobehavior”
- (O03) **Maëlann Roger** - “Exposure to pesticides in Magallana gigas larvae: impact to its microbiota and its susceptibility to OsHV-1 at the spat stage”

15:15 - 16:15 : *Poster & Flash Presentations*

16:15 - 17:00 : **SESSION** - Microbiome host interactions - Part 2

Chair: Marine Suchet

- (O04) **Thomas Moura** - “Comparative ecotoxicological effects of a copper-based nanopesticide and its conventional equivalent on Xenopus laevis tadpole and its gut microbiota”
- (O05) **Florian Chapeau** - “Effects of graphene oxide on Xenopus laevis after multi-route exposure: an integrated host-microbiota approach”
- (O06) **Jesse Ouwehand** - “Microbial custody: key microbiome inhabitant Sphingomonas alleviates silver nanoparticle toxicity in Daphnia magna”

Day 2 - Monday, October 20th, 2025

October 20, 2025

13:30 - 13:35 : Introduction of the day

Maria Osipenko

13:35 - 14:20 : **KEYNOTE** - *Effects of microplastics on bacterial communities in agricultural soils*

Dr. Clémence Thiour Mauprivez

14:20 - 15:05 : **SESSION** - Effects of contaminants on microorganisms: from species to communities - Part 1

Chair: Maria Osipenko

- (O07) **Camille Touchet** - “Microplastics and freshwater disease ecology: impacts on microbiota, life-history traits, and transmission potential of the snail Galba truncatula”
- (O08) **Koffi Anderson Hongo** - “Assessment of microbial diversity in lake Kassembié for microplastic degradation using 16S rRNA (V3-V4) region sequencing”
- (O09) **Marie Winter** - “Laboratory to field scale: the ecological relevance of laboratory tests for environmental reliable ecotoxicity assessment of polymers”

15:05 - 16:05 : *Poster & Flash Presentations*

16:05 - 16:50 : **SESSION** - Effects of contaminants on microorganisms: from species to communities - Part 2

Chair: Roxane Dhommée

- (O10) **Olivia F. Sieniawski** - “Surfactants in herbicide formulations influence nitrogen cycling in soil microcosms”
- (O11) **Maria Osipenko** - “Effect of plant-based products on soil microbial communities in Christmas tree plantations”
- (O12) **Neus Besolí-Mestres** - “Does urban runoff impact urban stream communities?”

Day 3 - Monday, October 27th, 2025

October 27, 2025

13:30 - 13:35 : Introduction of the day

Titouan Dionet

13:35 - 14:20 : **KEYNOTE** - *Better, not just newer: A case study of soil microbial pesticide risk assessment*

Dr. Christopher Sweeney

14:20 - 15:20 : **SESSION** - New methods and approaches in microbial ecotoxicology

Chair: Nicolas Gallois

- (O13) **Tifenn Primet** - “Toxic Foresight: Predicting Harmful Cyanobacterial Blooms”
- (O14) **Isiaka A. Adelere** - “Application of Bacillus safensis lau 13 metabolite for the control of growth and aflatoxin production by Aspergillus species on stored maize grains”
- (O15) **Camille Saint-Picq** - “Revealing marine plastic degraders using stable isotope tracers”
- (O16) **Titouan Dionet** - “Spore-tacular automation: deep learning analysis for aquatic hyphomycete ecotoxicological assessment”

15:20 - 16:20 : *Poster & Flash Presentations*

16:20 - 16:50 : **SESSION** - Microbial bioprocesses and bioremediation

Chair: Ioanna Gkoni

- (O17) **Göksu Celik** - “Biodegradability of tire additives: the role of freshwater and wastewater microbiomes”
- (O18) **Olivia Renard** - “S-metolachlor degradation in agricultural soils and groundwater: isolation of native degrading strains and microbial community profiling”

Day 4 - Monday, November 3rd, 2025

November 3, 2025

13:20 - 13:25 : Introduction of the day

Sofia Agosti

13:25 - 14:10 : **KEYNOTE** - *Impacts of humans on the environmental resistome and mobilome*

Dr. Edward Topp

14:10 - 14:55 : **SESSION** - Antimicrobial resistance

Chair: Sofia Agosti

- (O19) **Ioanna Gkoni** - “Influence of antibiotics and microbial coalescence on sediment microbial communities’ functions and diversity”
- (O20) **Anita Solem** - “Dissemination of antimicrobial resistance and potential pathogens through urban wastewater treatment plants”
- (O21) **Eleni Rafaila Lamprou** - “Plastisphere as a Hotspot for Antibiotic Resistance Gene Enrichment in Fertilized Agricultural Soils”

14:55 - 15:45 : *Poster & Flash Presentations*

15:45 - 16:30 : **SESSION** - Effects of contaminants on microorganisms: from species to communities - Part 3

Chair: Camille Touchet

- (O22) **Charly Dupont** - “Novel insight into rare earth element mediated stress resistance in Pseudomonas putida KT2440 using adaptative laboratory experiment”
- (O23) **Zahrasadat Alavikakhiki** - “Acute toxicity evaluation of 12 pharmaceuticals on microbial functions of periphyton”
- (O24) **Andrea Marchetto** - “Responses of Gut Microbial Species and Complex Communities to Xenobiotic Exposure Reveal Mechanisms of Resilience and Vulnerability in vitro”

16:30 - 16:40 : Presentation of EcotoxicoMic 2026

Dimitrios Karpouzas

16:40 - 16:55 : Awards & Closure of the third international webinar

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Poster Presentations List

P1 - Arrigoni Zoé - Road Dust contaminants and periphytic microalgae: community shifts and trophic transfer to Daphnia magna

P2 - Bourhane Zeina - Novel Bioactive Molecules in Thermal Waters: A New Frontier in Cosmetic Innovation

P3 - Caux Daphnée - Prior stress exposure influences microbial community assembly and litter decomposition in headwater streams

P4 - Chamorro Catherine - Effects and intracellular fate of cobalt (Co) in the freshwater microalga Chlamydomonas reinhardtii

P5 - Delcros Emeline - Elucidation of intracellular speciation and the effects of indium on the microalga Chlamydomonas reinhardtii

P6 - Khalfallah Fadwa - Urban land use shapes microbial life strategies along a management intensity gradient

P7 - Köhler Stella - Pesticide mixture effects on bioaccumulation and toxicity in biofilms

P8 - Langel Jessie-Lee - New Biomarkers for Sea Turtle Conservation: Insights from Shell Biofilms and Eggshell Trace Metals

P9 - Le Douarin Louis - Development of a multi-omic approach to assess the impact of the harbour eco-exposome on juvenile fish

P10 - Lounas Ryhane - Isolation and characterization of indigenous hydrocarbon-degrading bacteria from oil-contaminated Algerian soils using Nanopore technology

P11 - Mejia Camacho Ana Luisa - Fitness Costs Limit MDR E. coli Invasion but Not Gene Dissemination in Freshwater Sediment

P12 - Sepet François - River or dendrotelmata: Does habitat of origin shape the tolerance of aquatic hyphomycetes to lead and copper?

Oral Presentations

Microbiome - host interactions

Presentation O01

Impacts of chronic exposure to sodium fluoride or tebuconazole on the branchial, intestinal and epidermal microbiota of juvenile rainbow trout (Oncorhynchus mykiss)

Suchet Marine[1], Pannetier Pauline[1,2], Supliot Lalie[2], Danion Morgane[2], Cachot Jérôme[1], Bellec Laure[1]

[1]Environnements et Paléoenvironnements OCéaniques (France)
[2]Laboratoire de Ploufragan-Plouzané-Niort [ANSES] (France)

The holobiont concept has emerged as a key integrative approach in microbial ecotoxicology, as microbiota play crucial roles in growth and immunity. Recent studies showed that disruptions of microbial communities could alter the host health, and result from environmental changes, including exposure to pollutants. Tebuconazole (Tbz) is a fungicide used in agriculture and sodium fluoride (NaF) is a compound used in industrial processes, for the fluoridation of drinking water, and in dental care products. Both compounds can be detected in freshwater ecosystems, and due to their antifungal and antibacterial properties, one might expect them to disrupt the microbiota of aquatic organisms. Rainbow trout (Oncorhynchus mykiss) is frequently used as fish model in ecotoxicology, and is one of the most farmed fish worldwide. Gaining a better understanding of the microbiota of farmed fish, and how it is influenced, is a major challenge for food safety. The aim of this study was to assess the effects of chronic exposure to sodium fluoride (5 or 17 mg/L) or tebuconazole (69 µg/L) on the branchial, intestinal and epidermal microbiota of rainbow trout. Fish were exposed from 6 days post-fertilization to 7 months. DNA was then extracted from gills, mid-gut and epidermal mucus, and the V3-V4 region of the 16S rRNA gene was amplified by PCR. Sequencing was performed on a NextSeq2000 (Illumina) and data were processed using FROGS (v5). Diversity analyses were used to characterise the amplicon sequence variants (ASVs), in terms of Alpha and Beta diversity, as well as to assess the taxonomic composition of the bacterial communities. Differential abundances analyses (DESeq2 and LEfSe) will provide further insights into microbiota disturbances caused by the two compounds. Preliminary results indicate that the bacterial communities of this freshwater fish are affected by chronic exposure to sodium fluoride and tebuconazole, and in a tissue-specific manner.

