Abstractbook

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Welcome

Dear colleagues,

It is with great enthusiasm that we welcome you to the Food System Microbiomes 2025 International Conference! This second conference will explore the interconnectedness of microbiomes across food systems and their critical roles in addressing global challenges.

Microbiomes remain pivotal to advancing sustainable and resilient food systems. This year's conference will feature discussions on microbiomes for global health, mitigating climate change, enhancing circularity and sustainability, improving nutrition and human health, and addressing risks in the food system. We will also spotlight novel microbiome concepts, cutting-edge applications, and emerging technologies driving progress in these areas.

A special highlight of the conference will be an open session organised by early-career researchers, providing a platform to showcase their insights and contributions to the field.

The Food System Microbiomes 2025 International Conference is organised by the MicrobiomeSupport Association, continuing its mission to increase awareness and drive innovation in food system microbiomes. This event offers a unique platform to connect with leading experts, share groundbreaking research, and shape the future of microbiome science.

On behalf of the Food System Microbiomes Organizing Committee and the MicrobiomeSupport Association members, we wish you an inspiring time in Wageningen, the renowned "City of Life Sciences".

Angela Sessitsch

Hauke Smidt

Scientific Program

Day 1 (Tuesday, 25 November 2025) 13:00 – 20:00

11:00 – 13:00 Arrival & registration

13:00 – 13:15 Welcome (Angela Sessitsch & Hauke Smidt, MicrobiomeSupport Association)

13:15 – 14:00 Opening lecture: Nicola Segata (University Trento, IT) – Human and food microbiomes within a OneHealth perspective

14:00 – 15:40 SESSION 1 – INTERCONNECTEDNESS OF MICROBIOMES ACROSS FOOD SYSTEMS
Session chairs: Daniele Daffonchio (University of Turin, IT) and Jan Sikkema (Holomicrobiome Institute, NL)

14:00 – 14:25 Daniele Daffonchio (University of Turin, IT - The 'microbial terroir' promotes fruit quality, plant resilience against stresses and carbon sequestration in fruit tree agroecosystems
14:25 – 14:40 Sijmen Schoustra (Wageningen University & Research, NL & University of Zambia, ZM) - Ecological selection shapes microbiomes in traditional fermentation: from ecology inspired experiments to avenues of sustainable development
14:40 – 14:45 Science flash: I Nyoman Sumerta (The University of Melbourne, AU) - Seasonal tapping affects microbial community assembly and flavour formation in palm wine fermentation
14:45– 14:50 Science flash: Chiara Traina (University of Turin, IT) - Interconnections across microbiomes: how do plant holobionts and food fermentations relate? A focus on the Taggiasca olive tree ecosystem.
14:50 – 15:15 Jan Sikkema (Holomicrobiome Institute, NL) - The Holomicrobiome Institute: Interconnectedness of microbiomes
15:15 – 15:30 Francesca Cristetti (University of Turin, IT) - Characterization of endophytic and epiphytic microbial communities of Nebbiolo grapes
15:30 – 15:35 Science flash: Despoina Langari (Aristotle University of Thessaloniki, GR) - A multi-omics exploration of microbiome dynamics across fermentation styles of cv. Chalkidiki green olives: revealing microbial interconnectedness in table olive food system
15:35 – 15:40 Science flash: Marco van Es (Bac2nature, NL) - BRIDGING microbiome science and practice: Connecting soil, food, and health professionals

15:45 – 16:15 Coffee break & Poster Session 1

16:15 – 18:00 SESSION 2 – THE MANY PATHWAYS TO SUSTAINABLE FOOD SYSTEMS POWERED BY MICROBIOMES (ESR SESSION) - POWERED BY PECHAKUCHA
Session chairs: Kevin Jerez-Bogota (Aarhus University, DK) and Ricardo Garavito Duarte (North Carolina State University, USA)
Session sponsor: Applied Microbiology International

16:15 – 16:25 Presentation by session sponsor: Lucky Cullen & Chloe Radcliffe - Introducing Applied Microbiology International and *Sustainable Microbiology*
16:25 – 17:10 Pecha Kucha Presentations by ESRs
Eugenia Dadzie (University of Waterloo, CA)
Ricardo Garavito Duarte (North Carolina State University, USA)
Shana L. Hepping (Leiden University, NL)
Leonardo Menghi (University of Southern Denmark, DK)
Ally Miners (University of Waterloo, CA)
Sara Pipponzi (AIT-Austrian Institute of Technology, AT)

17:10 – 18:00 Moderated discussion

18:00 – 20:00 Welcome reception (included in the registration fee)

Day 2 (Wednesday, 26 November 2025) 09:00 – 21:00

09:00 – 10:30 SESSION 3 – MICROBIOMES FOR GLOBAL HEALTH
Session chairs: Gerlinde de Deyn (Wageningen University & Research, NL) and Alexandre Soares Rosado (KAUST, SA)

09:00 – 09:25 Gerlinde de Deyn (Wageningen University & Research, NL) - Soil health, soil microbes and one health
09:25 – 09:40 Jowenna Sim (University of South Australia, AU) - From soil to food chain: Microbial responses to triazole fungicides
09:40 – 09:45 Science flash: Joseph Selvin (Pondicherry University, IN) - Urbanization-driven alterations in sediment microbial communities and the prevalence of antimicrobial resistance in freshwater ecosystems
09:45 – 10:10 Alexandre Soares Rosado (KAUST, SA) - Extreme microbes, the ultimate frontier in environmental restoration and planetary health
10:10 – 10:25 Wisnu Adi Wicaksono (Graz University of Technology, AT) - One Health perspective: Large-scale (meta)genomic analyses elucidate the distribution and horizontal transmission of antimicrobial resistance genes from environmental sources to humans
10:25 – 10:30 Science flash: Elena Crotti (University of Milan, IT) - Uncovering antimicrobial resistance pathways in agri-food ecosystems

10:30 – 11:00 Coffee break & Poster Session 1

11:00 – 12:10 SESSION 4 – MICROBIOMES FOR MITIGATING CLIMATE CHANGE
Session chairs: Eiko Kuramae (Netherlands Institute of Ecology, NL) and Ana Portugal Melo (MIRRI, PT)

11:00 – 11:25 Eiko Kuramae (Netherlands Institute of Ecology, NL) - Climate costs of domestication: How rice microbiomes shifted from nitrogen fixers to N_2O emitters
11:25 – 11:50 Ana Portugal Melo (MIRRI, PT) - MIRRI-ERIC and MICROBES-4-CLIMATE: advancing culturomics and synthetic communities for climate action
11:50 – 12:05 Robin Martens (Wageningen University & Research, NL) - Predicting Microbial Functional Diversity for Decomposition along an Aridity Gradient
12:05 – 12:10 Science flash: Edoardo Zaccaria (Wageningen University & Research, NL) - Microbial seeding as an early-life intervention to reduce methane emissions in dairy cattle

12:10 – 13:00 SESSION 5 – MICROBIOMES FOR CIRCULARITY/SUSTAINABILITY
Session chairs: Rosa Doménech (ITENE, ES), Rosa Perez-Gregorio (University of Vigo, ES) and Angela Sessitsch (AIT Austrian Institute of Technology, AT)

12:10 – 12:35 Rosa Doménech (ITENE, ES) - Plant-growth promoting microorganisms to drive wheat microbiome modulation through sustainable practices
12:35 – 12:50 Aranksha Thakor (University of Waterloo, CA) - Engineering *Pseudomonas alloputida* for sustainable bioplastic production from dairy waste
12:50 – 12:55 Science flash: Simone Rampelli (University of Bologna, IT) - From soil to must: Harnessing vineyard microbiomes for circular viticulture and winemaking
12:55 – 13:00 Science flash: Dirkjan Schokker (Wageningen University & Research, NL) - Antimicrobial resistance dynamics in black soldier fly larvae valorizing waste streams

13:00 – 14:30 Lunch break & Poster Session 1

13:30 – 14:30 MicrobiomeSupport General Assembly

14:30 – 16:05 SESSION 5 – MICROBIOMES FOR CIRCULARITY/SUSTAINABILITY (continued)
Session chairs: Rosa Doménech (ITENE, ES), Rosa Perez-Gregorio (University of Vigo, ES) and Angela Sessitsch (AIT Austrian Institute of Technology, AT)

14:30 – 14:55 Rosa Perez-Gregorio (University of Vigo, ES) - Leveraging bioactive compounds and microbiomes for the development of sustainable, low-immunogenic wheat-based foods
14:55 – 15:10 Elisabetta Chiarini (University of Turin, IT) - Sustainable Kombucha fermentation: Microbial dynamics and chemical profiling from plant-based by-products
15:10 – 15:15 Science flash: Annelein Meisner (Wageningen University & Research, NL) - Steering microbiomes for diseases suppression in soilless cultivations systems via the addition of circular waste streams
15:15 – 15:20 Science flash: Enrique Cubas (ITENE, ES) - Exploiting crop microbiomes as a source of biocontrol and biostimulant microorganisms for sustainable agriculture in the Mediterranean
15:20 – 15:45 Angela Sessitsch (AIT Austrian Institute of Technology, AT) - Microbiome interconnectedness and employing microbiomes for a sustainable and healthy soya-based food system
15:45 – 16:00 Sofia Leonti (Wageningen University & Research, NL) - Facilitators and barriers to farmers' acceptance of microbiome technology and other similar technologies for sustainable crop production: a review
16:00 – 16:05 Science flash: Abelardo Margolles (CSIC-IPLA, ES) - Modulation of gut microbiota by oligosaccharide fractions derived from brewer's spent grain in a dynamic colonic fermentation model

18:00 Conference dinner: De Beekdalhoeve
(bus departure from conference venue @16:30)

Day 3 (Thursday, 27 November 2025) 09:00 – 18:15

09:00 – 10:20 SESSION 6 – MICROBIOMES FOR NUTRITION AND HUMAN HEALTH
Session chairs: Stephane Chaillou (INRAE, FR) and Christophe Courtin (KU Leuven, BE)

09:00 – 09:25 Stephane Chaillou (INRAE, FR) - The domino-like heath effect of fermented food-based diet: What strategies for untangling the complexity?
09:25 – 09:40 Maria Batool (University of Reading, GB) - Microbiota changes and growth impacts associated with oral iron supplementation in neonates
09:40 – 09:55 Julien Tap (micalisfme, FR) - Multiscale associations between diet and the gut microbiome in a nationwide French cohort
09:55 – 10:10 Elisa Di Stefano (APC Microbiome Ireland, IE) - Harnessing *Bifidobacterium* spp. for phytate degradation: activity, regulation, and potential to support early-life nutrition
10:10 – 10:15 Science flash: Davide Buzzanca (University of Turin, IT) - Development of a plant-based psychobiotic yogurt-like for the gut brain axis
10:15 – 10:20 Science flash: Ilario Ferrocino (University of Turin, IT) - Effects of probiotic supplementation on symptoms and microbiome characteristics in patients with non-celiac gluten/wheat sensitivity

10:30 – 11:00 Coffee break & Poster Session 2

11:00 – 12:05 SESSION 6 – MICROBIOMES FOR NUTRITION AND HUMAN HEALTH (continued)
Session chairs: Stephane Chaillou (INRAE, FR) and Christophe Courtin (KU Leuven, BE)

11:00 – 11:25 Christophe Courtin (KU Leuven, BE) - Leveraging food fermentations for health

11:25 – 11:40 Josep Rubert (Wageningen University & Research, NL) - Unveiling microbial lipid signatures: The metabolism of linoleic acid by clostridia and gammaproteobacteria
11:40 – 11:55 Frederick Warren (Quadram Institute, GB) - Spatiotemporal profiling of the human small intestinal microbiome
11:55 – 12:00 Science flash: Gloria Fackelmann (University of Trento, IT) - Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals
12:00 – 12:05 Science flash: Emma Saltzman (Monash University, AU) - Live bacteria in fresh foods contribute to human gut microbiome diversity

12:15 – 13:30 REGULATORY WORKSHOP
Chairs: Yolanda Sanz (CSIC, ES) and Javier Moreno (CSIC, ES)

12:15 – 13:00 Introductory talks
Yolanda Sanz (CSIC, ES) - MicrobiomeSupport Regulatory Task Force introduction
Javier Moreno (CSIC-UAM, ES) - Integrating gut microbiome insights into food safety risk assessments
Rosella Brozzi (EFSA, IT) - Scientific criteria for the characterisation of microorganisms of regulated products in the EU
Sandrine Claus (STARFISH Bioscience, FR) - Developing next-generation biosolutions for agriculture within the EU legislative framework -
13:00 – 13:30 Round Table discussion with Rosella Brozzi (EFSA, IT), Sandrine Claus (STARFISH Bioscience, FR), Céline Druart (Pharmabiotic Research Institute, FR), Javier Moreno (CSIC-UAM, ES) and David Yañez (CSIC, ES)

13:30 – 14:30 Lunch break & Poster Session 2

14:30 – 16:00 Project Exhibition
Session 1: How food system microbiomes contribute to food transition pathways (Microbiomes4Soy, Tribiome, Wheatbiome)
Session 2: How to predict emerging food system risks (HOLiFOOD, FoodSafeR)
Session 3: Unlocking microbial potential – accelerating discovery through integrated infrastructure (UNLOCK)

16:00 – 16:30 Coffee break & Poster Session 2

16:30 – 18:10 SESSION 7 – MICROBIOMES FOR MITIGATION OF RISKS IN THE FOOD SYSTEM
Session chairs: Floor van Meer (Wageningen University & Research, NL) and Martin Wagner (University of Veterinary Medicine Vienna, AT)

16:30 – 16:55 Marlous Focker (Wageningen University & Research, NL) - RESLIENCE thinking in management *Salmonella* spp in the pork supply chain
16:55 – 17:10 Eleftheria Trampari (Quadram Institute Bioscience, GB) - The ecology of persistence: How community complexity and composition shape *Salmonella*'s survival in the food chain.
17:10 – 17:15 Science flash: Mohak Gujare (Wageningen University & Research, NL) - Identifying prognostic microbiome biomarkers to predict post weaning diarrhea (PWD) in piglets and disentangling the effects of confounding factors
17:15 – 17:20 Science flash: Felix Spiegel (FFoQSI GmbH, AT) - Genomic characterization of persistent *Listeria monocytogenes* in European food processing facilities
17:20 – 17:45 Martin Wagner (University of Veterinary Medicine Vienna, AT) - The microbiome of biofilms in real food systems

17:45 – 18:00 Barbara Drigo (University of South Australia/Adelaide University, AU) - A novel risk assessment framework to address antimicrobial resistance in the Australian and Asia-Pacific vegetable supply chain
18:00 – 18:05 Science flash: Floor van Meer (Wageningen University & Research, NL) - The effect of climate change on food-borne disease outbreaks in the Netherlands
18:05 – 18:10 Science flash: Garance Leroy (IFREMER, FR) - Assessment of a microbiome engineering strategy using Lactic Acid Bacteria as bioprotective cultures to delay the spoilage of Gilthead Seabream (Sparus aurata) fillets

Day 4 (Friday, 28 November 2025) 09:00 – 13:00

09:00 – 11:10 SESSION 8 – NOVEL MICROBIOME CONCEPTS, APPLICATIONS AND TECHNOLOGIES
Session chairs: Paul Cotter (TEAGASC, IE) and Marnix Medema (Wageningen University & Research, NL)
Session sponsor: Quantum Design Europe

09:00 – 09:10 Presentation by session sponsor: Igor Poberay: Single-cell Insights: Integrated Microscopy Workstation for Manipulation and Analysis of Microbes and Their Microenvironment
09:10 – 09:35 Marnix Medema (Wageningen University & Research, NL) - Deciphering the chemical language of the microbiome using computational omics
09:35 – 09:50 Narciso M. Quijada (Institute of Functional Biology and Genomics (IBFG), ES) - The neglected side of the microbiome: hotspots in food production and the fungal resistome
09:50 – 10:05 Hrituraj Dey (University of Trento, IT) - Extending curatedFoodMetagenomicData(cFMD) for integrated analysis of food microbiomes
10:05 – 10:10 Science flash: Agata Szymanek (Perseus Biomics, BE) - Robust microbiome profiling with strain resolution using optical mapping
10:10 – 10:15 Science flash: Ananya Pawan Gupta (University of Turin, IT) - Phenotypic characterisation using BIOLOG: microbial strains from cocoa and their novel application
10:15 – 10:20 Science flash: Lakhansing A. Pardeshi (Wageningen University & Research, NL) - Conservation, evolution and recombination of tailocins in the genus *Pectobacterium*; and consequences for species and strain level interactions
10:20 – 10:45 Paul Cotter (TEAGASC, IE) - New developments in studying food-microbiome-gut interactions
10:45 – 11:00 Bhavya Sree Vadlamudi (Wageningen University & Research, NL) - Evolution on autopilot: Engineering functional stability in synthetic microbial communities
11:00 – 11:05 Science flash: Nehir Kizililsoley (WFSR, NL) - Leveraging advanced AI for enhanced food safety through pathogen analysis
11:05 – 11:10 Science flash: Irene Franciosa (University of Turin, IT) - Optimizing long-term storage and propagation strategies for the preservation and reuse of fermented sausage microbiome

11:15 – 11:45 Coffee break & Poster Session 2

11:45 – 12:30 Closing lecture: Michael Wagner (University of Vienna, AT) - The many faces of nitrification: From fundamental understanding to paths toward sustainable nitrogen management

12:30 – 13:00 Poster awards and closing (Hauke Smidt & Tanja Kostic, MicrobiomeSupport Association)

Poster Table

Poster Session 1 display times – 25.11.2025, 1 pm – 26.11.2025, 4:30 pm

Poster Session 1: Interconnectedness of microbiomes across food systems		
Poster#	**Presenter**	**Title**
PS1-S1-PP01	Tanu Shree Hissaria	Impact of carbon source and oxygen on volatile profiles of psychrotrophic food spoilage bacteria and human perception
PS1-S1-PP02	Francesca De Filippis	Metagenomics and volatilomics portraying of traditional table olives from the Mediterranean area
PS1-S1-PP03	Janja Trcek	Species composition and phylogenetic diversity of acetic acid bacteria communities in homemade vinegars
PS1-S1-PP04	Naser Reyhani	Regrounding microbiomes across food systems: A conceptual framework for place-based interventions
PS1-S1-PP05	Leo van Overbeek	OneMicrobiome: Understanding of microbiomes across environments for sustainable nutrition
PS1-S1-SF01	I Nyoman Sumerta	Seasonal sap tapping affects microbial community assembly and flavour formation in palm wine fermentation
PS1-S1-SF02	Chiara Traina	Interconnections across microbiomes: How do plant holobionts and food fermentations relate? A focus on the Taggiasca olive tree ecosystem
PS1-S1-SF03	Despoina Langari	A multi-omics exploration of microbiome dynamics across fermentation styles of cv. Chalkidiki green olives: Revealing microbial interconnectedness in table olive food system
PS1-S1-SF04	Marco van Es	Bridging microbiome science and practice: Connecting soil, food, and health professionals

Poster Session 1: The many pathways to sustainable food systems powered by microbiomes (ESR session)		
Poster #	**Presenter**	**Title**
PS1-S2-SF01	Shana L. Hepping	Microbiome as mediator: Lessons from the Food Pharmacy for integrating health and agriculture

PS1-S2-SF02	Leonardo Menghi	Oral and gut microbiome influences on the perception of plant-based and fermented foods
PS1-S2-SF03	Ally Miners	Alleviation of drought stress with microbial Inoculants to maximize crop yield
PS1-S2-SF04	Eugenia Dadzie	Harnessing microbial communities and synthetic biology for PET Upcycling into PHA bioplastics
PS1-S2-SF05	Sara Pipponzi	Lettuce biofortification through vitamin B12- producing bacteria

Poster Session 1: Microbiomes for global health		
Poster #	**Presenter**	**Title**
PS1-S3-PP01	Ifthikhar Zaman	Isolation and characterization of linear low-density polyethylene (LLDPE) degrading *Brucella intermedia* strain from soil
PS1-S3-PP02	Lene Lange	Microbiomes for both food security and improved use of the bioresources
PS1-S3-PP03	Katie Lawther	Exploring antimicrobial resistance in dairy farms: Multidisciplinary insights into AMR prevalence and diversity in neonatal calves and their environments.
PS1-S3-SF01	Joseph Selvin	Urbanization-driven alterations in sediment microbial communities and the prevalence of antimicrobial resistance in freshwater ecosystems
PS1-S3-SF02	Elena Crotti	Uncovering antimicrobial resistance pathways in agri-food ecosystems

Poster Session 1: Microbiomes for mitigating climate change		
Poster #	**Presenter**	**Title**
PS1-S4-PP01	Arjun Sham Valiyaveettil Shamgopal	Integrative analysis of plant growth-promoting and antifungal mechanisms in rhizosphere bacteria and their contribution to abiotic stress adaptation
PS1-S4-PP02	Giorgia Siviero	Evaluation of plant-microbe interactions in Introgression lines (ILs) of *Oryza rufipogon* X *Oryza sativa cv* Vialone Nano
PS1-S4-SF01	Edoardo Zaccaria	Microbial seeding as an early-life intervention to reduce methane emissions in dairy cattle

Poster Session 1: Microbiomes for circularity/sustainability		
Poster #	**Presenter**	**Title**
PS1-S5-PP01	Rym Saidi	Inoculated chickpea genotype and P-fertilization influence rhizosphere microbiota which drive symbiosis efficiency and growth performance under low-P conditions
PS1-S5-PP02	Gabriela Pinto Miguel	Unravelling the microbiota of disease-resistant berry grapes
PS1-S5-PP03	Esther Menendez	Temporal and functional profiling of wheat rhizoplane biofilm-forming bacterial communities reveals core traits for designing SynCom-based biofertilizers
PS1-S5-PP04	Giulia Amore Bonapasta	Resolving viral, microbial, and antimicrobial resistance networks in the rumen: A Hi-C metagenomics framework for sustainable livestock microbiomes
PS1-S5-PP05	Monica Majo-Cuervo	Integrative metagenomic and metataxonomic analysis of biofilm formation in the wheat rhizoplane as a model system
PS1-S5-PP06	Baris Ozdinc	Trinity of piglet gut biogeography development: Age, organ and tissue
PS1-S5-PP07	Anastasija Jušković	Effects of agro-management on soybean root and rhizosphere microbiome under field conditions
PS1-S5-PP08	Beatrix Wepner	Creating transition pathways for microbiome applications in the soyabean value chain: Insights from the MICROBIOMES4SOY project
PS1-S5-PP09	Rounak Chourasia	High-throughput exploration of microbial catalytic potential for AI/ML based prediction of sustainable hybrid fermentation outcomes
PS1-S5-PP10	Maria Hernandez-Soriano	From roots to results: Wheat control of soil microbial nitrogen cycling in living lab farms
PS1-S5-PP11	Yan Lin	Multi-component plant extracts outperform single compounds in mitigating intestinal antimicrobial resistomes in swine
PS1-S5-SF01	Simone Rampelli	From soil to must: Harnessing vineyard microbiomes for circular viticulture and winemaking
PS1-S5-SF02	Dirkjan Schokker	Antimicrobial resistance dynamics in black soldier fly larvae valorizing waste streams
PS1-S5-SF03	Annelein Meisner	Steering microbiomes for diseases suppression in soilless cultivations systems via the addition of circular waste streams

PS1-S5-SF04	Enrique Cubas	Exploiting crop microbiomes as a source of biocontrol and biostimulant microorganisms for sustainable agriculture in the Mediterranean
PS1-S5-SF05	Abelardo Margolles	Modulation of gut microbiota by oligosaccharide fractions derived from brewer's spent grain in a dynamic colonic fermentation model

Poster Session 2 display times – 27.11.2025, 9 am – 28.11.2025, 1 pm

Poster Session 2: Microbiomes for nutrition and human health		
Poster #	**Presenter**	**Title**
PS2-S6-PP01	Tanja Kostic	Flavour, odour and texture improvements of plant-based dairy products using microbial fermentation products
PS2-S6-PP02	Rocio Olmo	Potential of donkey milk microbiota for the development of functional fermented products
PS2-S6-PP03	Marieke Elfferich	Lettuce be healthy: The influence of agricultural practices on the lettuce microbiome and metabolome, and its importance for human health
PS2-S6-PP04	Nikoletta Vidra	ILSI Europe perspective review: Site-specific microbiota changes during pregnancy associated with biological consequences and clinical outcomes - opportunities for probiotic interventions
PS2-S6-PP05	Raffaele Magliulo	Development of a kombucha metagenome catalogue including a one-year longitudinal sampling
PS2-S6-PP06	Stefan Harper	The effect of increasing wheat arabinoxylan on the gut microbiome
PS2-S6-PP07	Gaia Vanzetti	Optimizing Taggiasca table olives fermentation: Development of autochthonous microbial starter culture
PS2-S6-PP08	Katja van Dongen	Studying interactions of foodborne xenobiotics and the human intestinal microbiome: An *in vitro* approach
PS2-S6-PP09	Anna M. Malinowska	The impact of the intake of partly fermented infant formula with 2'-FL, 3'-GL and bovine milk fat on the composition and functional properties of infant gut microbiome: Preliminary results
PS2-S6-PP10	Akshay Bisht	Differential carbohydrate fermentation in children with severe malnutrition: Recovery stage influences *in vitro* inulin utilisation

PS2-S6-PP11	Enriqueta Garcia-Gutierrez	Antioxidant characterisation of Murciano-Granadina goat milk kefir
PS2-S6-PP12	Jorge Pardellas Soto	Impact of green tea polyphenols on sourdough fermentation: Implications for gluten detoxification and microbial activity
PS2-S6-PP13	Alia Alwedyan	Snack your way to a healthier gut: Impact of dietary fibre accessibility on the gut microbiome
PS2-S6-PP14	Vineet Singh	Prebiotic potential of seed mucilages and their impact on the host (adult and toddler's) gut microbiome
PS2-S6-PP15	Yi-Wen Lin	*Lactococcus lactis subsp. lactis 1 TIP4,* a newly discovered lactic acid bacterium derived from fermented *Mesembryanthemum crystallinum*, boosts immunity and decreases inflammation in immune cells
PS2-S6-PP16	Louise-Eva Vandenborght	Yeast probiotic for gut health: From *in vitro* model to clinic
PS2-S6-PP17	Yolanda Sanz Herranz	Impact of the wheat production system on its nutritional properties and the gut microbiome
PS2-S6-PP18	Adel Bou Alia	Simulating the impact of drinking water microbiomes on the human gut microbiome
PS2-S6-PP19	Núria Alegre Hospitaler	“Missing microbes”: Systematically understanding gut microbiome compositional and functional differences across populations
PS2-S6-PP20	William Scott	Model-based insights into the potential probiotic role of *Flavonifractor plautii* for gut microbiota modulation
PS2-S6-PP21	Chiara Maria Calvanese	PROBIOGENOMIC approach to discover novel pro- and psychobiotic strains
PS2-S6-PP22	Nadiya Dunayevska	The food-gut microbiome axis: Exploring the potential of fermented foods to restore gut microbiome diversity
PS2-S6-PP23	Katarzyna Warchoł	Gut microbiota as a novel strategy to support fertility and hormonal equilibrium in endometriosis and polycystic ovary syndrome (PCOS)
PS2-S6-PP24	Maria Aspri	Unveiling the microbiome of PDO Halloumi cheese: A combined culture-dependent and metagenomic approaches
PS2-S6-SF01	Davide Buzzanca	Development of a plant-based psychobiotic yogurt-like for the gut-brain axis