Keywords: holobionte, symbiotoxicity, chronic exposure, aquatic pollutant, rainbow trout

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Presentation O02

Chemical–Microbiome Interactions in Larval Zebrafish: Microbiome-Dependent Effects of Azoxystrobin on Neurobehavior

Wray Chloe[1,2], Castañeda-Monsalve Victor[1], Jemlich Nico[1], Engelmann Beatrice[1], Rolle-Kampczyk Ulrike[1], Kader Siraz[1], Tyler Charles[2], Tal Tamara[1,3]

[1]Helmholtz Centre for Environmental Research GmbH - UFZ, CITE, Leipzig, Saxony (Germany)
[2]Biosciences, Geoffrey Pope Building, University of Exeter, Exeter EX4 4QD (United Kingdom)
[3]University Leipzig, Medical Faculty, Leipzig, Saxony (Germany)

Microbial colonization is essential for the development of a functional nervous system, yet exposure to environmental chemicals can disrupt microbiome composition, impact function, and alter the biotransformation of xenobiotics. Azoxystrobin, a widely used broad-spectrum fungicide, has previously been shown to induce shifts in microbial composition and alter pathways related to xenobiotic response in a defined, simplified ex vivo human gut microbiota (SIHUMIx). Here, we utilize larval zebrafish to investigate whether azoxystrobin-microbiome interactions also drive neurobehavioral changes, establishing a causal link to phenotypic effects in the context of a host. We derived microbiome-depleted zebrafish larvae and colonized a subset with SIHUMIx at 1 day post fertilization (1 dpf). At 4 dpf, larvae from both cohorts were developmentally exposed to azoxystrobin. Neurobehavioral responses were assessed at 5 dpf using the Visual and Acoustic Motor Response (VAMR) NAM. This 25-endpoint automated behavior battery quantifies responses to a range of visual and acoustic stimuli, allowing us to use behavior as a functional readout of neurodevelopment. Targeted metabolomics of amino acids, biogenic amines, and short chain fatty acids complemented behavioral endpoints to explore potential underlying mechanisms. Colonized larvae exposed to azoxystrobin exhibited dark-phase hyperactivity relative to colonized controls, a phenotype absent in exposed microbiome-depleted larvae. Colonized fish also exhibited higher serotonin levels, suggesting microbiome-mediated modulation of neurotransmitter availability that may underlie behavioral responses to azoxystrobin. Collectively, these findings support a role for host-associated microbes in xenobiotic biotransformation and highlight their potential to shape neurobehavioral responses to environmental chemicals.

Keywords: microbiome, zebrafish, azoxystrobin, metabolomics

Presentation O03

Exposure to pesticides in Magallana gigas larvae: impact to its microbiota and its susceptibility to OsHV-1 at the spat stage

Roger Maëlann[1], Morga Benjamin[2], Dégremont Lionel[2], Troncin Fanny[3], Tourbiez Delphine[2], Maurouard Elise[2], Akcha Farida[1], Bertucci Anthony[1]

[1]Unité Contamination Chimique des Ecosystèmes Marins (France)
[2]Unité Adaptation et Santé des Invertébrés Marins (France)
[3]Université de Bordeaux (France)

The Pacific oyster (Magallana gigas) is a key sentinel species in coastal ecosystems. It is increasingly exposed to complex mixtures of anthropogenic pollutants, including trace metals and pesticides. While ecotoxicological studies have explored the oyster exposome and its physiological impacts, the contribution of the microbiome to host health remains largely overlooked. This is particularly critical during early developmental stages, which are highly vulnerable to xenobiotics and coincide with the establishment of the host-associated microbiota. Given the recognised role of the microbiota in immune function, development, and environmental resilience, pollutant-induced disruptions to this symbiotic relationship—termed symbiotoxicity—deserve closer attention. This study aimed to investigate how early-life exposure to a complex pollutant mixture affects the oyster microbiome, and whether these changes influence susceptibility to viral infection. Six oyster families, selected for resistance or susceptibility to Ostreid herpesvirus 1 (OsHV-1), were either unexposed or exposed to an environmentally relevant mixture of eighteen contaminants (pesticides and metals used in pesticide formulations) for ten days during the larval stage. Later, at the juvenile stage, they were challenged with OsHV-1. Bacterial communities were characterised by high-throughput sequencing of the full-length 16S rRNA gene using Nanopore long-read technology. Our first findings showed that contaminant exposure reduced fertilisation success, except for one family. Alpha diversity metrics revealed no significant differences across conditions or families, but bacterial richness declined over time. Beta diversity analyses (PERMANOVA) showed significant effects of time (R^2 = 22.3%), oyster family (R^2 = 14.5%), and early-life contaminant exposure (R^2 = 3.2%) on bacterial community structure. While differences in mortality were observed between resistant and susceptible families, no differences in survival were detected between exposed and unexposed oysters during the OsHV-1 challenge. These results indicate that early-life exposure can alter microbiome structure but has limited impact on viral susceptibility.

Keywords: microbiome, oyster, pesticides, symbiotoxicity, oshv, 1, ecotoxicology

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Presentation O04

Comparative Ecotoxicological effects of a Copper-Based Nanopesticide and its Conventional Equivalent on Xenopus laevis tadpole and its Gut Microbiota

Moura Thomas[1], Chapeau Florian[1], Nguyen Van Xuan[1], Vivant Marion[1], Larue Camille[1], Candaudap Frédéric[1], Barret Maïalen[1], Chevalier Laurence[2], Gauthier Laury[1], Pinelli Eric[1], Mouchet Florence[1]

[1]Centre de Recherche sur la Biodiversité et l'Environnement (France)
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Concerns regarding copper use in agriculture and accumulation in the environment have led to restrictions on its use. Copper-based nano formulations have been proposed as an alternative. However, their release from soil into aquatic environments might threaten non-target organisms. Amphibians have already been heavily impacted by anthropogenic activities and their gut microbiota are likely to be sensitive to such products. Ecotoxicological data and studies on commercial formulations that specifically focused on aquatic systems are still scarce. The aim of this study was to determine the impact of a copper (Cu(OH)□)-based nanopesticide, Kocide 3000® (K3), compared to the non-nanosized equivalent Kocide 2000® (K2), at environmentally relevant concentrations (5 , 10 , 25 and 50 µg Cu L−1). For this purpose, the amphibians Xenopus laevis tadpoles were exposed for 12 days, after which toxicity endpoints were measured, and 16S rDNA gene sequencing was performed to characterize the bacterial composition in the gut. Copper salt (CuSO□·5H□O) was also tested to provide a benchmark for assessing copper-related toxicity alongside the complex commercial formulations. Exposure to all copper formulations resulted in measurable effects across the assessed physiological parameters. Regarding the intestinal microbiota response, bacterial communities were shown to be significantly altered. The effect of the two commercial products differs from that of copper alone, inducing differential modifications to the bacterial community structure, as evidenced by changes in the abundance of phyla. Only the nanopesticide K3 induced significant changes compared to the negative control at all tested concentrations. This study highlights the effects of copper nanopesticides on aquatic organisms and their associated microbiota, reinforcing the need for a holistic ecotoxicological approach.

Keywords: aquatic ecotoxicology, nanopesticide, copper, gut microbiota, amphibian

Presentation O05

Effects of graphene oxide on Xenopus laevis after multi-route exposure: an integrated host-microbiota approach.

Chapeau Florian[1], Moura Thomas[1], Nguyen Van Xuan[1], Barret Maialen[1], Dailhau Sandra[2], Vivant Marion[1], Flahaut Emmanuel[3], Gauthier Laury[1], Pinelli Eric[1], Mouchet Florence[1]

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[3]CIRIMAT (France)

Graphene-based nanomaterials, such as graphene oxide (GO), possess unique physicochemical properties that have favored their widespread industrial and biomedical use. However, GO is inevitably released into aquatic ecosystems throughout its life cycle, making a thorough ecotoxicological assessment essential for its safe application. Although amphibians such as Xenopus laevis are common toxicity models, they are rarely considered as holobionts, that is, integrated units of host and microbiota. This study fills this gap by examining the combined effects of direct (water column) and trophic exposure to GO on post-metamorphic X. laevis, with a particular focus on microbiota essential for host homeostasis, nutrient uptake, and immunity. To simulate realistic conditions, juvenile frogs were kept for 96 hours in aquaria containing GO at 0.1 and 10 mg/L, while feeding on previously added chironomid larvae, thus loading them with GO. At the end of the exposure, genomic DNA was extracted from intestinal and skin samples to profile bacterial communities using high-throughput 16S rRNA gene sequencing. In addition, liver mRNA sequencing was performed to reveal metabolic responses and transcriptomic changes related to GO exposure and microbiota disruption. GO caused significant intestinal dysbiosis, notably altering the relative abundance of Firmicutes and Bacteroidetes, two phyla often associated with digestive function and metabolic balance. On the skin, variations in the proportions of Proteobacteria suggest a potential weakening of microbial defenses against pathogens such as Batrachochytrium dendrobatidis. Concurrently, the liver transcriptome showed an upregulation of energy reallocation pathways, indicating compensatory metabolic adjustments possibly induced by microbiome disruption. These results demonstrate that GO acts as an environmental stressor destabilizing the amphibian holobiont, from microbial assemblages to host physiology. Integrating microbiome analyses into ecotoxicological frameworks thus enables a more comprehensive risk assessment of emerging nanomaterials and underscores the need to consider host-microbiota interactions in environmental safety assessments.