PS2-S6-SF02	Ilario Ferrocino	Effects of probiotic supplementation on symptoms and microbiome characteristics in patients with non-celiac gluten/wheat sensitivity
PS2-S6-SF03	Gloria Fackelmann	Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals
PS2-S6-SF04	Emma Saltzman	Live bacteria in fresh foods contribute to human gut microbiome diversity

Poster Session 2: Microbiomes for mitigation of risks in the food system		
Poster #	**Presenter**	**Title**
PS2-S7-PP01	Melisa Jaramillo Zapata	Microbiological food safety: Risk mitigation of foodborne pathogens by applying omics approaches within the food system
PS2-S7-PP02	Yasmine Trabelsi	Human-derived *Lactobacillus* postbiotics as biopreservatives in functional food development: Antifungal efficacy and metabolomic profiling
PS2-S7-PP03	Cintia Mayr	Microbial composition and pathogen resistance in Sauerkraut: Effects of farming practice, potato peel, and fermentation stage
PS2-S7-PP04	Zoe Kampff	The cell surface-associated rhamnose-glucose polysaccharide represents the receptor of *Streptococcus thermophilus* bacteriophage P738
PS2-S7-PP05	Serena Giacomozzi	Strategies for microbiome mapping in raw milk cheese: Findings from a pilot study
PS2-S7-PP06	Alessandra De Cesare	Predicting biological hazards in raw milk cheese using microbiome data
PS2-S7-PP07	Shiva Dubey	Microgreens microbiome: Impact of sanitation on microbial community shifts
PS2-S7-PP08	Amal Alghamdi	The leaf rust biocontrol mediated by an endophytic *Bacillus subtilis* strain
PS2-S7-PP09	George-John Nychas	Multi-omics profiling reveals microbial ecology of fish spoilage under different packaging conditions
PS2-S7-PP10	Luuk van Ooijen	From food to FASTA: Metagenomics for rapid foodborne bacterial pathogen detection
PS2-S7-SF01	Mohak Gujare	Identifying prognostic microbiome biomarkers to predict post weaning diarrhea (PWD) in piglets and disentangling the effects of confounding factors

PS2-S7-SF02	Felix Spiegel	Genomic characterization of persistent *Listeria monocytogenes* in European food processing facilities
PS2-S7-SF03	Floor van Meer	The effect of climate change on food-borne disease outbreaks in the Netherlands
PS2-S7-SF04	Garance Leroy	Assessment of a microbiome engineering strategy using lactic acid bacteria as bioprotective cultures to delay the spoilage of Gilthead Seabream (*Sparus aurata*) fillets

Poster Session 2: Novel microbiome concepts, applications and technologies		
Poster #	**Presenter**	**Title**
PS2-S8-PP01	Koen Venema	A complete pipeline for microbiome modulation – from simple high-throughput screening to well-conducted clinical trails
PS2-S8-PP02	Sandro Gepiro Contaldo	Bridging data and disease: A reproducible metagenomic workflow framework within MIRRI-IT's HPC platform
PS2-S8-PP03	Sara Pipponzi	First Insights into soil microbiome preservation: Strategies, challenges, and future directions
PS2-S8-PP04	Pavlo Hrab	Marine sponge microbiomes for sustainable food preservation
PS2-S8-PP05	Wannes Van Beeck	Ferme Scholen: A safe and engaging gateway to microbiology for the high school curriculum through fermented vegetables and their microbiome
PS2-S8-SF01	Agata Szymanek	Robust microbiome profiling with strain resolution using optical mapping
PS2-S8-SF02	Ananya Pawan Gupta	Phenotypic characterisation using BIOLOG: Microbial strains from cocoa and their novel application
PS2-S8-SF03	Lakhansing A. Pardeshi	Conservation, evolution and recombination of tailocins in the genus *Pectobacterium*; and consequences for species and strain level interactions
PS2-S8-SF04	Nehir Kizililsoley	Leveraging advanced AI for enhanced food safety through pathogen analysis
PS2-S8-SF05	Irene Franciosa	Optimizing long-term storage and propagation strategies for the preservation and reuse of fermented sausage microbiome

Opening Keynote Lecture

OP-KN01 Human and food microbiomes within a One-Health perspective

Nicola Segata

University of Trento, Italy

Session 1: Interconnectedness of microbiomes across food systems

S1-PL01 The 'microbial terroir' promotes fruit quality, plant resilience against stresses and carbon sequestration in fruit tree agroecosystems

Daniele Daffonchio

Department of Agriculture, Forestry and Food Sciences, University of Turin, Italy

Microbiomes are inherently and tightly linked to the functional biology of any living multicellular organism, including animals and plants. Different microbiomes are associated to the different organs and compartments of plants and provide physiological and ecological services that contribute to shape host evolution and domestication. Plant microbiome is also increasingly emerging as a factor that contribute to the quality of the agricultural products. In this talk the concept of 'microbial terroir' is discussed in the light of the quality of fruit, the capacity of microorganisms of relieving host's stresses and saving resources and enhancing the stock of carbon in the agroecosystem, all features to be incentivized to combat the challenging effects of the changing climate. Examples related to grapevine vineyards, date palm oases and olive tree orchards are provided to discuss the role of microbial terroir in orchard sustainability and resilience.

S1-ST01 Ecological selection shapes microbiomes in traditional fermentation: From ecology inspired experiments to avenues of sustainable development

Sijmen Schoustra

Genetics, Wageningen University & Research / University of Zambia, Netherlands

Traditional fermentation is integral to many food systems, especially in low and middle income countries. However, ecological principles that govern microbiome composition and functioning in fermentation are not well studied, hampering the used of traditional fermented foods to promote sustainable development.

In fermentation, transformation of raw materials relies on microbiomes sourced from the environment that are shaped by ecological selection. Exactly what ecological variables shape microbiomes in traditional fermentation is not well understood. Drawing from ecological theory we developed various experiments to assess how ecological selection shapes microbiomes in traditional fermentation. Upon selection, we expect that in the short term species sorting drives community assembly, while in the longer term fixation of novel mutations in specific microbial taxa will result in more specific adaptation.

Here we use a traditional milk-based fermented food from Zambia, mabisi, to assess the effects processing variation, novel substrates and location affect microbiome composition and functioning. First, we conducted a survey collecting around 200 mabisi samples from local processors alongside with interviews to document specifics on processing variation. We profiled microbiomes for their species composition (ASVs) using amplicon sequencing and metabolic profiles with GC-MS. For mabisi six main processing variations exist. Results showed that various processing parameters could explain variation in microbiome profiles. Next, we conducted field experiments where we asked three independent processors to conduct mabisi microbial community along three different processing variations over 10 processing cycles. While we started with an initially uniform microbiome, this microbiome (16S amplicon sequencing profiles) diverged in a reproducible way based on processing method, independent of processor. Finally, we assessed how various relevant functional properties (pH, propensity to produce B-vitamins, key aroma profiles and others) depend on community assemble and selection.

Our results not only advance our fundamental understanding of eco-evolutionary forces that shape microbiomes, it also allows for practical application. Based on our work, the Zambia Bureau of Standards to develop a code-of-practice for mabisi processing, formalizing small-scale traditional processing, thus promoting sustainable development and livelihoods.

S1-SF01 Seasonal sap tapping affects microbial community assembly and flavour formation in palm wine fermentation

I Nyoman Sumerta, Kate Howell

School of Agriculture, Food and Ecosystem Sciences, University of Melbourne, Australia

Palm wine is a traditional alcoholic beverage, widely found in tropical and sub-tropical countries and plays significant roles in culture and tradition. Palm wine is made from naturally fermented palm sap where a complex microbial community emerges through interactions of microbial species including yeasts and bacteria. In this study, we analysed the spatial dynamic of microbial communities to elucidate the fermentation process and flavour formation in relation to season of sap tapping. Fermenting sap from three different palm tree species across the island of Bali, Indonesia were sampled in the wet and dry seasons. Our results reveal that the dominant microbial species primarily drives the fermentation process with minimal influence from the season of sap tapping on reducing diversity indices and increasing variations. It is observed in microbial groups, which were responsible for ethanol production such as *Saccharomyces cerevisiae* and *Zymomonas mobilis* significantly differentiated by season of sap tapping while acid fermenting bacteria were considerably affected. Lactic acid bacteria, acetic acid bacteria, and human-associated fungi exhibited greater sensitivity to season factor, correlating with the acidity profile of freshly tapped sap. Microbial shifting was positively correlated to the formation of aroma profile, suggested by the similar pattern of volatile organic compounds and small molecules characters over seasonal factor. Volatile organic compounds were discriminated by season suggesting less affection on esters as dominant group but benzenoid, acid, and aldehyde groups were more altered. The presence of minor taxa showed an essential role on enhancing the variety of aroma and flavour profile of palm wine and differentiate palm wine characters across season of sap tapping. These findings enhance understanding of microbial dynamics linked to ecological factors in palm wine fermentation, revealing aroma differentiation in palm wine and suggesting strategies for product development, microbial management, and quality optimization to elevate this traditional product in the future.

S1-SF02 Interconnections across microbiomes: How do plant holobionts and food fermentations relate? A focus on the Taggiasca olive tree ecosystem.

Chiara Traina[1], Livio Antonielli[2], Johanna Ley[2], Ilario Ferrocino[1], Kalliopi Rantsiou[1], Tanja Kostic[2], Luca Cocolin[1]

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Microbiomes form a continuum from the environment to the plant holobiont and the food systems, interacting with one another and influencing the plant health and ultimately the sensory traits of the fermented products. The Taggiasca olive tree (*Olea europaea* L.) native to Liguria, North-West Italy, exemplifies this connection, with its fruits undergoing a traditional spontaneous fermentation, where the native microorganisms shape the final product's quality. In this study, a metabarcoding approach was used to characterize the microbial ecology of above- (brined olives, olives, leaves, barks) and below-ground (soils, rhizospheres) compartments of the Taggiasca olive tree and the final fermented products in year 2023 to detect a potential microbial transfer from the tree to the food. Alpha diversity results showed that bacterial diversity was more conserved across compartments than the fungal one, where more significant differences were observed. For beta-diversity, below-ground compartments and leaves in both bacterial and fungal datasets showed more intra-group dissimilarities than olives and brined olives, while Bray-Curtis dissimilarity matrix among samples showed a less dissimilar fungal composition across brined olives and leaves; barks and leaves; barks and rhizospheres, compared to the bacterial one. The main bacterial indicator genera across all samples were *Amnibacterium*, *Halomonas* and *Sphingomonas*, while the main fungal ones were *Cladosporium*, *Zygotorulaspora* and *Hyphopichia*. Indicator ASVs such as *Cladosporium* (ASV18) were shared across all compartments, while *Microbacterium* (ASV172) was present in all compartments except barks, suggesting that certain microorganisms are capable of transferring across plant compartments and persisting into the final fermented product. In the future, the integration of multiple -omics and the consideration of multiple harvest seasons could help investigate the connection of microbiota with the quality of the fermented food products. This study provides the first comprehensive insight into the microbiota associated with the Taggiasca olive tree, offering valuable information on its interactions with the environment and potential implications for food quality.

S1-PL02 The Holomicrobiome Institute: Interconnectedness of microbiomes

Jan Sikkema

Holomicrobiome Institute, Netherlands

Microbiomes exist everywhere—in soil, water, plants, and animals—forming a vast "holomicrobiome" that surrounds us. Recent advancements enable scientists to map and analyze microbiome composition, function, and effects. As a result, microbiome research is expanding rapidly, with promising applications in circular agriculture, sustainable livestock farming, healthier food production, reduced greenhouse gas emissions, improved water quality, and medical diagnostics and treatments.

The Holomicrobiome Institute, funded by the Netherlands National Growth Fund, will integrate fundamental microbiome research across agriculture, food production, healthcare, and water management, recognizing the need for a holistic approach. Leveraging developments in computation and artificial intelligence, it will model and predict microbiome interactions, accelerating the development of applications such as microbial fertilizers, sustainable food ingredients and products, new diagnostic tools, and safer medical treatments.

Our food system, spanning a multitude of different ecological niches, is a highly diverse playground of interconnecting microbiomes. Microbiomes in specific niches of the food chain influence the composition and activities of microbiomes further downstream. These interconnections can have both beneficial impacts such as a.o. characteristic flavours or gut health promoting effects, as well as negative outcomes in terms of reduced shelf life or even outgrowth of pathogens. In this presentation a few examples of interconnections will be discussed and the newly established Holomicrobiome Institute will be introduced.

The Holomicrobiome Institute will bring together research institutions, businesses, governments, and societal stakeholders, and we expect that this ecosystem will drive innovation in safe and effective microbiome-based solutions. Funding is available for activities conducted at Dutch research institutes and companies; we are happy to discuss partnering with international stakeholders for shared innovation programs.

S1-ST02 Characterization of endophytic and epiphytic microbial communities of Nebbiolo grapes

Francesca Cristetti, Vasileios Englezos, Paola Di Gianvito, Luca Cocolin, Kalliopi Rantsiou

DISAFA, University of Turin, Italy

Vineyards offer an ideal habitat for the growth of different microorganisms. Vineyard-specific conditions, such as climatic factors, soil, geographical location, and local practices, strongly influence microbial diversity. Epiphytic microbial communities inhabit the surface of berries, contributing to plant-environment interactions and shaping the microbial composition of grapes at harvest. In contrast, endophytic microorganisms reside within plant tissues and contribute to plant growth, stress tolerance, and the production of secondary metabolites. Understanding the diversity and distribution of epiphytic and endophytic microorganisms is essential, as their distinct origins and functions can influence grape-associated microbial dynamics and consequently affect fermentation processes and wine quality. This study aimed to explore the fungal and bacterial communities associated with distinct compartments of grapes (skin/pulp) and to investigate the role of geography in the communities assembly. Grapes were collected at harvest from thirty-eight Nebbiolo vineyards across seven geographical zones, grouped into two macro areas in Piedmont and one in Lombardy. After harvest, berries were frozen and processed under sterile conditions to separate skins from pulp. To ensure the separation, the berries were washed sequentially under sterile conditions, while the skins were soaked in an isotonic solution to detach microorganisms. Fungal and bacterial communities were investigated by high-throughput sequencing on bacterial 16S rRNA and fungal 26S rRNA encoding genes. Distinct microbial profiles were observed between the two compartments. This study provides important insights into vineyard microbial ecology, revealing how epiphytic and endophytic communities are distributed with potential implications for microbial dynamics and, therefore, wine quality.

S1-SF03 A multi-omics exploration of microbiome dynamics across fermentation styles of cv. Chalkidiki green olives: revealing microbial interconnectedness in table olive food system

Despoina Langari, Fani Mantzouridou

Department of Chemistry, Aristotle University of Thessaloniki, Greece

The integration of high-throughput omics technologies such as metataxonomics and metabolomics offers a comprehensive framework for monitoring and elucidating the complex microbial ecosystems of fermented foods. Despite these advancements, the combined application of such tools to table olive fermentation remains limited. This study applies a multi-omics strategy to track microbial community dynamics and their association with volatile organic compounds (VOCs) during the spontaneous fermentation of Spanish-style (SS) and natural (NF) cv. Chalkidiki green olives at industrial scale. Microbial genomic DNA was extracted directly from the brine samples and subjected to sequencing of the V3-V4 region of the 16S rRNA gene and of the ITS2 region to characterize the bacterial and fungal communities, respectively. VOCs were analyzed by headspace SPME-GC-MS. Spearman's correlation was performed using SPSS software (v. 29.0, SPSS Inc., Chicago, USA). Notable differences in bacterial composition were observed between the two processing methods. *Secundilactobacillus* and *Lactiplantibacillus* were dominant in SS, whereas NF exhibited greater diversity including also *Pediococcus parvulus*, *Loigolactobacillus* coryniformis and *Oenococcus kitaharae*. However, both fungal communities were dominated by genus *Pichia*. Volatilomic analysis resulted in the identification of more than 95 VOCs, including acids, alcohols, carbonyls, esters, phenols, hydrocarbons, terpenoids and miscellaneous compounds. The ecological differences were reflected in distinct correlation profiles. In SS, *Lactiplantibacillus* and *Secundilactobacillus* were strongly ($\rho>0.9$) correlated with 2,3-butanediol and ethyl heptanoate, respectively. *Pichia* was strongly correlated with acetic acid and ethyl lactate. In contrast, in NF *Lactiplantibacillus* was strongly correlated with benzaldehyde. *O. kitaharae* exhibited strong correlations with 2-ethyl-1-butanol, methyl salicylate, linalool and α-terpineol, *P. parvulus* with 1-propanol and 2-methyl-3-buten-2-ol, while *Lob. coryniformis* with 2-methylbutanal. Additionally, *Pichia membranifaciens* displayed strong correlations with 2-heptanol and (E)-2-hexen-1-ol. These findings highlight the intricate microbiome–metabolome interconnections involved in fermentation dynamics. This multi-omics monitoring supports the development of science-driven fermentation strategies to optimize the production of cv. Chalkidiki table olives.

S1-SF04 *BRIDGING Microbiome Science and Practice: Connecting Soil, Food, and Health Professionals*

Marco van Es

Bac2nature, Netherlands

Microbiomes form invisible yet critical networks linking soil health, food quality, and human well-being. While scientific understanding of these connections is rapidly evolving, translating microbiome research into meaningful practices for professionals in healthcare and the vegetable sector remains a key challenge.

Within the Dutch *Soils2Guts* project, efforts are underway to activate the societal value of microbiome knowledge by engaging directly with practitioners. For healthcare professionals, this includes the development of educational modules and preventive strategies that incorporate microbiome literacy and support nature-based health promotion. In the vegetable supply chain, collaborations are being built between soil scientists, growers, retailers, and food safety experts to explore how farming practices that enhance microbial richness can improve both sustainability and food system resilience.

This presentation will share examples of interventions that translate microbiome interconnectedness—from soil to vegetable to gut—into practical insights. These include co-created exposure pilots, storytelling workshops, and participatory formats that help embed microbiome awareness into daily practice. By bridging scientific research with real-world application, this work contributes to building a more health-oriented and ecologically grounded food system.

Session 2: The many pathways to sustainable food systems powered by microbiomes (ESR session)

S2-SF01 Microbiome as mediator: Lessons from the food pharmacy for integrating health and agriculture

Shana Hepping, Gerard Breeman, Eefje Cuppen

Public Administration, Leiden University, Netherlands

The microbiome, an invisible yet profoundly interconnected ecosystem of microbes, is increasingly recognized as a powerful entry point for reimagining relationships across food, health, and environment. The Soils2Guts consortium seeks to analyze these relationships by investigating the microbial connection between soils, plants and guts. Within this broader project, this study is situated and looks into the integration between agrifood and healthcare systems into one Healthy and Sustainable Food System, and how the microbiome can function not only as a biological connection, but as an societal and discursive entry point, thereby exploring the microbiome's potential to catalyze sustainability transitions.

Drawing on a case study of the Food Pharmacy in the Netherlands, this study examines how the microbiome is mobilized in practice. The Food Pharmacy is a cross-sector initiative promoting regenerative agriculture and preventive health through a community-based intervention including food boxes and cooking workshops. Specifically, we set out to explore how professionals and policymakers engage with the microbiome concept: does it open up new forms of collaboration and mutual understanding? Or does it compete with dominant frames such as nutrient-centric or individualized health advice?

The research employs a interpretivist design, being qualitative interviews with key stakeholders. Analysis is guided by frameworks on boundary work, innovation, and socio-ecological transitions, focusing on how new ideas travel across institutional domains, how they are resisted or embraced, and how they may function as leverage points for systemic change. Early findings suggest that while the microbiome holds integrative and imaginative potential, its translation into practice is hampered by conceptual ambiguities, regulatory fragmentation, and professional silos.

This research contributes to emerging scholarship on microbiomes as boundary objects; connecting diverse communities of practice across the food-health-environment nexus. It highlights the need for actor-sensitive approaches that attend to how microbiome discourse is negotiated, embedded, and potentially institutionalized. Ultimately, the study argues that microbiome thinking, if cultivated carefully, can support more relational and systemic understandings of food, health and sustainability, helping to bridge fractured regimes and create a more integrated food system.

S2-SF02 Oral and gut microbiome influences on the perception of plant-based and fermented foods

Leonardo Menghi, Davide Giacalone

Department of Green Technology, University of Southern Denmark, Denmark

Shifting toward diets aligned with environmental sustainability and human health is a pressing societal concern. In this context, increasing fermented food intake offers a valuable opportunity, combining a low ecological footprint with the support of gut microbiome configurations equipped with redundant health-supporting functionalities. However, broader adoption remains limited by phenotypic differences in sensory perception. Intriguingly, accumulating evidence supports a contribution of the human microbiome to interpersonal variations in chemoperception, potentially influencing the dietary integration of fermented and plant-based foods.

Against this backdrop, this contribution offers a concise overview of biological mechanisms linking the human microbiome to sensory perception, with a focus on plant-based and fermented foods. This is framed by two case studies involving adults (S1; n = 100, 58% women, 18–30 y) and adolescents (S2; n = 232, 43% girls, 13–17 y). In both studies, participants provided hedonic and intensity ratings of oral sensations elicited by commercial (S1) or model (S2) plant-based foods, alongside assessments of psychological traits related to food choice, dietary data (food diaries in S1, FFQs in S2), and salivary and gut (S1) microbiota samples, later profiled via 16S rRNA gene sequencing (S1) or shotgun metagenomics (S2). Across both samples, higher abundance of dysbiotic gut taxa and cariogenic, SCFA-deficient salivary bacteria was associated with enhanced responsiveness to bitterness, sourness, and astringency, and lower adherence to plant-based diets. The findings will be discussed in light of their potential to inform personalized strategies that leverage this bidirectional framework to support sustainable and health-promoting dietary habits.

S2-SF03 Alleviation of drought stress with microbial inocualnts to maximize crop yield

Ally Miners, Trevor Charles

Biology, University of Waterloo, Canada

Drought is a major environmental stressor that diminishes soybean yield. Climate change has exacerbated drought frequency and intensity, threatening global food security and contributing to agricultural economic decline. Application of plant growth-promoting bacteria (PGPB) has been shown to mitigate drought stress and boost plant productivity through various mechanisms. However, beneficial microbes are often ineffective in field trials, despite showing promising results in growth chamber studies under sterile conditions. In this study, four microbial inoculants belonging to the genera *Stutzerimonas* and *Pseudomonas* were evaluated on their ability to rescue soybean growth under drought stress. These strains possessed several plant-beneficial traits, including nitrogen fixation, phosphate solubilization, production of 1-aminocyclopropane-1-carboxylate (ACC) deaminase, as well as iron-chelating siderophores. Field soil from Southwestern Ontario was used to investigate inoculant efficacy under a native plant microbiome, since competition with native microbiota, cross-feeding, and biogeochemical cycling influence the activity of PGPB inoculants. By evaluating the performance of PGPB amid complex interactions with native plant microbiota, the most promising strains for enhancing crop yield were identified.

S2-SF04 Harnessing microbial communities and synthetic biology for PET upcycling into PHA bioplastics

Eugenia Dadzie, Trevor Charles, Aranksha Thakor

Biology, University of Waterloo, Canada

Plastic pollution, particularly from polyethylene terephthalate (PET), presents a persistent environmental challenge due to its durability and resistance to degradation. At the same time, bioplastics such as polyhydroxyalkanoates (PHAs) offer a biodegradable alternative to conventional plastics, but their adoption is limited by high production costs and reliance on refined feedstocks. Bridging this gap calls for strategies that couple waste remediation with value-added biomanufacturing in a circular framework.

This work integrates microbial ecology, functional metagenomics, and synthetic biology to develop a microbial platform capable of converting PET-derived monomers, terephthalic acid (TPA) and ethylene glycol (EG), into PHAs. Environmental enrichment cultures from plastic-impacted sites were used to identify microbial communities capable of metabolizing PET breakdown products. Genes of interest were captured through functional metagenomic screening and introduced into *Pseudomonas putida* KT2440, a genetically tractable and industrially relevant chassis with native PHA-producing capacity.

The engineered strains combine PET-derived carbon assimilation with biopolymer biosynthesis, creating a route for the biological upcycling of plastic waste. This approach highlights the potential of leveraging microbiomes not only as reservoirs of catabolic diversity, but as foundational tools for propagating sustainable material flows. By aligning waste valorization with microbial biotechnology, this work contributes to the development of circular, microbiome-driven solutions to plastic pollution.

S2-SF05 Lettuce biofortification through vitamin B12- producing bacteria.

Sara Pipponzi[1], Stefanie Primisser[2], Livio Antonielli[1], Emilio Stefani[3], Stephane Compant[1], Angela Sessitsch[1], Tanja Kostic[1]

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Vitamin B12 is produced exclusively by certain bacteria and archaea. Since plants neither require nor synthesize vitamin B12, they typically do not contain this essential nutrient. Therefore, individuals who adhere to vegan or vegetarian diets are at risk of deficiency and associated health problems.

An *in silico* genome analysis was performed on 66 bacterial genomes, including a reference strain known to produce vitamin B12. The genomes were analyzed using the Rapid Annotations using Subsystems Technology (RAST) server and the MetaCyc database to verify the presence and completeness of the vitamin B12 metabolic pathway. Bacterial strains containing the metabolic pathway were selected for further analysis.

The ability of the selected strains to produce vitamin B12 was confirmed by analyzing pure culture extracts using high-performance liquid chromatography with diode-array detection (HPLC-DAD). The most promising strains were then tested for their ability to produce vitamin B12 in lettuce seedlings grown under sterile conditions, both with and without cobalt chloride supplementation. HPLC-DAD analysis of the purified lettuce extract revealed that *Methylobacterium* sp. strain P1-11 can produce detectable amounts of vitamin B12 in vivo.

This is the first time a bacterial endophyte has been used to produce vitamin B12 *in planta*, suggesting the potential of endophytic bacteria to enhance the nutritional value of plant-based foods. This finding paves the way for further research and potential future applications.

Session 3: Microbiomes for global health

S3-PL01 Soil health, soil microbes and one health

Gerlinde De Deyn

Soil Biology, Wageningen University & Research, Netherlands

Currently > 8 billion people inhabit planet Earth, all in need of food, clean water, air, energy, and shelter. Despite all our technical innovations humans remain critically dependent on natural resources, yet we consuming these faster than they can regenerate and thereby cross our planetary boundaries and compromise health. We urgently need to shift to sustainable production and consumption to safeguard our natural resources and to ensure healthy future generations on a healthy planet. Microbiomes can play a key role in this transition as regulators of elemental cycles, detoxifiers and producers of health promoting biochemicals. However, microbiomes do not operate in isolation and their composition and functioning is dependent on the environmental context. In this talk I will explore the global status of soil health, the role of soil microbes and their linkages to the one health concept.