Keywords: aquatic ecotoxicology, nanomaterials, graphene oxide, amphibian, microbiota

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Presentation O06

Microbial custody: key microbiome inhabitant Sphingomonas alleviates silver nanoparticle toxicity in Daphnia magna

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[2]National Institute of Public Health and the Environment (RIVM) (Netherlands)

The expanding application of nanotechnologies increases the likelihood of environmental exposure to metallic nanoparticles of hosts and their associated microbiomes. While microbial resistance to metal toxicity has been widely studied in isolation, less is known about how these interactions play out within host-microbe systems. In this study, we investigated the role of silver ion-resistant bacteria from the Daphnia magna microbiome in modulating host responses to silver nanoparticles (AgNPs). Using germ-free and mono-associated D. magna neonates, we assessed how specific bacterial strains influence host sensitivity to AgNPs. We identified Sphingomonas yanoikuyae, a core microbiome member, as silver-resistant. Mono-association with S. yanoikuyae conferred similar AgNP tolerance as seen in naturally colonized neonates, while germ-free and Microbacterium-associated neonates showed increased sensitivity. In these latter groups, toxicity was primarily driven by dissolved silver ions, whereas in Sphingomonas- and naturally colonized neonates, particulate silver played a greater role. Notably, S. yanoikuyae accumulated more silver ions in vivo than other isolates. Our findings highlight the critical role of microbiota in influencing nanoparticle speciation and modulating nanotoxicity within host organisms.

Keywords: bacterial resistance, metal speciation, metal, based nanoparticles, microbiome, aware ecotoxicology, microbiome, host

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Effects of contaminants on microorganisms : from species to communities

Presentation O07

Microplastics and freshwater disease ecology: impacts on microbiota, life-history traits, and transmission potential of the snail Galba truncatula

Touchet Camille[1], Chapuis Elodie[1]

[1]MIVEGEC (France)

Microplastics are emerging contaminants representing a major challenge for society and research. Two decades of studies documented their accumulation and spreading at a global scale but their effects on organisms and ecosystem functioning remain only partially understood. They threaten the environment as well as animal and human health, yet their role in host–parasite interactions remain poorly understood, especially in freshwater ecosystems where both plastic pollution and zoonotic disease risks are high. To address this gap, we investigate the effects of microplastic pollution in the vulnerable Camargue wetlands on the freshwater snail Galba truncatula. This species is the main European host of the liver fluke Fasciola hepatica, a trematode parasite infecting humans and livestock and causing severe health issues and economic losses. Because microorganisms play key roles in immunity, including host susceptibility to parasitic infection—and are highly sensitive to environmental perturbations, we hypothesize that microplastic exposure alters the snail microbiota, affecting both life history traits and transmission potential. To test this hypothesis, snails will be reared at the laboratory under four experimental conditions: exposed to (1) microplastics only, (2) parasite only, (3) combined microplastics + parasite, (4) control. Experimental infection will be conducted using F. hepatica larvae and the transmission potential of snails will be evaluated by quantifying the production of metacercariae, i.e. the infective stage for mammals. Survival, growth and reproduction will be monitored throughout the snail's life cycle. Finally, the snail microbiota diversity, both from field and laboratory populations will be characterized through 16S metabarcoding. This integrative design links pollution biology with disease ecology, providing the first experimental evidence on how microplastics can influence host microbiota and parasite transmission.

Keywords: plastic pollution, microplastics, freshwater ecosystems, wetlands, microbiota, host parasite, zoonosis, snails, f. hepatica, g. truncatula

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Presentation O08

Assessment of microbial diversity in lake Kassembié for microplastic degradation using 16S rRNA (V3–V4) region sequencing

Hongo Koffi Anderson[1], Attahoua Ines Estelle Kouadio[1]

[1]Université Nangui Abrogoua (Côte d'Ivoire)

Microplastic pollution poses a growing threat to aquatic ecosystems, particularly in understudied tropical regions such as Lake Kassembié in Côte d'Ivoire. This study aims to evaluate the microbial diversity of the lake and identify native bacterial communities with the potential to degrade microplastics, using high-throughput sequencing of the 16S rRNA V3–V4 regions. Water samples were collected and filtered from different lake zones. Environmental DNA was extracted and sequenced using the Illumina platform. Bioinformatic analysis was performed using QIIME 2 to process and classify the microbial communities. The results reveal high microbial diversity, with dominant phyla including Proteobacteria, Firmicutes, and Bacteroidota. Notably, several bacterial genera known for their plastic-degrading capabilities were detected: Acinetobacter (Kass47–48), Pseudomonas (Kass23–24), Bacillus (Kass39–40, Kass42–43, Kass37–38, Kass47–48), and Stenotrophomonas (Kass37–38). These genera are reported in the literature for their ability to produce enzymes such as hydrolases and laccases that facilitate the breakdown of synthetic polymers. These preliminary findings highlight the presence of indigenous microbial taxa in Lake Kassembié that may contribute to natural microplastic degradation. The study offers a foundation for further functional metagenomic analysis and potential development of eco-friendly bioremediation strategies using native microbial resources.

Keywords: degradation, microbiome, lake, microplastic

Presentation O09

Laboratory to Field Scale: The Ecological Relevance of Laboratory Tests for Environmental Reliable Ecotoxicity Assessment of Polymers

Winter Marie[1], Broll Gabriele[2], Bodo Philipp[3], Diaz Cecilia[1], Schlich Karsten[1]

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Polymeric compounds are included into various agrotechnical products. Given that synthetic polymers and modified natural polymers are subject to REACH, biopolymers can be regarded as important substitute components. Due to their natural origin, they remain unregulated, even though their complex molecular structures could lead to increased accumulation potential in the environment. As regulatory requirements and hazard evaluation concepts are missing, the potential ecotoxicological impact is unknown. Our main aim was therefore to develop a systematic ecotoxicological hazard assessment including terrestrial ecotoxicity screening tests for (bio)polymers. Potential nitrification (ISO 15685) and extracellular enzymatic activity (ISO 20130) tests were combined with molecular biological analysis using qPCR (target: amoA). By this, we aim to connect soil function with microbial diversity and specific gene expression potential. In order to ensure the reliability of the data collected and prove the ecological relevance, a combination of laboratory tests and field studies has been utilized. For testing, we focused on alginate, cellulose fibers and active char formulated in a seed coating with sugar beet. The treated soil was incubated under laboratory conditions in glass vessels (without seed) and under field exposure in small-scale lysimeters (with seed). The components were applied as single substances (1000 mg/kg) and as cryomilled formulations (1 and 3 coatings/2.5 kg). Additionally, seed coatings (1 and 3 coatings/2.5 kg) were exposed (field exposure). The tests were conducted 28, 100 and 365 days after the treatment of the test soil. Overall, the laboratory results of 28 and 100 day exposure overestimated the effects observed under field conditions, indicating that the laboratory approach is a conservative and protective tool for hazard assessment. Molecular biological tests are currently being carried out. An overview of the results will be presented in the webinar.

Keywords: hazard assessment, polymers, functional ecotoxicity, molecular biological analysis

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Presentation O10

Surfactants in herbicide formulations influence nitrogen cycling in soil microcosms

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Soil plays a critical role in biogeochemical cycles that regulate the transformation of essential elements such as nitrogen (N). However, the functionality of the soil microbiome is vulnerable to anthropogenic influences, such as the application of glyphosate-based herbicides (GBHs) in agriculture. GBHs contain glyphosate (GLY) as the active ingredient and various co-formulants, like surfactants (SFs). Although often labelled “inert”, SFs are mostly used to reduce surface tension, enhancing herbicide efficiency. Previous research has shown that SFs alter microbial communities, raising significant concerns about the broader ecological impacts of SFs. Here, we used agricultural soil microcosms to investigate how SFs influence the activity of key microbial players involved in N cycling and their impact on greenhouse gas formation. Oxic and anoxic soil microcosms were established in triplicate with either EU application rates (15 mg/kg) or ‘hotspot’ concentrations (150 mg/kg) of GLY, GBH, or the GLY alternative, the SF pelargonic acid. Chemical analysis assessed compound degradation, gas production, and ion transformation. DNA and RNA were extracted for 16s rRNA gene sequencing, metagenomics, and metatranscriptomes to determine community composition, gene profiling, and activity. Consumption of nitrate and production of nitrite was seen in the anoxic microcosm, with varying differences between treatments. Microbial community shift reflected this, with key denitrifiers either stimulated or inhibited. Key genes in the nitrification cycle and denitrification cycle were seen in the oxic and anoxic microcosms, respectively. In the oxic microcosm, different treatments led to elevated and decreased gene expression in key genes (e.g, amoA – subunit of ammonium monooxygenase) involved in the N-cycle, indicating that SFs and active compounds may be driving microbial community and functional changes. Overall, our findings show that GBHs and SFs alter microbial activity and N-cycling. Thus, raising concerns about the impact of inert ingredients and the need for transparency in herbicide formulations.