S3-ST01 From soil to food chain: Microbial responses to triazole fungicides

Jowenna Sim[1], Barbara Drigo[1], Casey Doolette[1], Sotirios Vasileiadis[2], Dimitrios Karpouzas[2], Enzo Lombi[3]

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Fungicides are essential in modern agriculture for safeguarding crop productivity. However, their broader ecological impacts on agroecosystems, including plant–microbe interactions, soil health, and the integrity of the food system, remain insufficiently understood. This study evaluated the effects of two widely used triazole fungicides, flutriafol and tebuconazole, across ten South Australian cropping soils selected to represent a range of pH, organic carbon content, and textures. We employed enzymatic and functional gene assays, alongside shotgun metagenomics in three representative soils, to assess microbial functional responses and their potential implications for food system safety. Both fungicides stimulated microbial enzymatic activity and increased functional gene abundances associated with carbon and nitrogen cycling, as well as aromatic compound metabolism, particularly in high-organic-carbon soils, suggesting enhanced microbial functional capacity. However, these functional stimulations were accompanied by the selective enrichment of resistance traits. Soil-specific effects were observed, with both fungicides increasing the abundance of clinically relevant β-lactamase genes (*bla*$_{GES}$, *bla*$_{IMP}$), the colistin resistance genes *mcr*, biocide resistance genes linked to metals with documented dietary exposure pathways, such as mercury and cadmium, as well as the mobile genetic elements (e.g., IS1, IS21, IS1182), suggesting enhanced potential for horizontal gene transfer. Notably, the abundance of several food-associated potential pathogen genera, including *Listeria* spp*., Enterococcus* spp*., Vibrio* spp*.,* and mycotoxin-producing *Aspergillus* spp*. and Fusarium* spp*.*, increased under fungicide treatment, alongside corresponding phage signatures. These findings underscore the complex soil–fungicide–microbiome interactions, where stimulation in microbial function is also associated to increased resistance and food-related pathogen risks. Such insights are critical for informing sustainable pesticide practices that balance crop protection with long-term food system safety.

S3-SF01 Urbanization-driven alterations in sediment microbial communities and the prevalence of antimicrobial resistance in freshwater ecosystems

Joseph Selvin, Vishnu Prasad Nair, G Seghal Kiran

Microbiology, Pondicherry University, India

Urbanization poses significant threats to freshwater ecosystems, yet its effects on sediment microbial communities remain underexplored. Our study investigates the influence of urbanization on bacterial diversity, community structure, and functional potential in two contrasting aquatic systems in southern India: the semi-urban Sankaraparani River (Puducherry) and the urban Buckingham Canal (Chennai). Sediment samples were analyzed using 16S rRNA gene sequencing to characterize microbial communities. The Sankaraparani River exhibited higher microbial diversity, predominantly composed of Acidobacteria, Chloroflexota, and Planctomycetes—taxa commonly associated with near-natural environments, including nitrogen-fixing and methane-oxidizing bacteria. In contrast, the Buckingham Canal showed reduced diversity and was enriched with pollution-associated taxa such as Pseudomonadota, Bacillota, and Bacteroidetes, including sulfur- and nitrogen-reducing bacteria indicative of anthropogenic impact.

In addition to community composition, we assessed the prevalence of antimicrobial resistance (AMR) across freshwater environments of Puducherry. Environmental screening revealed the presence of antibiotic-resistant bacteria in both sediment and lake water ecosystems. A novel plasmid belonging to the repUS12 replicon type was identified in *Bhargavaea beijingensis* strain PS04, harboring *ermT* and *tet(L)* genes that confer resistance to macrolides, lincosamides, and tetracyclines. In Thiruvandarkoil Lake an important rural water body and potential drinking water source resistant isolates were subjected to whole genome sequencing. Genomic analysis revealed cephalosporin resistance mediated by *blaVEB-6* (in *Proteus mirabilis* PS01), *blaSHV-12* and *ompK36* mutation (in *Klebsiella quasipneumoniae* PS02), and *blaSHV-12*, *blaACT-16*, *blaCTX-M*, and *blaNDM-1* (in *Enterobacter hormaechei* PS03). Notably, an *mcr-9*-positive *Enterobacter hormaechei* was detected—marking the first environmental report of *mcr-9* in India.

These findings underscore the ecological consequences of urbanization on freshwater sediment microbiomes and highlight the emergence and environmental dissemination of AMR genes, raising concerns about ecosystem health and public safety. This work emphasizes the urgent need for integrated monitoring and bioremediation strategies to manage microbial pollution and antimicrobial resistance in aquatic environments.

S3-PL02 Extreme microbes, the ultimate frontier in environmental restoration and planetary health

Alexandre Soares Rosado

Biological and Environmental Sciences and Engineering Division (BESE), KAUST – King Abdullah University of Science and Technology, Saudi Arabia

Microbiomes are central to terrestrial ecosystems: they regulate soil fertility, sustain plant growth, drive nutrient cycles, and buffer against disturbance. In the face of climate change, land degradation, and pollution, these microbial communities are increasingly recognized as key to restoring ecological stability and biodiversity.

Our research examines how microbiomes can be harnessed to improve soil quality, reduce chemical inputs, and remediate contamination. Through multi-omics, we characterize soil microbial communities and their functions to design strategies for soil improvement. In mangroves, we identified novel taxa and enzymes capable of degrading plastics, while studies on extremophiles revealed their potential to mitigate oil pollution and other stressors. These findings highlight the applied value of microbial approaches to today's environmental challenges.

We also investigate unique environments such as Terra Preta soils in the Amazon and volcanic systems in Saudi Arabia, which harbor diverse and efficient microbial consortia. These ecosystems provide models for enhancing fertility and resilience that can inform restoration globally. Building on this, we are testing microbial applications in Mars simulation chambers, assessing their ability to support plant growth and soil functionality under extreme extraterrestrial conditions.

At this conference, I will present new data on extremophilic black fungi, particularly Rhinocladiella, and how their physiology may inform soil amelioration strategies. I will also discuss genomic insights into novel extremotolerant bacteria isolated from NASA's Phoenix mission spacecraft assembly cleanrooms. These resilient microbes, adapted to oligotrophic, radiation- and chemical-stressed environments—encode genes for biofilm formation, DNA repair, and metabolites such as ε-poly-L-lysine and zeaxanthin, underscoring their potential for biotechnology and planetary protection.

Framed within One Health and planetary health perspectives, these efforts emphasize the pivotal role of microbiomes in advancing sustainability. Microbial interventions can regenerate soils, strengthen food security, mitigate pollution, and support human wellbeing, providing solutions from Earth's vulnerable ecosystems to future space exploration.

S3-ST02 One Health perspective: Large-scale (meta)genomic analyses elucidate the distribution and horizontal transmission of antimicrobial resistance genes from environmental sources to humans

Wisnu Adi Wicaksono[1], Núria Alegre Hospitaler[2], Samuel Bickel[1], Gabriele Berg[1]

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By the year 2050, it is projected that drug-resistant pathogens may be responsible for approximately 10 million deaths annually. This significant concern highlights the importance of understanding the role of environmental microbiota in the development of antibiotic resistance, in order to inform effective mitigation strategies. Natural environments, which often exhibit high microbial diversity and prevalence, are recognized as important reservoirs of antimicrobial resistance (AMR) genes. To thoroughly understand the evolution, emergence, and dissemination of antimicrobial resistance, it is crucial to investigate the distribution of antibiotic resistance genes (ARGs) across interconnected ecosystems, emphasizing the complex interactions among humans, animals, and the environment, as outlined by the One Health framework. In this study, we analyze a comprehensive dataset that includes over 19,000 metagenome-assembled genomes (MAGs) and 4,000 metagenomic samples from soil, food, oral microbiomes, and the human gut. Our goal is to examine the distribution and transfer of ARGs across these interconnected microbiomes. Specifically, we seek to address the following research questions: 1) What are the primary carriers of ARGs, and what factors most significantly influence the resistome? 2) Which taxa are likely to contribute to the emergence and dissemination of antimicrobial resistance across different environments? 3) How do changes in bacterial community structure correlate with variations in ARG profiles across different biomes? 4) What environmental and biological factors impact the presence and distribution of ARGs?

S3-SF02 Uncovering antimicrobial resistance pathways in agri-food ecosystems

Elena Crotti[0], Francesco Riva[0], Valentina Riva[0], Arnaud Dechesne[1], Emanuele Ferrari[2], Federico Lazzaro[3], Andrea Di Cesare[2], Barth Smets[1], Francesca Mapelli[0], Ester Eckert[2]

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Within the One Health framework, monitoring the spread of antibiotic resistance genes (ARGs) via horizontal gene transfer (HGT) in agri-food systems is essential to assess the potential risks to human health. Freshwater ecosystems and plant compartments, both of which may receive treated wastewater, represent key routes for AMR diffusion. In freshwater habitats, extracellular DNA (eDNA) is frequently highlighted as a critical factor in ARG spread. However, its fate and uptake within food webs—particularly its interactions with higher organisms like zooplankton—remain poorly characterized. Additionally, limited research has explored plant-related niches, such as phyllosphere and rhizosphere. As these compartments can be exposed to reclaimed water through irrigation, they could act as reservoirs for AMR determinants, potentially introducing them into the food chain. Aim of this contribution is to evaluate the movement of ARGs through natural transformation and conjugation in the abovementioned underexplored niches.

We first investigated the impact of the zooplankton *Daphnia obtusa* on eDNA, evaluating its uptake by *Acinetobacter baylyi* BD413, a model naturally competent bacterium. Using transformation assays, molecular techniques, and proteomic analyses, our results showed that zooplankton (and their associated microbiota) influence eDNA degradation, topology and uptake, thus suggesting a role in AMR diffusion in freshwater. We then assessed natural transformation on the lettuce phylloplane using *A. baylyi* BD413. Results confirmed that transformation can occur on the leaf surface, revealing a potential entry point for ARGs into an epiphytic bacterium with endophytic capabilities. Lastly, considering the importance of Enterobacteriaceae within the One Health and AMR perspective, an environmental isolate of *Klebsiella variicola* was selected as ARG donor. A broad-host-range plasmid, encoding a fluorescent marker gene and an ARG, was transferred to native rhizosphere microbiota from lettuce roots. Plasmid transfer was confirmed via cell sorting and 16S rRNA gene amplicon sequencing. In conclusion, our data underscore the importance of studying AMR spread through HGT in agri-food systems, to support the development of robust risk assessment tools and strategies for mitigation.

Session 4: Microbiomes for mitigating climate change

S4-PL01 Climate costs of domestication: How rice microbiomes shifted from nitrogen fixers to N_2O emitters

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Crop domestication has boosted global food production but also reshaped plant–microbe interactions with major climate implications. Here, we compare the rhizosphere microbiomes of wild and domesticated rice to assess how domestication altered nitrogen cycling processes. Using shotgun metagenomics and quantitative PCR, we find that wild rice harbors a microbiome enriched in nitrogen-fixing genes and exhibits higher nitrogenase activity, while domesticated rice enriches for genes involved in nitrous oxide (N_2O) production. Greenhouse assays confirm that soils inoculated with wild rice microbiomes display stronger N-fixing activity regardless of plant genotype, whereas soils associated with domesticated rice emit significantly more N_2O. Root metabolomics further reveal that wild rice exudates correlate positively with the abundance of microbial N-fixation genes, whereas domesticated rice exudates favor N_2O-producing taxa. Supplementing soils with wild rice metabolites restores microbial nitrogen fixation and nitrogenase activity. Collectively, our findings demonstrate that rice domestication shifted root-associated microbial functions from nitrogen fixation toward N_2O emission, illustrating an overlooked climate cost of crop domestication.

S4-PL02 MIRRI-ERIC and MICROBES-4-CLIMATE: Advancing culturomics and synthetic communities for climate action

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MIRRI-ERIC, the Microbial Resource Research Infrastructure, is a pan-European ERIC that coordinates microbial Biological Resource Centres and services. It provides access to curated microorganisms, data, and expertise, supporting research, innovation, and European priorities for sustainable food systems and climate action.

MICROBES-4-CLIMATE (M4C), coordinated by MIRRI-ERIC, is a Horizon Europe project that brings together leading Research Infrastructures to study soil and plant microbiomes under climate stress. It develops interoperable services, experimental approaches, and data workflows to understand microbial responses to drought, heat, and other factors, strengthening resilience in agroecosystems and related environments.

Within M4C, one goal is the establishment and validation of synthetic microbial communities (SMCs). It standardises sampling, isolation, and preservation, identifies new microbial isolates, and designs SMCs with key ecosystem functions that protect plants under stress. These resources and workflows are preserved in partner collections, ensuring long-term availability for research and innovation.

In parallel, culturomics provides a complementary approach to broaden the range of microbial strains available for such efforts. By diversifying cultivation conditions and applying high-throughput MALDI-TOF MS dereplication and genome-based identification, it uncovers microbial diversity often missed by conventional approaches. Such strains can enhance soil and plant health, support climate-resilient farming, and accelerate microbiome-based innovation for climate change mitigation.

S4-ST01 Predicting microbial functional diversity for decomposition along an aridity gradient

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Soil microbial communities are rarely represented in soil models or with extreme simplifications due to their complexity. Acknowledging that temperature and moisture are the primary controls over microbial functional diversity, this research aims to determine the extent to which soil functional diversity can be predicted based on these factors. We used the aridity index (AI), as this easy-to-measure metric includes temperature and moisture. Following the YAS framework, a widely accepted trait-based approach to characterize soil microbial communities, we hypothesized that under an identical food source, the functional strategies employed by the community will go from high growth yield (Y) in humid areas to higher investment in stress tolerance (S) in arid areas. We should also expect a trade-off between investment in S and Y, while relative investment in A (resource acquisition) should remain constant. We further hypothesized that AI is a decent predictor of the microbial investments into the Y, A, and S traits. We used the DEMENTpy model, an in silico simulator, to derive YAS investments for hypothetical soil microbial communities at five sites along an aridity gradient in Spain. We validated model simulations using mass loss from Rooibos tea samples from each site and employed a Dirichlet regression model to predict YAS investments, using AI. Contrary to the hypotheses, increasing aridity changes community investment from Y to A, with limited changes in S. The A strategy could be predicted considerably well based on AI, while Y and S could not. Together with further validation of our modeling results with experimental data, our findings lay the groundwork in deriving simple mathematical formulations that can be integrated into Earth system models, allowing for upscaling from genomes to Earth system processes.

S4-SF01 Microbial seeding as an early-life intervention to reduce methane emissions in dairy cattle

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Mitigating methane (CH_4) emission from dairy cattle is critical for reducing agriculture's climate impact. Early-life microbiome modulation offers a promising intervention strategy. This study evaluated whether rumen microbiome composition in calves could be steered towards a composition associated with lower CH_4 emission by early-life inoculation with rumen fluid from cows with divergent methane emission phenotypes. Donor cows were classified as high (HMR) or low (LMR) methane emitters based on . Microbial community analyses (16S rRNA and metagenomic sequencing) indicated modest but significant differences in microbiome composition related to CH_4 emission phenotype (redundancy analysis, RDA: R^2 = 3.49%, P = 0.003, 18 differentially abundant bacterial genera, different co-correlation networks), although individual animal variation had a stronger overall influence. Calves were inoculated orally five times during their first 3 weeks of life (100 mL per inoculation event) with either rumen fluid from HMR cows, LMR cows, or water (control) and followed up to 52 weeks of age. Microbial seeding did not affect feed intake, body weight, or growth performance. However, calves inoculated with microbiota from LMR donors showed significantly lower CH_4 intensity (g/kg body weight, -3.3%, P = 0.05) and a toward reduced CH_4 yield (g/kg DMI, -2.7%, P = 0.07) compared to calves inoculated with microbiota from HMR donors. Microbial analyses confirmed a significant influence of inoculation treatment on calf rumen microbiome composition (RDA R^2 = 2.94%, P = 0.001), revealing a closer resemblance to the donor cows' microbiota rather than unrelated donors ($P < 0.05$). Comparable results were found in the archaea community, further supporting the consistency of microbial responses. In conclusion, early-life microbial seeding significantly influenced the rumen microbiome composition and reduced CH_4 emission in calves up to 52 weeks of age without negative impacts on growth or intake. Future research should explore improved methods of microbial sampling and delivery, along with long-term persistence and functional implications, building upon this proof-of-principle study.

Session 5: Microbiomes for circularity/sustainability

S5-PL01 Plant-growth promoting microorganisms to drive wheat microbiome modulation through sustainable practices

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The use of Plant Growth-Promoting Microorganisms (PGPMs) is becoming increasingly valued as a sustainable agricultural practice to enhance crop health and productivity while reducing environmental impact. Their ability to establish long-term in the soil microbiome, along with their contrasting and synergistic modes of action, make them a viable alternative for the gradual replacement of hazardous chemicals. As part of TRIBIOME project, over 150 PGPMs were isolated from wheat roots and surrounding soils (BBCH 51-57) from Italy, Spain and South Africa. Top candidates were rigorously screened for their ability to promote wheat grow through rapid, controlled and cost-effective *in vitro* culture assays, mimicking environmental stress conditions. *Bacillus* sp. exhibited a positive effect on aerial and root development in *Triticum durum* at the mid-development stage (9 days), compared to control plantlets, under both normal and drought conditions. In addition to driving the shift towards sustainable farming, TRIBIOME lays the foundation for a circular agricultural economy by repurposing pretreated wheat residues as a second-generation substrate for cultivation of the top *Bacillus* sp. isolate, which reached $3 \cdot 10^7$ colony forming units per mL in 48 h. By reusing waste to produce newly isolated microorganisms and validating their growth-promoting activities, this project paves the way for wheat agriculture that supports growing population and adapts to climate change. The project's progress points to a future where technology and sustainability are combined to improve not only wheat cultivation, but also other essential crops.

S5-ST01 Engineering *Pseudomonas alloputida* for sustainable bioplastic production from dairy waste

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Despite increasing awareness and regulations for limiting single-use plastic products, the world still produces up to 500 million tons of plastic waste each year. A large amount of this waste cannot be managed, and as a result becomes an environmental pollutant. There is an imminent need to replace some of these materials with biodegradable and renewable alternatives.

Polyhydroxyalkanoates (PHAs) are microbially produced, biodegradable, and biocompatible polymers with physical properties that are comparable to petroleum-based commercial plastics. Medium-chain-length (mcl) PHAs are particularly attractive due to their flexibility and durability, characteristics which are essential for many packaging applications. While the prospect of these polymers has been around for decades, the high cost of production has limited their commercial viability as a sustainable alternative. This challenge primarily stems from the high cost of the fatty acid-based feedstocks that are normally required for mcl-PHA production. One way to combat this hurdle is to produce these products using low- or no-cost food waste. This project introduces our attempt at producing low cost mcl-PHA using waste lactose from dairy processes. Lactose is a large constituent of many dairy waste by-products, making it an ideal target for valorization.

The microbial chassis, *Pseudomonas alloputida* KT2440, is a well-established platform for PHA biosynthesis but lacks the ability to metabolize lactose or its breakdown product, galactose. We have successfully genome-engineered *P. alloputida* to efficiently utilize lactose and galactose, allowing substantially decreased production costs while addressing an existing waste management issue. Furthermore, by harnessing functional metagenomics-based gene discovery and synthetic biology, we have engineered our strains to efficiently convert waste lactose to produce a range of high-value mcl-PHA and scl-mcl-PHA copolymers.

By converting abundant and readily available food waste into high value, biodegradable materials using microbial platforms, this work demonstrates the potential of microbe-enabled solutions for circularity and sustainability in the bioeconomy.

S5-SF01 From soil to must: Harnessing vineyard microbiomes for circular viticulture and winemaking

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Viticulture relies on complex microbial ecosystems that shape grapevine health, soil fertility, and, ultimately, wine quality. In the Vino Nobile di Montepulciano area, recent metagenomic and functional studies have highlighted the presence of plant growth-promoting bacteria (PGPB) with key functional traits that can be harnessed to enhance both vineyard sustainability and wine production.

This study presents the biodiscovery and characterization of PGPB and enologically relevant microbial strains isolated from vineyard soils, plant rhizospheres, and grape musts in the Vino Nobile di Montepulciano terroir, focusing on their potential applications in sustainable viticulture and winemaking.

We applied shotgun metagenomics and culturomics to 320 samples collected during the 2022–2024 seasons. We identified microbial consortia enriched in biofertilization, biocontrol, stress tolerance, and fermentation-related functions, with key genera including *Pseudomonas* and *Bacillus*. These strains exhibited enhanced capacities for phosphorus solubilization, nitrogen fixation, and the production of bioactive compounds such as indole-3-acetic acid (IAA) and siderophores, demonstrating their potential to support vine growth while reducing chemical inputs. Moreover, we isolated enologically relevant microbial strains from grape musts, harboring genetic traits linked to fermentation processes and the valorization of must-derived substrates, suggesting their potential role in shaping wine quality.

This study provides the first integrated evaluation of native PGPB and enological microbes from Montepulciano vineyards, laying the foundation for a microbiome-based sustainable food production system. By integrating these beneficial microbes as biofertilizers and enological probiotics, we offer a scalable approach to regenerative viticulture, reducing agrochemical dependency, enhancing terroir expression, and promoting sustainable wine production.

S5-SF02 Antimicrobial resistance dynamics in black soldier fly larvae valorizing waste streams

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This study investigated the potential of black soldier fly larvae (BSFL) for waste valorization within circular food production systems, with a particular focus on the associated microbial and antimicrobial resistance (AMR) gene landscape. Reared on various residual streams, BSFL microbiota were assessed to understand both their composition and potential AMR risks. While Pseudomonadota was consistently abundant across treatments, the study revealed concerning prevalence of Tetracycline resistance genes, particularly concentrated in frass derived from larvae fed dairy processing plant sludge. Integration of taxonomic data with AMR gene profiles identified *Acinetobacter colistiniresistens* and *Pseudomonas aeruginosa* as key bacterial contributors to multiple AMR gene clusters within the BSFL system. These findings demonstrate that while BSFL offer a promising avenue for waste valorization, careful consideration and further research are crucial to mitigate potential risks associated with the accumulation and transfer of antimicrobial resistance genes.

S5-PL02 Leveraging bioactive compounds and microbiomes for the development of sustainable, low-immunogenic wheat-based foods

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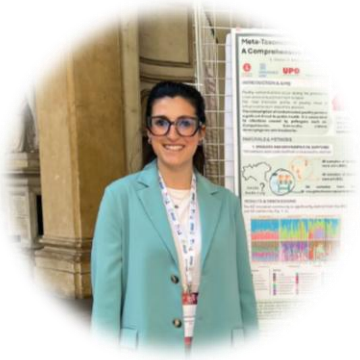
Consumer preferences are shifting towards environmentally friendly, clean-label, and resilient food systems. Along with this, there is a growing demand for allergen-free and health-conscious foods, as consumers become increasingly aware of food sensitivities, allergies, and intolerances. Among immune reactions to food, food allergies are particularly concerning for consumers due to the immediate and severe reactions that can lead to life-threatening outcomes. At the same time, there is rising awareness of non-celiac gluten sensitivity and celiac disease. However, many individuals with these conditions remain undiagnosed and are left to manage their symptoms without clear medical guidance, making them a persistent concern for both consumers and the scientific and healthcare communities.

Alternative grains, such as rice, corn, or quinoa, are commonly used in gluten-free diets, but they often lack the same nutritional benefits or culinary qualities as wheat. Low-immunogenic wheat products could offer a better alternative by maintaining the nutritional value and texture of traditional wheat-based foods while catering to dietary restrictions. In this context, developing low-immunogenic foods that align with current consumer demands is an exciting area of research in food science and agriculture.

Offering low-immunogenic wheat products can help food manufacturers meet the needs of a growing niche market for specialty foods. Recent studies have highlighted the critical role of microbial communities in food sustainability, spanning human health, agricultural practices, and environmental sustainability. In the case of wheat-based foods, some microbial communities have been shown to break down gluten proteins, reducing their immunogenicity. However, the effects of food matrixes on microbiota ecology and function remain underexplored.

Additionally, bioactive compounds have demonstrated the ability to modulate wheat gluten immunogenicity by influencing the bioaccessibility, bioavailability, and immunogenic potential of gluten peptides. As part of the WHEATBIOME framework, novel cellular models are being developed to better understand the impact of bioactive compounds, food and human microbiota, and immunogenic proteins on food taste and immunogenicity. This holistic approach—from farm to fork—aims to design sustainable, low-immunogenic foods that align with modern consumer needs.

S5-ST02 Sustainable Kombucha fermentation: Microbial dynamics and chemical profiling from plant-based by-products



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Kombucha is a fermented beverage with ancient origins, produced by a SCOBY (*Symbiotic Culture of Bacteria and Yeasts*), which consists of yeasts, acetic and lactic acid bacteria. The beneficial properties associated with this beverage are well known, and due to the growing consumer interest in functional foods, kombucha has recently attracted renewed attention. This study aimed to characterise the microbial community involved in kombucha fermentation, introducing an innovative element: the use of plant-based by-products (pineapple, carrot, fennel) as flavouring agents. This approach aligns with the principles of circular economy. Microbial populations were analysed using culture-dependent and independent methods. An amplicon sequencing metataxonomic analysis targeting the 16S rRNA and 26S rRNA genes was performed. High-performance liquid chromatography was employed to identify sugars and organic acids, while volatile organic compounds (VOCs) were analysed via gas chromatography-mass spectrometry. Fermentation was monitored over 8 days (0, 1, 4, 6, and 8) at 24 °C. Additionally, shelf-life tests were conducted at 4 °C on days 7 and 14 to evaluate microbial viability and product stability. The results showed a predominant presence of yeasts belonging to the *Schizosaccharomyces* and *Zygosaccharomyces* genera. The main genus of acetic acid bacteria is *Komagataeibacter*, which creates the characteristic kombucha biofilm and produces acetic acid. The microbial groups reached a final concentration of 6 $\log_{10}$ CFU/ml after the second fermentation. Organic acid analysis indicated a significant increase in acetic acid level, accompanied by a corresponding pH decrease over time (Dunn's test, $p < 0.05$). Forty VOCs were identified, with concentrations increasing throughout fermentation and storage, suggesting ongoing metabolic activity. The presence of the *Schizosaccharomyces* genus is associated with an increase in VOCs, highlighting its role in fermentation processes. Notably, pineapple-flavoured kombucha samples exhibited higher VOCs levels (Dunn's test, $p < 0.05$), suggesting an impact of flavouring by-products on microbial metabolism and the resulting aroma profile. Overall, the final product demonstrated promising attributes, including diverse flavour notes and natural carbonation. However, further development and comprehensive sensory evaluation are necessary. This work enhances the understanding of kombucha's microbial ecology and supports its potential as a sustainable beverage.

S5-SF03 Steering microbiomes for diseases suppression in soilless cultivations systems via the addition of circular waste streams

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Soilless growing systems are globally increasing by ca. 250% in 2050 and include the production of fruit vegetables, leafy greens and small fruit as well as ornamentals. The use of chemical plant protection products must be further minimized in the future. Alternative approaches are needed to prevent plant diseases, such as Pythium, and Fusarium in these soilless cultivation systems. Microorganisms can suppress the growth or establishments of pathogens in the root zone. This natural process is called disease suppression. However, soilless growing media may lack a microbial community that suppresses diseases, as soilless growing media have a low microbial diversity compared to soils at the start of plant growth and the microorganisms present may not contribute to disease suppression. Microbiomes in compost and spent mushroom substrates have a long history for their disease suppressive capacity. Therefore, they may be good options to consider in soilless cultivation systems.