Keywords: biogeochemical, cycles, nitrogen, glyphosate, based herbicides, surfactants

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Presentation O11

Effect of plant-based products on soil microbial communities in Christmas tree plantations

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In the context of a transition toward more sustainable agriculture, biological products such as biopesticides, biofertilizers, and biostimulants are experiencing rapid growth. However, their impact on the structure and functioning of soil microbial communities remains poorly documented. As part of the European X-Tree project (EUROSTAR), which aims to develop a sustainable cropping system for Christmas tree production, a bio-based solution combining a bioherbicide (based on essential oils) and a biostimulant (derived from plant extracts) is being studied. The goal of my PhD research is to explore the effects of these products on the dynamics of soil microbial communities, in terms of abundance, taxonomic and functional diversity. Experiments are conducted at different scales (laboratory, greenhouse, and field), using a combination of biochemical (soil respiration, enzymatic activity), molecular (high-throughput sequencing, qPCR), and chemical (chromatography) approaches. At the laboratory scale, a microcosm experiment involving over 300 samples was conducted, it gave us initial insight into how the different products influence soil microbial community dynamics. The next phase of the research will focus on greenhouse-scale studies to further investigate these effects under more complex environmental conditions. The objective is to better understand how these natural inputs influence microbial communities and their associated ecosystem functions. This research contributes to shedding light on the response mechanisms of microbial communities to new agricultural practices.

Keywords: microbial ecotoxicity, soil microorganisms, biological herbicides, biostimulants, soil pollution

Presentation O12

Does urban runoff impact urban stream communities?

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Chemical pollutants mobilized by rainfall generate surface runoff, which affects freshwater ecosystems, particularly in urban areas. Pollutants are transported and often discharged untreated into nearby streams, especially during the “first flush” phase. We investigated the chemical composition and ecological impacts of urban runoff on the Güell stream (Girona, Spain), focusing on benthic biofilms and macroinvertebrate communities. We conducted a Control-Impact experimental design to monitor five independent rainfall events during spring. Different compounds reached the stream via urban runoff at high concentrations, including dissolved organic carbon (28 mg L-1), as well as specific pollutants such as 1,3-diphenilguanidine (37 µg L-1) and zinc (34 µg L-1). Other pollutants, such as carbendazim and Ibuprofen-1-OH, were already present in the stream due to upstream pollution sources. Runoff pulses determined both physical and chemical disturbances, including biofilm detachment from small flood events and pollutant-induced shifts in biofilm structure and function. At the impacted site, several structural (e.g. chlorophyll-a content, r=-0.67) and functional variables (e.g. basal fluorescence, r=-0.75; phosphatase activity, r=-0.83) in the biofilm were negatively correlated with accumulated rainfall over the preceding week prior to the sampling. These events coincided with a peak in pollutant concentrations, suggesting that recent rain events might have caused ecological impacts in the stream. Macroinvertebrate abundance increased following rainfall episodes, likely reflecting seasonal patterns rather than direct effects of runoff. Overall, our results highlight that multiple factors influence stream communities’ responses to urban runoff. Recurrent pulse disturbances could pose long-term risks to ecological integrity, particularly under scenarios of increasing urbanisation and climate-driven extremes.

Keywords: urban runoff, pollutants, pulse disturbances, stream, biofilms, macroinvertebrates

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Presentation O22

Novel insight into rare earth element mediated stress resistance in Pseudomonas putida KT2440 using adaptative laboratory experiment.

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Rare earth element (REE) corresponds to the 15 lanthanides series (Z=57 to 71), scandium (Z=21) and yttrium (Z=39) (Connely et al., 2005). Due to their wide applications in high-technologies products, demands -and consequently extraction- of these metals are in constant increase (Mwewa et al., 2022). This has inevitably led to rising levels of REE in both soils and waters in areas close to large cities, industrial complexes and agricultural areas (Gonzalez et al., 2014 ; Ramos et al., 2016 ; Gomes e al., 2022). The emerging of REE as pollutant raised questions about their ecotoxicology impact. Few studies have focused on toxicity to bacteria, even though they are recognized as drivers of key ecosystem processes and can act as early sentinels of environmental perturbations. Furthermore, data on toxicity of REEs and on the molecular mechanisms underlying bacterial responses to these metals are still scarce. The soil-dwelling bacterium Pseudomonas putida KT2440 employs REE as a cofactor for a periplasmic pyrroloquinoline quinone-dependent alcohol dehydrogenase and appears to possess a complete molecular mechanism dedicated to the sensing, uptake, and utilization of these metals. (Wehrmann et al., 2017 ; Wehrmann et al., 2018 ; Wehrmann et al., 2019). Here we use adaptive laboratory experiment to gain insight into the tolerance of P. putida to REE toxicity. Serial propagation under gradually increasing REE stress levels yielded resistant populations from which two strains showing a stable and significantly higher resistance were isolated. Sequencing of their genomes revealed that each evolved strain has a single substitution in the same uxpB gene, encoding a phosphatase. By using deletion-overexpression approach and phosphatase activity measurements, we confirmed involvement of this gene in REE resistance. Then, effect of the mutations was determined to understand REE resistance mechanisms and allowed to extrapolate key point of REE toxicity toward P. putida KT2440.

Keywords: rare earth elements, phosphatase, experimental evolution

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Presentation O23

Acute toxicity evaluation of 12 pharmaceuticals on microbial functions of periphyton

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Pharmaceutical contaminants in freshwater ecosystems pose significant ecological risks, particularly for periphyton that underpin primary production and nutrient cycling. This study investigates the functional responses of periphyton exposed to selected pharmaceuticals. While antibiotics are designed to target bacteria and are expected to affect microbial communities, other classes of pharmaceuticals may also exert unforeseen impacts. In this context, we aimed to compare the toxicity of different pharmaceutical classes on both autotrophic and heterotrophic microorganisms within periphyton, focusing on functional endpoints. Twelve pharmaceuticals from diverse therapeutic classes—including antibiotics, non-steroidal anti-inflammatory drugs, cardiovascular and anticancer compounds—were selected based on environmental occurrence and ecotoxicological relevance. Short-term exposure experiments (up to seven days) were conducted in microcosms under controlled conditions, using eight-point concentration gradients and three to four replicates per treatment. Functional endpoints included photosynthetic efficiency (proxy for autotrophic function) and extracellular β-glucosidase activity (reflecting heterotrophic function). The screening phase revealed distinct response patterns depending on the depending on the pharmaceutical and the endpoint studied. For photosynthetic efficiency, we observed: immediate inhibition with no recovery (e.g., Erythromycin); transient inhibition followed by recovery (e.g., Atenolol); gradual inhibition over time (e.g., 5-Fluorouracil); and no observable effect at tested concentrations. For β-glucosidase activity, some pharmaceuticals completely inhibited activity (e.g., Ofloxacin), whereas others (e.g., 5□Fluorouracil) triggered pronounced stimulation, increasing activity by up to 100% over controls. Preliminary results also suggest changes in chlorophyll content and shifts in the relative abundance of green algae, cyanobacteria, and diatoms. Based on these functional screening results, six pharmaceuticals with the strongest effects will be selected for untargeted metabolomics analysis to identify early molecular signatures below functional effect thresholds. This multi-level approach—combining functional assays and metabolomics—aims to improve understanding of how pharmaceuticals affect periphyton and to support development of metabolomic biomarkers for early detection of contamination in freshwater ecosystems.

Keywords: pharmaceuticals, periphyton, microbial ecotoxicology, functional endpoints, photosynthetic efficiency, β, glucosidase activity

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Presentation O24

Responses of Gut Microbial Species and Complex Communities to Xenobiotic Exposure Reveal Mechanisms of Resilience and Vulnerability in vitro

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Persistent exposure to endocrine-disrupting chemicals (EDCs) threatens human health. While gut bacteria can metabolize xenobiotics and modulate their toxicity, the gut microbiome-EDC interactions are understudied. This work aimed to (i) assess EDC ecotoxicity on gut bacteria, (ii) explore interactions between tolerant and sensitive species and evaluate EDC-induced ecological shifts in gut-derived microcosms, and (iii) evaluate microcosms' role on EDCs bioavailability and transformation. We screened 38 EDCs (13 phenols, 9 phthalates, 8 per- and polyfluoroalkyl substances (PFAS), 8 pesticides) at various concentrations (30µM-1000µM) on 38 core gut bacteria. The ability of tolerant species to protect sensitive ones was assessed via cross-feeding assays. Ecological effects were studied by exposing feces-derived microcosms to 22 EDCs and analyzing 16S rRNA sequencing data via QIIME2 suite. Monoculture assays showed PFAS and phenols inhibited one-fourth of strains by at least 25%. Longer-chain PFAS, parabens, and lower-weight phthalates had stronger inhibitory effects. Sensitivity was associated with phylogeny and physiology, with Gram-negative, non-motile, obligate anaerobes more vulnerable. Pseudomonadota and Bacteroidota species were the most resilient and sensitive to EDCs, respectively. In co-cultures, resistant strains mitigated (Enterococcus faecalis) or exacerbated (Streptococcus salivarius) EDC toxicity on sensitive Bacteroides species. Triclosan, triclocarban, bisphenol B, butylparaben, and PFDA prominently altered the structure and composition of microbial communities. Microcosms reduced butylparaben and diethyl phthalate bioavailability by 25–75%. Our findings indicate that EDCs altered bacterial growth in an EDC- and species-specific manner, disrupting gut microbial ecology. However, microbe-microbe interactions and species' metabolic capabilities may mitigate their impact on gut microbiome health.