Here, we studied if the addition of compost or spent mushroom substrate (SMS) to soilless cultivation systems would suppress root-zone diseases in cucumbers via changes in microbiome composition. We hypothesized that the addition of compost or spent mushroom substrate (SMS) to seeds would suppress disease symptoms by *Pythium aphanidermatum* in cucumber plants via a changed microbiome. Thereto, a greenhouse experiment was performed where green compost or SMS were added during the seedling phase. *Phytium aphanidermatum* was added before the seedlings were placed on stonewool mats. Disease symptoms were measured during cultivation and mats were sampled for long-read nanopore sequencing of bacterial (16S), fungal (ITS) communities. Both SMS and green compost decreased disease symptoms in comparison to the positive control without compost added and the addition of spent mushroom substrate decreased the disease symptoms most. Our results further show that differences in microbiome composition may explain these results. However, when repeating the experiment in a different year with a different batch of compost a slightly different result was observed, namely that green compost and not SMS suppressed Pythium best. Our results indicate that the addition of circular waste streams, such as compost can improve diseases suppression in soilless systems, but that more research is needed on how to steer for disease suppressive composts.

S5-SF04 Exploiting crop microbiomes as a source of biocontrol and biostimulant microorganisms for sustainable agriculture in the Mediterranean

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The consequences of climate change, like increasingly warm and humid climatic conditions, are expanding the geographical range and host spectrum of phytopathogens, facilitating their spread in new agricultural ecosystems. This trend is further aggravated by the abiotic stress, which compromises the ability of crops to cope with emerging infections. In this context, it is essential to develop resilient agricultural strategies that mitigate the impact of climate change on crop health. ITENE, as part of TRIBIOME and ESCUDO projects, has isolated more than 200 microorganisms directly from the microbiome of strategic Mediterranean crops in Spain, with the most promising produced in second-generation media from agricultural by-products. *Pantoea* sp. and *Pseudomonas* sp., isolated from rice crops, exhibited strong biostimulant properties and effective biocontrol against *Gaeumannomyces graminis* (take-all disease). Moreover, both strains achieved high viable cell counts (>10^8 CFU/ml) from pretreated rice husk. *Bacillus* sp., isolated from vineyard rhizosphere and cultured in grape pomace (>10^8 CFU/ml), is a promising candidate for biocontrol of *Guignardia bidwellii* (black rot disease) and *Diaporthe ampelina* (excoriosis disease). Another *Pseudomonas* strain, isolated from wheat rhizosphere and cultured in wheat straw hydrolylsate (>10^8 CFU/ml) also demonstrated biostimulant properties through nutrient mobilization, siderophore production, ACC deaminase activity, and phytohormone synthesis. Additionally, it exhibited tolerance to abiotic stresses, including acidic and alkaline pH, high salinity, and the presence of heavy metals. This work demonstrates the potential of leveraging native microbiome solutions and agricultural by-products to develop sustainable biocontrol and biostimulant agents. The circular approach not only promotes environmental sustainability but also enhances the resilience and productivity of key Mediterranean crops, representing a promising strategy for future agricultural practices in the region.

S5-PL03 Microbiome interconnectedness and employing microbiomes for a sustainable and healthy soya-based food system

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Microbiomes have highly important roles for ecosystem functioning and carry out key functions that support planetary health, including nutrient cycling, climate regulation, and water filtration. Microbiomes are also intimately associated with complex multicellular organisms such as humans, other animals, plants, and insects and perform crucial roles for the health of their hosts. Microbiomes are connected within and transferred between different habitats and may have positive or negative effects on planetary and human health. Also, microbiomes play an important role in sustainable and healthy food systems. They are key to sustainable primary production and may be used in food/feed production and thereby may support human and animal gut health. In this talk, we will report on the EU-funded project MICROBIOMES4SOY, which explores the role of microbiomes in a soya-based food system serving as a model system to exemplify the contribution of microbiomes to healthy and sustainable diets.

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S5-ST03 Facilitators and barriers to farmers' acceptance of microbiome technology and other similar technologies for sustainable crop production: A review.

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With reference to the increasing global food demand and the prevalence of environmental issues like climate change, sustainable agriculture has been placed at the center of attention for resilient food systems. However, to achieve the sustainable production of yields in the available arable land, novel sustainable technologies – such as microbiome technology – would have to be embedded in agricultural production systems, a prerequisite for which is farmers' willingness to accept and adopt the innovations. In this regard, we conducted a scoping review to explore and unravel the factors that appear to influence crop farmers' acceptance of microbiome technology, drawing also upon evidence on similar sustainable technologies. A scoping review is generally conducted to map the available findings in a scientific field, identify the most central concepts, and point out knowledge gaps. Nonetheless, due to the novelty of innovations that harness the benefits of soil microbes, literature on microbiome technology is still pretty scarce. Thus, we focused on similar technologies as well (conservation agriculture, organic farming, manure treatment, precision agriculture, and others that emerged), insights on which can inform and guide future research on microbiome technology.

Based on evidence from 51 articles on farmers from Europe, USA, and China, we categorized the influential factors according to the approach of Agricultural Innovation Systems in (i) economic (cost & profitability, farm size & resources, market access), (ii) institutional and policy (subsidies & government support, policy effectiveness, institutional & targeted support), (iii) agronomic and infrastructural (land & farm characteristics, environmental challenges, infrastructure & digital connectivity), (iv) technological (perceived usefulness, perceived complexity, compatibility & trialability), (v) social and cultural (social norms & farming culture, peer influence & social learning), (vi) individual and behavioural (individual demographics, attitudes values & environmental awareness, risk cognition & openness to innovation, self-efficacy & technological literacy). A comprehensive overview was provided regarding (a) the documented effects of the eighteen different factors on farmers' behaviour, (b) similarities and differences between regions, (c) methodologies used, and (d) remarks on the quality of the studies. Finally, knowledge gaps were reported and areas for future research were discussed.

S5-SF05

Modulation of gut microbiota by oligosaccharide fractions derived from brewer's spent grain in a dynamic colonic fermentation model

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Cereal processing residues mainly consist of cellulose (40%), hemicellulose (HC) (30%), and lignin (20%), polysaccharides with bioactive properties which make the valorization of these residues attractive. One possible use is as a source of prebiotic ingredients. This study investigates alternatives for valorizing HC-rich waste, such as Brewer's Spent Grain (BSG), using mild physicochemical processes (e.g., alkaline or hydrothermal) that favor subsequent enzymatic hydrolysis (e.g., endo-xylanase, Ultraflo or Rohalase®) and controlled fermentation with lactic acid bacteria (LAB) isolated from BSG to produce fractions rich in prebiotic polysaccharides.

The aim of this study was to evaluate *in vitro* the microbiota-modulating capacity of a selection of extracts obtained from BSG. To this end, a dynamic model of the human intestinal microbiota (doi.org/10.1016/j.lwt.2021.110921) was employed to assess the long-term adaptation of the microbiota to the tested ingredients. The taxonomic variation over time was studied by sequencing the full 16S rRNA gene. Additionally, SCFA and ammonium production in response to two test ingredients were examined: an enzymatically modified BSG substrate (BSG-Enz) and a BSG substrate fermented with a consortium of LAB (*Lactobacillus kimchii*, *Lactococcus lactis*, *Lactiplantibacillus pentosus* and *Pediococcus pentosaceus*) (BSG-Ferm), as compared to a control substrate (galactomannan).

The dynamic model was inoculated with a fecal inoculum and, after stabilization, the tested ingredient was fed in the system three times a day for one week. Specifically, the ingredients tested were: control (week 1), BSG-Enz (week 2), and BSG-Ferm (week 3). Finally, it was returned to the control substrate (week 4).

Analysis of SCFAs revealed a decrease in propionic acid during administration of the test substrates, which was more pronounced with BSG-Ferm. Conversely, an increase in butyric acid was observed. Similarly, variations in ammonium were observed during the adaptation periods between substrates. These concentrations decreased once the microbiota stabilized with each substrate, which was more pronounced with BSG-Enz. Notably, *Bifidobacterium* and *Akkermansia* increased with both BSG-Enz and BSG-Ferm. These results confirm the ability of the tested ingredients to modulate beneficial groups of the intestinal microbiota and support the possibility of using enzymatic or fermentation processes to obtain prebiotic ingredients from BSG for its valorization.

Session 6: Microbiomes for nutrition and human health

S6-PL01 The domino-like health effect of fermented food-based diet: What strategies for untangling the complexity?

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Food is a key modulator of the Human gut microbiome and therefore diet-based strategies represent high-value solutions to consumer health-related problems. In this context, the role of fermented foods in human health has become recently an important focus of research. The intuitive notion that fermented food consumption has an impact on health has been developed through a variety of studies using different analytical strategies. A holistic integration of these studies reveals that this effect is probably like a domino game, involving interconnected mechanisms that act simultaneously on each other (diversity of living food microorganisms, diversity of food metabolites and nutrients, direct or indirect molecular effects on the gut microbiota or on the host cells, regularity of consumption etc.). However, there are so many factors that can cause variability in the effects of fermented foods, including the fact that defining a “healthy” Human gut microbiota remains a challenge, due to its high heterogeneity within healthy populations, it is crucial to consider how future research in this area could expand the available data on the health effects associated with the consumption of these foods.

The aim of my presentation will be to present the latest research findings on this challenge, both as an introduction to the various presentations that will be given during this session of the conference, but also to initiate discussion on the needs for future research. In particular, I will discuss the need to establish causal links between these dietary changes, microbiota modulation and the clinical benefits observed, which requires integrated approaches combining multi-omic analyses, observational studies, clinical trials, metabolic modelling and experimental systems that reproduce human gastrointestinal conditions. The collection of this type of data may require innovative technologies, particularly AI, to facilitate collection and improve the quality of the data collected.

S6-ST01 Microbiota changes and growth impacts associated with oral iron supplementation in neonates

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Iron deficiency (ID) is the primary cause of childhood micronutrient malnutrition worldwide and can lead to anaemia, impaired metabolic function, and stunted growth. Oral iron supplements are commonly used to prevent or treat ID and iron deficiency anaemia (IDA). Neonatal piglets are valuable models for ID in human infants since they rapidly develop the condition if they do not receive exogenous iron. This, along with their shared physiological characteristics with humans, results in piglets being useful models for exploring the underlying mechanisms in response to different iron treatments. Both IDA and oral iron availability can skew the gut microbiota, which may contribute to physiological changes in young infants.

This study explored the impact of IDA and different iron treatments on gut microbial composition and diversity using a neonatal piglet model for human infants. Twenty-four piglets were litter-matched into 4 sex-balanced treatment groups at 1-day old: 1. Control (no iron treatment); 2. Intramuscular iron (IM, 200mgs) injection; 3. Iron-supplemented sow milk replacer (oral-iron, 150 mg/kg feed); 4. IM & oral iron for 4 weeks. We examined the effect of iron treatments on growth, metabolism and the gut microbiota using 16S rRNA gene sequencing. During analysis, comparisons between oral iron (n=12) and intramuscular iron injection (n=6) were also enabled by combining treatment groups. The results showed that all types of iron treatments prevented anaemia by sustaining sufficient concentrations of Hb and other iron-dependent blood parameters, and by maintaining host-derived metabolite concentrations. However, oral iron supplementation was associated with significant reductions in weight gain (~ 0.5Kg, $p<0.05$) and abundances of Lachnospiraceae ($p<0.05$) in piglets compared to their IM iron treated siblings, and significant reductions in lactobacilli ($p<0.05$) were observed in all iron treated siblings compared to IDA siblings. Our results highlight that shift in gut microbiota due to IDA and Iron supplementation has significant impacts on piglet growth. This could have important consequences for oral iron supplementation recommendations, especially in small-for-age infants in LMICs and is especially relevant for iron-replete infant who consume iron-rich formula milk.

S6-ST02 Multiscale associations between diet and the gut microbiome in a nationwide French cohort

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Understanding the intricate relationship between the human diet and the gut microbiome is crucial for developing strategies toward a healthy and sustainable diet. In the French Gut project, we implemented a multiscale framework to link dietary intake to gut microbiome structure and function. Leveraging a standardized processing pipeline, we utilized a semi-quantitative Food Frequency Questionnaire and applied machine learning with data-driven methods to extract dietary patterns, including PHATE-based clustering. This last method allowed us to distinguish “dietary branches” and more precisely identify eater types that reflect clear variations in dietary habits among the French Gut participants, driven by fiber sources or mainland regions. Metagenomic analyses pinpointed specific gut microbiome signatures of eater types at different analytical levels (species, functions, and strain), exemplified by the diet-linked distribution of *Agathobacter rectalis* strains. As a complementary and objective approach to dietary profiling, we employed a food exposome pipeline to assess dietary exposure by analyzing food-derived residual DNA in stool samples. Together, these findings provide a comprehensive, multiscale blueprint for characterizing diet–microbiome interactions at the population level, highlighting the value of combining a priori and data-driven dietary assessment methods. Our result will pave the way for healthy and sustainable precision nutrition strategies grounded on real-world dietary habits.

S6-ST03 Harnessing *Bifidobacterium* spp. for phytate degradation: activity, regulation, and potential to support early-life nutrition.

Elisa Di Stefano[1], Elisabeth O'Flaherty[1], Kieran James[1], Francesca Bottacini[2], Ciaran Lee[3], Maria Esteban Torres[1], Gerald Mercier[4], Audrey Boniface-Giraud[4], Muriel Derrien[5], Raphaelle Bourdet-Sicard[4], John MacSharry[6], Paul D. Cotter[7], Fionnaula McAuliffe[8], Ken Nally[3], Douwe van Sinderen[1]

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Phytic acid (as phytate) is the main phosphorus storage compound in plant seeds, strongly binding minerals such as iron and zinc, reducing their bioavailability and contributing to micronutrient deficiencies in populations consuming plant-based diets. This is particularly critical in low- and middle-income countries, where cereal- and legume-based porridges dominate infant diets. While phytases are well characterised in microbes like *Aspergillus niger* and *Escherichia coli*, a few bifidobacteria have been studied to identify this functionality. Given their role as early gut colonisers, bifidobacteria may be harnessed as probiotics for *in situ* phytate degradation.