Keywords: exposome, edcs mixtures, xenobiotic metabolism, gut microbial ecology, microcosms

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New methods and approaches in microbial ecotoxicology

Presentation O13

Toxic Foresight: Predicting Harmful Cyanobacterial Blooms

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Planktothrix rubescens is a filamentous cyanobacterium capable of producing toxins that pose risks to human health and aquatic ecosystems. Lake Bourget, the largest natural lake in France, has experienced recurrent P. rubescens blooms since its first occurrence in 1996. After a disappearance in 2010, the species re-emerged in 2015, displaying irregular bloom dynamics. A key feature of P. rubescens is its buoyancy regulation, enabling persistence at various depths of the water column, with a main stratum observed around the thermocline at 15 m depth. Previous studies have sought to identify the environmental drivers of these blooms, yet the system is shaped by complex, nonlinear interactions among multiple variables. To address this challenge, we applied Empirical Dynamic Modelling (EDM), an equation-free, data-driven framework based on state-space reconstruction. This approach allows us to disentangle causal drivers and capture the state-dependent responses of P. rubescens to environmental forcing. Our analysis highlights the central role of both water column stratification and phosphorus input in shaping bloom dynamics. Furthermore, by altering causal driver values in winter, we explored scenarios that revealed their delayed impact on bloom intensity during late summer. Finally, starting from the 15 m stratum, we were able to predict the vertical spreading of P. rubescens throughout the water column. These findings demonstrate the potential of EDM to provide mechanistic insights into bloom dynamics of toxic cyanobacteria and to assess how changes in key environmental drivers may influence future risks for lake ecosystems and human health.

Keywords: toxic cyanobacteria, empirical dynamic modelling, planktothrix rubescens

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Presentation O14

Application of Bacillus safensis lau 13 metabolite for the control of growth and aflatoxin production by aspergillus species on stored maize grains

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The uncontrolled rise in the use of synthetic chemicals for post-harvest preservation of farm produce had resulted to ecological deterioration and contamination of crop products with harmful chemical residues. Thus, the use of bioactive materials as substitute to the common synthetic chemicals for the control of post-harvest microbial contamination of crops has gained tremendous attention due to their eco-friendliness, cost effectiveness and sustainability. This study aims to evaluate the antifungal effect of B. safensis LAU 13 metabolites (METOX) for the control of Aspergillus species growth and aflatoxin production on stored maize grains. The METOX was produced by B. safensis LAU 13 during three days of cultivation through submerged fermentation. Characterization of METOX by gas chromatography-mass spectrometry (GC-MS) revealed the presence of bioactive compounds predominantly aldehyde derivatives, 4-Dodecen-1-al (13.5%) and Octanal,3,7-dimethyl (13%). The METOX exhibited potent inhibitory effect against the aflatoxin-producing strains of A. flavus and A. niger isolated from stored maize grains as it induced 62% and 16% fungal growth inhibition against the isolated strains A. flavus and A. niger, respectively. Hence, the result obtained herein suggests that the METOX produced by B. safensis LAU 13 has promising application as a bioactive material for sustainable control of the growth of aflatoxin-producing fungal species in stored grains.

Keywords: bacillus safensis, aspergillus species, aflatoxin, metox, eco, friendly

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Presentation O15

Revealing marine plastic degraders using stable isotope tracers

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Plastic biodegradation in natural environment is performed by the microbial biofilm living on its surface (so-called "plastisphere"), whose molecular mechanisms remain a black box. Here, we present the DNA-stable isotope probing (DNA-SIP) coupled with -OMICs techniques as a powerful tool to describe the microorganisms actively involved in plastic biodegradation. We produced two types of 13C-labeled polyhydroxyalcanoates with short chain length (13C-scl-PHA) (Odobel et al., 2025) and medium chain length (13C-mcl-PHA), which were incubated as sole carbon source with natural marine plastispheres. Rapid biodegradation into carbon dioxide (CO2) was found for scl-PHA, where much longer biodegradation rates were observed in the case of mcl-PHA. DNA-SIP coupled with 16S rRNA metabarcoding identified different active biodegraders according to the polymer types (mainly Marinobacter sp., Cellvibrionaceae and Alteromonas sp. for scl-PHA and Leptonema sp.for mcl-PHA). Further analysis of 13C-labeled metagenome-assembled genomes (MAGs) enables us to reconstruct several genomes, some of which revealed numerous copies of depolymerases. This revealed different combinations of depolymerase gene organization, forming homodimers and sometimes fused heterodimers, increasing the biodegradation efficiency of these species and give them a selective advantage in the community. Overall, these results illustrate the potential of the stable isotope tracers to explore the functional reservoir of the plastisphere for discovering new processes involved in the plastic end-of-life in the marine environment.

Keywords: dna, sip, omics, plastic, biodegradation

Presentation O16

Spore-tacular automation: deep learning analysis for aquatic hyphomycete ecotoxicological assessment

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Aquatic hyphomycetes are key decomposers in freshwater ecosystems, making them valuable bioindicators for ecotoxicological assessment. However, traditional methods for evaluating their responses to environmental stressors rely on time-consuming manual spore counting and subjective identification, limiting high-throughput applications. This study presents hyphsporea (Hyphomycetes Spores Recognition with Enhanced Algorithms), a novel YOLO-based deep learning tool designed for automated detection, counting, and classification of aquatic hyphomycete spores in ecotoxicological bioassays. The method was developed using microscopic images from sporulation assays of eight common aquatic hyphomycete species exposed to nutrient or fungicide (tebuconazole) gradients. The deep learning model was trained on annotated spore images to recognize species-specific morphological characteristics and accurately quantify spore production under various stress conditions. Performance evaluation included precision, recall, and accuracy metrics compared to manual counting by expert mycologists. Results demonstrated that hyph-sporea achieved high accuracy in spore detection and classification, with processing times reduced per sample. The automated system successfully captured species-specific responses to stressors, including bell-shaped dose-response curves for nutrients and dose-dependent inhibition patterns for fungicide exposure. The method eliminated inter-operator variability and enabled standardized, reproducible measurements across large datasets. This innovative approach represents a significant advancement in microbial ecotoxicology, providing researchers with a robust, standardized tool for high-throughput assessment of fungal responses to environmental stressors. The method's automation capabilities make it particularly valuable for regulatory testing, environmental monitoring, and ecological research requiring rapid, objective evaluation of fungal community in freshwater ecosystems.

Keywords: aquatic hyphomycetes, microbial ecotoxicology, deep learning, automated detection

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Microbial bioprocesses and bioremediation

Presentation O17

Biodegradability of Tire Additives: The Role of Freshwater and Wastewater Microbiomes

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Tires are a major source of environmental contaminants, releasing complex chemical mixtures through physical abrasion and leaching. Although tire-derived chemicals are widespread in various environmental compartments, including freshwater systems and wastewater treatment plants, their environmental fate and persistence remain poorly understood. Ready biodegradability tests (RBTs) are key screening tools used to assess whether chemicals are rapidly degraded or potentially persistent. However, RBT outcomes often show high variability across replicates, conditions, and laboratories partly due to differences in microbial composition within the environmental inoculum. Microbial community presence, abundance, and activity strongly influence both lag phases and degradation kinetics, yet the inoculum remains largely a “black box” in routine RBTs. This study investigates the biodegradability of 11 representative tire-derived chemicals, including 6PPD, diphenylguanidine, benzothiazoles, and benzotriazoles, while simultaneously characterizing the microbial community through 16S rRNA gene amplicon sequencing. We assessed the impact of test concentration, inoculum source (freshwater vs. wastewater), and chemical toxicity to inocula, and explored structure-biodegradability relationships. Initial results indicate that none of the tested compounds are readily biodegradable, though seven were classified as ultimately or inherently biodegradable. Our findings emphasize the importance of incorporating microbial community profiling to better interpret biodegradation outcomes. These insights are essential for improving the reliability of RBTs and strengthening environmental risk assessments for tire-associated contaminants.

Keywords: biodegradation, tire additives, freshwater, wastewater, microbiome

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Presentation O18

S-metolachlor degradation in agricultural soils and groundwater: isolation of native degrading strains and microbial community profiling

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The herbicide S-metolachlor is frequently detected in groundwater, along with its transformation products, raising concerns about its persistence and the quality of drinking water in contaminated areas. By combining in situ monitoring and laboratory experiments, this study focused on understanding the factors driving S-metolachlor degradation, which is essential for developing efficient remediation strategies. Soil and groundwater samples were collected from an agricultural site in southwestern France, which was selected for its recurrent groundwater contamination (up to 3.4 µg/L of metolachlor ESA) and monitored across hydrological variations and fertilization events. These environmental samples served as inocula for enrichment cultures, incubated in a minimal medium with S-metolachlor as the sole carbon source, and a carbon-rich medium supplemented with the pesticide. Microbial community diversity and predicted nitrogen-related functions were assessed for both in situ samples and enrichments using Illumina MiSeq sequencing (16S and ITS rRNA), coupled with PICRUSt2 functional inference. Bacterial and fungal strains were isolated and tested for their degradation potential over 21 days, in carbon rich conditions (1 mg/L of S-metolachlor). Strains from the genera Pseudomonas, Variovorax, Sphingopyxis, Caulobacter, Gibellulopsis, Alternaria and Papiliotrema, as well as a mix of all isolated strains, reached S-metolachlor degradation rates ranging from 10% to 55%. Transformation products were detected at concentrations nearly 100-fold lower than the degraded parent compound. To explore bioremediation strategies under more realistic conditions, microcosm experiments using agricultural soil slurries were conducted. The performance of a reconstructed microbial consortium composed of the isolated native degrading strains was assessed, along with the influence of nitrate inputs on pesticide degradation rates and microbial functions. This is, to our knowledge, the first study reporting S-metolachlor-degrading strains from these genera, which provides new insights into the microbial diversity involved in pesticide degradation and enriches the literature supporting bioremediation strategies based on native microbial resources.

Keywords: smetolachlor degradation, enrichments, degrading strains, bacteria and fungi, agricultural soils, groundwater

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Antimicrobial resistance

Presentation O19

Influence of antibiotics and microbial coalescence on sediment microbial communities' functions and diversity

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Microbial communities play a central role in ecosystem functioning by driving processes such as nutrient cycling, organic matter degradation, and contaminant transformation. Yet, their stability is increasingly challenged by chemical pollution and physical disturbances that promote microbial coalescence. Among chemicals, antibiotics, which are frequently detected in soil and aquatic ecosystems, can disrupt microbial diversity and biogeochemical cycles enhancing the dissemination of antimicrobial resistance(AMR), while soil intrusion can introduce exogenous microorganisms and/or genetic materials that may destabilize sediment communities. To investigate these combined effects, we conducted a 27-day controlled microcosm experiment using natural river sediments with contrasting organic matter content. Treatments included the presence or absence of antibiotics(sulfamethazine or ofloxacin) and/or soil inputs(with sterilized soil serving as a negative control), thereby simulating chemical and physical disturbances. Specifically, two sediment types were used, exposed to three antibiotic treatments(ofloxacin, sulfamethazine, or no antibiotic) and three soil treatments(sterile soil, non-sterile soil, or no soil). All treatments were performed in triplicates. Heterotrophic microbial activities(enzymatic activities and aerobic respiration)were generally higher in Tillet sediments, which were richer in organic matter, compared to Leysse sediments. Soil addition had stronger effects on enzymatic activities than antibiotics, particularly influencing phosphatase and β-glucosidase responses. Respiratory responses varied depending on sediment type and antibiotic treatment. Sulfamethazine treatment led to microbial adaptation to the mineralization of the antibiotic, but only in Leysse sediments and in the absence of soil. Finally, qPCR analyses revealed increased abundance of AMR gene markers(sul1, dfrA, blaOXA20, and int1) under combined disturbance scenarios, particularly with sulfamethazine and sterile soil treatments. Overall, our findings demonstrate that microbial coalescence and pharmaceutical pollution interact to reshape sediment microbial communities, altering enzymatic functions, respiration, sulfamethazine biodegradation and resistance gene dynamics. These results highlight the ecological risks of multiple stressors and the need for integrated approaches to safeguard biodiversity and ecosystem resilience.

Keywords: pharmaceuticals, antimicrobial resistance, enzymatic activities, respiration, biodegradation

Presentation O20

Dissemination of antimicrobial resistance and potential pathogens through urban wastewater treatment plants

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Urban wastewater contains a mixture of pollutants, including antibiotic residues and potentially toxic metals, and may also serve as a source of antimicrobial resistance and pathogens, aiding dissemination to the environment. Considering the growing global health risks accompanying antimicrobial resistance, it becomes crucial to understand its dissemination beyond clinical settings, especially in environments connecting humans and natural environments. In this study, three wastewater treatment plants (WWTPs) in Norway and Greece were investigated. Bacterial communities were characterized with regards to composition and the occurrence of selected indicators. Furthermore, antibiotic resistance genes and phenotypical resistance patterns of indicator bacteria were analysed, along with concentrations of antibiotic residues and potentially toxic metals. Several antibiotics were detected in inlet, outlet and sludge samples from the WWTPs. Cefotaxime, ciprofloxacin, and meropenem were all measured in concentrations exceeding suggested predicted no effect concentrations. Several potentially toxic metals were also found at concentrations proposed to pose selective pressure towards antimicrobial resistance. Bacterial communities differed significantly between the three treatment plants and between sample types (Permanova, p

Keywords: antimicrobial resistance, pathogens, wastewater, environment, amr, antibiotic resistance, antibiotic resistance genes

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Presentation O21

Plastisphere as a Hotspot for Antibiotic Resistance Gene Enrichment in Fertilized Agricultural Soils

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Agricultural soils represent a significant reservoir for organic contaminants and plastic pollutants, often introduced through practices such as the application of manure and sewage sludge. These biosolids are known to contribute to the spread of antibiotic resistance genes (ARGs), thereby increasing the likelihood of resistant microorganisms colonizing plastic surface, a new microbial niche known as the 'plastisphere'. We hypothesize that the plastisphere serves as a hotspot accelerating the evolution and dissemination of ARGs compared to the surrounding bulk soil. To test this hypothesis, a controlled microcosm experiment was conducted using conventional macro-fragments of low-density polyethylene (LDPE) plastic embedded in soil. The soil was treated twice, at 120-day intervals, with either manure or sewage sludge—both fumigated and non-fumigated—to allow a comparative assessment of the effects of biosolids application and microbial loads on ARG dynamics on the soil and plastisphere. Samples were collected from both the plastisphere and the surrounding soil, and analyzed for the presence and abundance of selected genetic markers, including tetQ (tetracycline resistance), sul1 (sulfamethoxazole resistance), dfrA (trimethoprim resistance), intI1 (class 1 integron integrase), and 16S rRNA (for total bacterial abundance). The results showed that, in most cases, tetQ and sul1 were significantly more abundant in non-fumigated samples across both soil and plastisphere niches. Notably, dfrA exhibited higher abundance specifically on the plastisphere, suggesting selective enrichment. In contrast, no significant differences were observed for 16S rRNA and intI1, indicating similar overall bacterial abundance and integron prevalence across treatments. To complement these targeted analyses, selected samples were submitted for shotgun metagenomic sequencing to explore the broader resistome and microbial community structure associated with the plastisphere and surrounding soil under different treatment conditions, and the analysis is ongoing. This additional data will provide deeper insights into the environmental and potential human health implications of plastisphere-associated ARG dynamics.

Keywords: plastisphere, args, microbial evolution, fertilization

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Poster Presentations

Poster P01

Road Dust contaminants and periphytic microalgae: community shifts and trophic transfer to Daphnia magna

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Tire Wear Particles (TWPs), a major component of road dust (RD), pose a significant threat to aquatic ecosystems. Abrasion of tires on roads generates microplastic-like particles that are transported to freshwater ecosystems via storm runoff. These particles release several pollutants, including metals such as zinc (Zn) and copper (Cu), polycyclic aromatic hydrocarbons (PAHs), and organic additives like 6PPD and its oxidation product 6PPD-Q. TWPs and their leachates have harmful effects on aquatic microorganisms, including growth inhibition and oxidative stress in phytoplankton species, with diatoms often among the most sensitive class. Moreover, studies have shown that microalgae, have a strong capacity to bioconcentrate both metals and organic pollutants, making them useful bioindicators. However, the impact of RD exposure and its associated contaminants on periphytic and zooplankton community structure and biodiversity remain poorly documented, as does the transfer of contaminants through the first levels of the aquatic trophic chain. Our research project will investigate the transport and effects of RD and TWPs in aquatic ecosystems. Contaminants including Zn, PAHs, 6PPD, and 6PPD-Q will be quantified in both exposed and reference sites. Periphytic microalgae will be sampled in lacustrine environments under RD and TWP pressure, near a spillway. Community structure and diversity, particularly of diatoms, will be assessed and compared between polluted and non-exposed sites. To evaluate trophic transfer, laboratory bioassays will be conducted by feeding Daphnia magna with contaminated versus uncontaminated periphyton. Bioaccumulation of pollutants in daphnids will be quantified and linked to effects on survival, growth, reproduction, and behavior. Our study will provide new insights into the transfer of RD and TWPs in aquatic ecosystems and help better characterize the ecotoxicological risks for freshwater microorganisms.

Keywords: tire wear particle, road dust, microorganisms, trophic chain, contaminant, ecotoxicology, periphyton, zooplankton, diatom, daphnia

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Poster P02

Novel Bioactive Molecules in Thermal Waters: A New Frontier in Cosmetic Innovation

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The management and conservation of natural resource is a global challenge to promote environmental and economic sustainability. Pyrenees region is rich in thermal springs with recognized therapeutic properties. These sulfurous waters are distinguished by their varied physical and chemical characteristics, as well as the presence of ions and minerals with interesting effects. However, the microbiome and bioactive metabolites present in these waters and their possible effects on the skin are unknown. Our aim is to characterize the microbial community and their relative metabolites in thermal waters in the Pyrenees. Samples were collected from 10 thermal sites. We applied a multidisciplinary approach that integrates chemical, molecular (16S rRNA gene metabarcoding), and metabolomic profiling to explore microbiome functionality. Physicochemical parameters, including salinity, pH, conductivity and redox potential, were measured. Additionally, the concentrations of ions and minerals were analyzed. Microbial community composition and diversity were determined. Bioinformatic and statistical analysis allow to characterize the community. Metabolites were analyzed by using a synergic non-targeted approach with UHPLC (1D and 2D) ESI-timsTOF and by direct infusion on ESI-FTICRMS (12T) to highlight the metabolome of interest by high-resolution profiling. The microbial communities were dominated by sulfur-oxidizing bacteria affiliated to Thiothrix, Sulfuricurvum and Acinetobacter genus. Non-metric multidimensional scaling (NMDS) analysis revealed that community diversity was shaped by physicochemical factors such as pH, temperature and chemical ion composition. Linear discriminant analysis effect size (LEfSe) showed a significant difference in taxa abundance according to each thermal water. The characterized metabolites belong to the sterol, organic acid, and fatty acid families. Metabolites with anti-inflammatory potential were identified and linked to specific microbial genera. Glucuronic acid was associated with the Flavobacterium genus and hexadecanoic acid with Thiothrix. These results demonstrate that technological advances provide unprecedented insights into ecological functions, revealing novel bioactive metabolites with promising applications in pharmaceutical and cosmetic innovation.

Keywords: thermal water, multidisciplinary approach, microbiome, metabolites, cosmetics

Poster P03

Prior stress exposure influences microbial community assembly and litter decomposition in headwater streams

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In the context of global change, headwater rivers face various anthropogenic and environmental stressors that impact biodiversity and ecosystem functions. This study evaluates how prior exposure of microbial communities (aquatic hyphomycetes and diatoms) to nutrient deficiency (nitrogen and phosphorus) or fungicide contamination (tebuconazole) influences their ability to colonize and decompose leaf litter. Aquatic hyphomycetes sporulation and diatom cultivation were conducted under two stressful conditions: nutrient deficiency or exposure to 10 µg.L-1 tebuconazole. Four microbial assemblages were then created under non-stressful conditions: (i) bacteria alone, (ii) bacteria + diatoms, (iii) bacteria + hyphomycetes, and (iv) bacteria + diatoms + hyphomycetes. These assemblages were placed in contact with sterile maple leaf discs for 1.5 days to allow colonization, then transferred to fresh medium for 30 days. Samples were collected at 1.5, 10, and 30 days to assess decomposition rates, stoichiometric composition (C:N:P), and microbial communities via qPCR. Initial results showed significant effect of microbial assemblage composition on decomposition, with increased efficiency when hyphomycetes and diatoms were associated, indicating that hyphomycetes are the primary contributors to litter decomposition and suggesting functional complementary between these groups. Stoichiometric analysis revealed differentiated effects of assemblages on nitrogen and phosphorus fixation dynamics in leaves. However, no significant treatment effects were detected, suggesting resilience of microbial communities or recovery mechanisms. qPCR analyses of microbial composition are ongoing to characterize microbial succession and identify mechanisms of differentiated colonization. These results will contribute to improving understanding of the links between microbial community structure and decomposition processes in an environmental stress context.

Keywords: aquatic hyphomycetes, diatoms, decomposition, microbial colonisation, environmental stressors

Poster P04

Effects and intracellular fate of cobalt (Co) in the freshwater microalga Chlamydomonas reinhardtii

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The global transition to low-carbon technologies has drastically increased the demand for cobalt (Co), a key component of lithium-ion batteries. This trend raises concerns about Co release into aquatic ecosystems and its potential toxicity to primary producers such as microalgae, which form the basis of freshwater food webs. While previous studies have partly described Co effects on algal physiology, little is known about its intracellular fate and subcellular distribution – critical processes to understand detoxification strategies and Co effects on microalgae. This study aimed to characterize both the physiological and intracellular responses of Chlamydomonas reinhardtii to increasing free Co2+ concentrations (0.001 – 31.3 nM). A combination of growth and subcellular assays, metal accumulation measurements, and subcellular fractionation was applied. Subcellular parameters showed distinct responses to increasing free Co2+ concentrations: cell size decreased with a minimum at 7.3 nM before partially recovering; chlorophyll a content declined dose-dependently; and cell granularity exhibited a biphasic trend, strongly decreasing at low doses but surpassing control levels at 31.3 nM, suggesting structural and metabolic adaptations. These subcellular alterations were reflected at the whole-cell level, as growth inhibition was detected above 0.2 nM, with EC20 and EC50 values of 0.81 ± 0.2 nM and 2.36 ± 0.3 nM free Co2+, respectively. Subcellular fractionation revealed that Co was predominantly sequestered in the heat-stable protein (HSP) fraction – rising from 56 % at background levels to 83 % at 31.3 nM, suggesting a detoxification mechanism via binding to thiol-rich peptides like phytochelatins. These findings provide novel mechanistic insights into Co toxicity and detoxification in microalgae. Beyond this work, the dataset establishes a framework for extending the study of battery-derived metals across microalgal species, testing realistic metal mixtures, and scaling up to mesocosm experiments with riverine biofilms – ultimately bridging controlled laboratory studies and ecosystem-level risk evaluation.

Keywords: bioaccumulation, cell physiology, batteries, metals, environmental impacts, subcellular partitioning

Poster P05

Elucidation of intracellular speciation and the effects of indium on the microalga Chlamydomonas reinhardtii

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With the development of new low-carbon and communication technologies, previously little-used metals such as indium are now being released into natural waters, emerging as new environmental contaminants. This issue is made worse by changes in the quantity and quality of freshwater caused by climate change. In this context, it is essential to study the impact of these contaminants on aquatic organisms and to develop new, rapid and reliable tools for water quality biomonitoring. This study explores the effects of indium on the model microalga Chlamydomonas reinhardtii under controlled laboratory conditions. The objectives were to (i) assess the impact of indium on growth and other physiological parameters and (ii) characterize its intracellular accumulation and subcellular localization. The methodology combined ecotoxicological (assessment of indium effects by flow cytometry) and analytical (quantification and subcellular fractionation of indium by ICP-MS). Exposure of C. reinhardtii to increasing concentrations of indium (from 0.087 µmol/L to 34.8 µmol/L) resulted in intracellular accumulation of indium following Michaelis-Menten-type kinetics, without affecting growth or the physiological parameters measured (cell size and granularity, pigment content, oxidative stress). Indium was mainly localized in the "granule" fraction (detoxified) and, to a lesser extent, in the "organelle" fraction (sensitive). These results highlight the tolerance of C. reinhardtii to indium, and pave the way for the development of future biomonitoring tools for emerging contaminants in aquatic ecosystems.

Keywords: microorganisms, metals, aquatic ecosystems, biomonitoring

Poster P06

Urban land use shapes microbial life strategies along a management intensity gradient

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Understanding how urbanisation affects the taxonomic and functional properties of soil microbial communities is critical for developing new approaches in microbial ecotoxicology. Here, we combined high-throughput sequencing (Illumina) with enzymatic assays, fungal functional guild inference (FUNGUILD), bacterial life strategy classification (oligotrophs vs. copiotrophs), and microbial co-occurrence network analysis to characterise 135 urban soil communities (bacteria and fungi) across eight contrasting land-use types in the city of Blois (France). Each land use was classified according to management intensity (1 = least managed, 4 = most intensively managed). This integrative framework enabled us to link land-use intensity with shifts in microbial assembly rules and ecosystem functions. We show that intensively managed sites (e.g. showcase gardens, sports fields) exhibit reduced fungal biomass, higher bacterial abundance, lower taxonomic and functional diversity, and decreased nitrogen-related enzyme activities compared to less managed or unused areas. Network analyses revealed that urban soils harbour fragmented and less connected microbial interaction structures relative to semi-natural ecosystems, providing a new perspective on ecosystem fragility under anthropogenic pressure. By coupling taxonomic, functional, and network-based approaches, our study proposes an innovative methodological framework for assessing urban soil microbial responses to anthropogenic disturbance. This approach provides new tools for microbial ecotoxicology to better integrate belowground biodiversity into sustainable urban ecosystem design and management.

Keywords: urban soil, microbial communities, land, use, management intensity, urban green spaces, biodiversity

Poster P07

Pesticide mixture effects on bioaccumulation and toxicity in biofilms

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Pesticides are commonly found in aquatic ecosystems, where they can harm non-target biofilms, which consist of algae, bacteria and fungi. These biofilms play essential roles in the aquatic food webs and are useful indicators of water contamination because of their rapid response to contaminants and ability to accumulate pesticides. Toxicity and bioaccumulation of pesticides to biofilms can depend on pesticide properties like logKOW, water solubilityand mode of action (MoA). However, most studies assess single pesticides, overlooking that they normally occur in mixtures in the environment with potentially interactive effects. Therefore, understanding the mixture effects (synergistic, antagonistic and additive) is important as otherwise the toxic effect could be incorrectly predicted. This study aims to determine the influence of pesticide properties on bioaccumulation and toxicity, and to assess the impact of these properties on mixtures, using an artificial freshwater biofilm composed of the cyanobacterium Synechococcus bacillaris and the diatom Phaeodactylum tricornutum. We performed two experiments: one where biofilms were exposed to a gradient of concentrations of five individual pesticides for 24h to establish dose-response curves, and a second where the biofilm was exposed to the ten binary mixtures to analyse the mixture effect. Photosynthesis inhibition was measured and pesticides were quantified in both the extracted biofilm and the water samples using LC-MS/MS. All pesticides inhibited photosynthesis in a dose-dependent manner. Toxicity increased in the following order: acetochlor, diuron, terbuthylazine, hexazinone and tebuconazole. Bioaccumulation showed no correlation with logKOW. The mixture effect could not be linked to the MoA alone but was also influenced by the chemical properties. In general, a high difference in the properties lead to a synergistic effect while a smaller difference lead to antagonistic or additive effects. These results highlight the complexity of pesticide interactions within aquatic biofilms.

Keywords: pesticides, mixture toxicity, biofilm

Poster P08

New Biomarkers for Sea Turtle Conservation: Insights from Shell Biofilms and Eggshell Trace Metals

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Sea turtles are considered “umbrella species” because they are essential to the preservation of marine environments. Their natural life cycles may be threatened by illegal fishing, water pollution, climate change, and human impacts on their feeding and nesting grounds. Thus, understanding the life history of marine turtles is essential to their conservation. However, current monitoring approaches are limited, costly, and invasive. Our study explores the potential of two complementary biomarkers: (i) metagenomic profiling of biofilms from the shells of nesting female sea turtles, which are hypothesized to reflect the microbial communities encountered along their migratory routes, and (ii) trace metal element (TME) concentrations in eggshells, which are expected to be induced by maternal transfer due to the turtles’ trophic environments. These two biomarkers could discriminate the trophic environments used by the turtles. Biofilm samples and eggshells were collected from 11 and 52 individuals, respectively, of two sea turtle species: the leatherback (Dermochelys coriacea) and the hawksbill (Eretmochelys imbricata). Sampling took place across three beaches on the Caribbean Island of Martinique during the 2024 nesting season. We sequenced the V1–V4 region of the 16S rRNA gene from the biofilm samples to characterize the associated microbial communities, including eukaryotes and protists. ICP-MS analyses provided complementary elemental profiles. The two biomarkers, both microbial and elemental, show a similar pattern with a strong interspecific difference, highlighting their potential as complementary tracers of turtle life history and movements. This proof-of-concept study demonstrates that combining microbial and geochemical signals could provide a new, less invasive way to study marine turtle ecology. Such approaches may ultimately inform conservation strategies by identifying habitat use and resilience across nesting populations.

Keywords: sea turtles, microbial communities, biofilms, metagenomics, trace elements, conservation, leatherback, hawksbill

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Poster P09

Development of a multi-omic approach to assess the impact of the harbour eco-exposome on juvenile fish

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Ports have undergone ecological restoration work to compensate the decline in fish stocks. Artificial reefs installed for this purpose in many French habours, including Port-Vendres, are used as nurseries by coastal fish. However, due to human activities, the quality of harbour waters is disrupted by chemical pollutants (metals, pesticides, medicines) and biological pollutants (microbial communities of urban origin). All these chemical and biological inputs, which are part of the harbour eco-exposome, represent a risk for port ecosystems. In order to assess whether the port eco-exposome can affect coastal fish's health, comparative analyses of the metabolome of Diplodus vulgaris juveniles were carried out between two ecologically contrasting areas, the port of Port-Vendres and a nearby natural nursery area. The diversity and structure of their microbiota communities were also explored. Juveniles present in the port area showed metabolic profiles that differed, as they developed, from those of juveniles in the natural area. Our study highlighted metabolites that were under-expressed in juveniles in the port area, compared to those in the natural area at the intermediate stage of their development. The associated microbiota also differed in terms of composition and/or abundance at the end of development. The pollution potentially present in the port area is probably responsible for the differences observed. Thus, based on these initial results, this multi-omic approach appears to be a very promising tool for assessing the long-term effect of low-level chronic pollution on juvenile fish. At the same time, the integration of data on water contamination, using passive samplers, is also being considered.

Keywords: ecological restoration, eco exposome, multi omics, metabolome, microbiome

Poster P10

Isolation and characterization of indigenous hydrocarbon-degrading bacteria from oil-contaminated Algerian soils using Nanopore technology

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Oil industry activity in southern Algeria has caused significant soil pollution, severely impacting the local microbial biodiversity. This study aimed to isolate cultivable hydrocarbon-degrading bacteria from crude oil-contaminated soils collected at a production site in the region, and to evaluate their potential for petroleum hydrocarbon biodegradation. Dehydrogenase activity and biocontrast testing on MSM agar (crude oil as the only carbon source) allowed for the selection of 08 isolates based on their prominent clear zones (ranging from 0.7 to 3.8 cm), indicating active biodegradation. These isolates were then genetically characterized through 16S rRNA gene sequencing using the MinION Nanopore platform (Oxford Nanopore Technologies), and sequence comparisons were performed using the GenBank (NCBI) database. The identified strains showed alignment with species such as Aeromonas hydrophila, Stenotrophomonas maltophilia, Enterobacter xiangfangensis, Pseudomonas aeruginosa, and Serratia marcescens. A bacterial consortium composed of Aeromonas hydrophila, Stenotrophomonas maltophilia, and Pseudomonas aeruginosa demonstrated notable biodegradation capacity, achieving 86% degradation of crude oil (1% v/v) within 8 days. These findings highlight the promising potential of these Indigenous bacterial strains for large-scale biotechnological applications in environmental bioremediation.

Keywords: crude oil pollution, nanopore sequencing, soil contamination, environmental bioremediation.

Poster P11

Fitness Costs Limit MDR E. coli Invasion but Not Gene Dissemination in Freshwater Sediment

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The spread of antibiotic resistance is a global health concern, with wastewater treatment plants (WWTPs) recognized as key environmental hotspots. These facilities release antibiotic-resistant bacteria (ARB) and low concentrations of antibiotics, creating conditions that may promote resistance spread. Multidrug resistance (MDR) plasmids are central to this process, as they enable transfer of antibiotic resistance genes (ARGs) across bacterial communities, but often impose a fitness cost that reduces host survival in the absence of selection. Understanding the fate of ARB and MDR plasmids in natural environments is important for assessing the environmental dimension of antibiotic resistance. In this study, we tested whether MDR Escherichia coli CV601 can establish in freshwater sediment communities and disseminate ARGs under environmentally relevant antibiotic concentrations. A 10-day static microcosm experiment was conducted using sediment from Lake Vänern, Sweden, with five treatments: (i) control (sediment + filtered river water), (ii) antibiotic mixture (trimethoprim 10 µg/L, cefotaxime 4 µg/L, ciprofloxacin 1 µg/L), (iii) E. coli CV601 (6,000 cells/mL, no plasmid), (iv) an MDR E. coli CV601 carrying dfrA14, blaCTX-M-15, and qnrS, and (v) the MDR E. coli CV601 plus antibiotics. Our results show that MDR E. coli exhibited reduced invasion capacity compared to the non-plasmid strain, consistent with a fitness cost. Nevertheless, plasmid-borne ARGs were detected in sediment within one day, indicating rapid dissemination to native bacteria. The addition of antibiotics in water at environmental concentrations did not significantly influence invasion or ARG spread, likely because the levels were below selective thresholds. In conclusion, MDR plasmids limit bacterial establishment in sediments but still allow ARG dissemination. Continuous emissions of MDR E. coli from WWTPs may therefore contribute to the persistence of resistance genes in natural communities. These findings highlight the ecological significance of fitness costs in shaping antibiotic resistance dynamics in the environment.

Keywords: fitness, cost, sediment, arb, arg, e. coli

Poster P12

River or dendrotelmata: Does habitat of origin shape the tolerance of aquatic hyphomycetes to lead and copper?

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Aquatic hyphomycetes (AHs) are pivotal decomposers of submerged organic matter in freshwater ecosystems. However, their ability to perform this crucial ecosystem process is sensitive to anthropogenic pollution of their habitats. In this context, our understanding of the capacity of AHs to cope with metals remains poorly understood. We explored their the tolerance to trace metals elements (TME) using dendrotelmata (water-filled tree holes, WTHs) as study systems. They act as pollutant traps, including for TME. Specifically, we aimed to assess the tolerance of AHs strains to copper and lead, isolated from WTHs and from the river of Massane reserve (Southern France), which likely contains much lower metal concentrations. We collected different types of organic matter from both habitats in March 2025. From this, we isolated Tricladium species and Alatospora acuminata, AHs species that were found in both habitats. We identified the strains by morphological identification and ITS barcoding. For the metal tolerance assay, we grew fungal plugs on 1% Malt and 2% extract agar at 18 °C under six increasing concentrations of copper, lead, or both metals combined from 0 to 1000 mg/L (0, 7.5, 15, 50, 150, 500, 1000). We measured colony growth every three days over a two-week period and calculated radial growth rate as the endpoint to determine concentration of the metal that causes a 50% reduction in fungal growth (EC50 values). We observed an enhanced copper tolerance reflected in higher EC50 for Tricladium strains from polluted backgrounds, but no difference for Alatospora acuminata.

Keywords: aquatic hyphomycetes, water filled tree holes, metal tolerance, combined metal effects

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