In this study, 120 human-derived *bifidobacterial* strains (*B. longum*, *B. catenulatum*, *B. pseudocatenulatum*, *B. breve*, *B. adolescentis*, *B. bifidum*, *B. dentium*) were screened for phytase activity, revealing a species-specific distribution of this activity. Phytase-encoding genes were identified in *B. longum* subsp. *longum* and *infantis*, and *B. catenulatum*. Functional characterisation of the purified phytase from *B. longum* subsp. *longum* (PhyBL) revealed its ability to completely degrade sodium phytate, with a dephosphorylation limit at $InsP_2$. An insertional mutation was introduced in the genome of *B. longum* subsp. *longum* NCIMB8809 to disrupt *phyBL*, which led to > 90 % loss of phytase activity, indicating that this is the primary phytase produced by this strain. Top-performing strains and an engineered *B. breve* UCC2003 constitutively expressing *phyBL* were used to ferment Ghanaian weaning porridge Tom Brown. Over 40% phytic acid was degraded by *B. breve* UCC2003:*phyBL*, while wild-type phytase-producing bifidobacteria achieved degradation of ~10%. Phosphate starvation was identified as a key regulatory factor controlling *phyBL* transcription in *B. longum* and may account for the low level of phytate degradation by the wild-type strains in porridge. Iron absorption and ferritin formation were assessed in a Caco-2/HT29-MTX transwell system from i) fermented and *in vitro* digested (INFOGEST) porridges, or ii) *in vitro* digested porridge incubated in the apical chamber with the phytase active bifidobacteria.

These findings deepen our understanding of phytase distribution and activity in the *Bifidobacterium* genus, laying the groundwork for tailored solutions to enhance micronutrient absorption from phytate-rich foods.

S6-SF01 Development of a plant-based psychobiotic yogurt-like for the gut brain axis

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Plant based fermented foods may improve gastrointestinal health and provide other health benefits, including the release of molecules with the potential to modulate pathways of the microbiota–gut–brain-axis. Several lactic acid bacteria (LAB) can synthesize a wide range of metabolites such as neurotransmitters and are considered as Psychobiotics bacteria (PB). This study was focused on the development of a plant-based, yogurt-like (containing rice, chickpea and pea flour) fermented with selected PB and tested for their ability to colonize the human gut in a invitro gastrointestinal model.

A total of 71 LAB was isolated from Italian typical fermented foods. A whole genome sequencing was performed to identify isolates with potential psychobiotic genes. A total of 18 potential psychobiotic strains were tested *in vitro* for their ability to survive the gastrointestinal tract (GIT) and screened for antibiotic resistance/sensibility. The ability of the strains to produce GABA, catecholamine, epinephrine, norepinephrine, dopamine, acetylcholine and serotonin production was then evaluated. *Lentilactobacillus diolivorans* (B92), *Levilactobacillus brevis* (TO10) and *Limosilactobacillus fermentum* (TO24) were selected and used to produce a plant-based, yogurt-like (YL). The impact of a long-term administration of YL on gut microbiome was evaluated using the Simulator of the Human Intestinal Microbial Ecosystem (SHIME®). Fecal inoculum was prepared from one patient with depressive disorder. The metataxonomic analysis showed the persistence of *L. brevis* and *L. fermentum* during the washout period in lumen and mucin samples. Beta diversity PCoA didn't show a strong separation, suggesting that the treatment didn't drastically change the microbiota composition. Detection of genes and neurotransmitters either short-chain fatty acids will be evaluated.

S6-SF02 Effects of probiotic supplementation on symptoms and microbiome characteristics in patients with non-celiac gluten/wheat sensitivity

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Non-celiac gluten/wheat sensitivity (NCGWS) remains a controversial condition lacking a clear pathophysiological mechanism and specific biomarkers. This randomized, double-blind, placebo-controlled trial aimed to explore the effects of probiotic supplementation to allow the reintroduction of gluten/wheat in NCGWS individuals.

Thirty NCGWS participants were randomized to receive either a probiotic formulation (*n*=15) (*Lactiplantibacillus plantarum*, *Lacticaseibacillus paracasei*, *Ligilactobacillus salivarius*) or a placebo (*n*=15) for six-weeks. The intervention included a four-week gluten-free, low-FODMAPs diet (T1), followed by a two-week gluten reintroduction (T2). At baseline (T0), T1, and T2, participants completed a modified Gastrointestinal Symptom Rating Scale (GSRS) questionnaire and provided fecal samples. Gut microbiome was analyzed using shotgun sequencing, and volatilomic profiling was performed via comprehensive two-dimensional gas chromatography (GC×GC).

In the probiotic-treated group, 47% of participants exhibited improved tolerance to gluten reintroduction, whereas no improvement was observed in the placebo arm (p=0.003). At T2, probiotic-treated participants showed a shift in gut microbiome composition, with significantly higher relative abundance of beneficial bacteria (such as *Lactiplantibacillus plantarum*, *Bifidobacterium adolescentis* and *Coprococcus catus*) and lower species correlated to gut inflammation (such as *Bacteroides vulgatus*, and *B. dorei*). Changes in metagenomic functions related to bacteriocin transport and biosynthesis, carbohydrates metabolism, and protein degradation occurred in probiotic-treated individuals. Gluten-tolerant individuals exhibited higher abundance of genes involved in gliadin hydrolysis and increased propanoic acid levels.

Probiotics treatment may improve gluten tolerance in individuals with NCGWS. The beneficial effect could be related to the increased abundance of microbial genes involved in gluten digestion.

S6-PL02 Leveraging food fermentations for health

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Food fermentation is undertaken for a variety of purposes; however, its positive implications for human health have received increasing attention. Fermentative processes can contribute to nutritional enhancement through the biosynthesis of essential micronutrients, such as vitamin B12, and through the degradation of antinutritional factors. Moreover, the consumption of foods containing viable, non-pathogenic microorganisms (beyond probiotics) has been associated with improved health status in several recent studies. Microbially derived metabolites, including lactic acid and short-chain fatty acids, are now increasingly recognised as mediators of host physiological responses, exerting effects on gastrointestinal, neurological, and systemic functions.

In the context of grain-based fermentations, additional mechanisms may underlie the health-promoting potential of these foods. Grains are characterised by high levels of starch, dietary fibre, and storage proteins that are structurally and functionally distinct from animal-derived proteins. They are also rich in components like phytate and fermentable oligosaccharides like fructan. Fermentation has the capacity to modulate the structure of these consitutents at a molecular level and to influence their digestion, absorption and fermentation in the gastrointestinal tract. These modifications may further potentiate the beneficial effects of fermented cereal-based products on human health.

This presentation will dive deeper into these topics, examine the molecular mechanisms driving transformations in (grain-based) food fermentations and provide illustrative examples of how fermentation technology can be leveraged for human health.

S6-ST04 Unveiling microbial lipid signatures: The metabolism of linoleic acid by clostridia and gammaproteobacteria

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During digestion, approximately 5-10% of dietary lipids reach the large intestine, where they interact with gut microbes. However, the interaction between lipids and the gut microbiota has remained largely unexplored. To address this gap, we investigated the interaction between linoleic acid (LA), a prevalent dietary polyunsaturated fatty acid (PUFA), and the human gut microbiota, focusing on how LA influences microbial composition and metabolism. We hypothesized that LA selects for several microbial species that cooperate to produce fatty acid units, which are then used to synthesize complex microbial lipids.

To test our hypothesis, we combined untargeted lipidomics, metagenomics, and isotopically labeled linoleic acid to study the microbial lipids resulting from interactions between gut microbiota and LA. First, we used static bioreactors and human feces to identify the gut microbes responsible for producing microbial lipids and their associated metabolic pathways and microbial lipids. Secondly, we employed a simulator of the human intestinal microbial ecosystem (SHIME) to validate our findings.

Our findings reveal that LA modulates microbial composition and metabolic activity. By integrating isotope-tracking lipidomics and metagenomics, we identified that specific gut microbes actively metabolize LA, incorporating it into complex lipids and producing bioactive PUFAs, such as eicosapentaenoic acid. The administration of LA shifted the gut microbiota composition, with species within the Gammaproteobacteria class, such as Klebsiella, becoming more prevalent. This shift occurred as LA activated its fatty acid metabolic pathways, generating a diverse array of microbial lipids, primarily fatty acids, phospholipids, and sphingolipids. Long-term *in vitro* feeding using SHIME corroborated these observations, demonstrating that bioactive long-chain PUFAs, such as linolenic acid, eicosapentaenoic acid, and docosahexaenoic acid, were synthesized shortly after LA exposure. Species within the Gammaproteobacteria class were identified as key contributors to the biosynthesis of these bioactive lipids. Given their potential impact on health and disease at the intestinal and systemic levels, we envision microbial lipids being targeted as markers of gut health.

S6-ST05 Spatiotemporal profiling of the human small intestinal microbiome

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Background: The human intestinal microbiota is a complex and diverse microbial community which plays a key role in maintaining homeostasis. There is biogeographical diversity in the human gut microbiome, with distinct microbial communities found in the duodenum, ileum and colon. While colonic microbiome has been extensively studied due to the relative ease of sampling stool, the composition and temporal dynamics of the small intestinal microbiome remains less clear due to the inherent challenges in accessing the small intestine. We applied naso-ileal intubation techniques to obtain longitudinal timeseries of ileal and duodenal luminal contents, providing a unique window into the dynamics of this important microbial community during meal ingestion.

Methods: 10 healthy participants were recruited. Enteral feeding tubes were inserted into the duodenum and ileum, enabling the collection of intestinal content samples for up to 3 hours postprandially from the duodenum, and for up to 8 hours from the ileum. Metagenomic sequences were assembled into Metagenome Assembled Genome's, to estimate species level abundances and annotate gene functions as well as carrying out strain level analysis.

Results: We reveal the microbiome of the small intestine to be highly dynamic during ingestion of a meal. In the fasted state, the duodenal microbiome is dominated by the facultative anaerobes *Streptococcus* and *Neisseria*. The ileal microbiome is more diverse, and while dominated by *Haemophilus* and *Streptococcus* also includes abundant obligate anaerobes from the genera *Faecalibacterium*, *Bacteroides* and *Blautia*. During consumption of a meal, large shifts in microbiome composition were observed, with an increase in overall microbial diversity and a marked increase in oral bacteria from the genera *Rothia*, *Pauljensia* and *Streptococcus*. This also includes potentially potentially pathobionts such as *Fusobacterium nucleatum*. Furthermore, we identify correlations between the small intestinal microbial community and metabolite profiles and gut hormone (GLP-1 and GIP) responses.

Conclusions: The findings of this study reveal the small intestinal microbiome to be more dynamic during food ingestion than previously appreciated. We identify a route for oral bacteria, to passage from the oral cavity to the ileum via the food bolus. Finally, we identify that the small intestinal microbiome may play a role in modulating the metabolic environment of the small intestine and gut hormone responses.

S6-SF03 Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals

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The gut microbiome is shaped by diet, however various studies conducted over the years have yielded mixed results, highlighting a need to better characterize diet-specific gut microbes and overcome large interpersonal variability of the gut microbiome with substantial sample sizes. To this end, we investigated the gut metagenomes of 19,817 omnivores, 1,088 vegetarians, and 656 vegans across five different cohorts and three countries (USA, UK, and Italy). We found the gut microbiome to accurately predict self-reported diet patterns (mean AUC = 0.85). Signature microbes for omnivorous diets, such as *Ruminococcus torques*, *Bilophila wadsworthia*, and *Alistipes putredinis*, were significantly correlated with meat (red > white) consumption, as determined by detailed food frequency questionnaires (FFQs), and scored worse on a cardiometabolic health scale. Vegan gut signatures correlated with overall fruit and vegetable consumption and scored highest on a cardiometabolic health scale, while vegetarian microbes were significantly linked to dairy consumption, with intermediate cardiometabolic health scores. Diets that include dairy products were enriched in microbes sequenced directly from dairy foods, in particular *Streptococcus thermophilus*, pointing towards the possibility of food-to-gut microbial transfer. Several microbial signatures in vegans overlapped with soil and plant-growth-promoting microbes, suggesting that agricultural practices could also contribute towards the microbes transferred to our gut via food. Ongoing functional profiling reveals diet-pattern differences, with an enrichment of amino acid metabolism in omnivores and functions characteristic of plant niches in vegans. Our work confirms and expands upon previous findings to show that the inclusion or exclusion of major food groups can shape our gut microbiome, even indirectly through possible microbial acquisition from foods or unlikely processes in the food chain, which may have downstream effects on our cardiometabolic health. We also go beyond the impact of diet on human microbiomes to incorporate data on plastic-degrading microbial genes detected across human-associated microbiomes to show how elevated exposure to plastics is reflected in the potential for human microbiomes to degrade common, commercially available plastics. This work advances our understanding of the various factors shaping the gut microbiome in the Anthropocene, from westernized diets to plastic use and misuse.

S6-SF04 Live bacteria in fresh foods contribute to human gut microbiome diversity

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Human gut microbiome diversity is integral to health; yet the mechanisms that shape and sustain this intricate ecosystem remain poorly understood. Dietary patterns can modify the gut microbiome through variations in nutrient or bioactive provision and utilisation with sequence-based studies suggesting foods carry bacteria in addition to pathogens. Bacterial transmission from food to the human gut microbiome requires ingestion of viable cells capable of withstanding food processing, storage and transit through the gastrointestinal tract. This work shows show that a diet of fresh produce and cooked meals harbor up to 10^7 live bacteria, predominantly Bacillota, Pseudomonadota and Actinomycetota, capable of surviving food processing and transiting to the human gut. In contrast, processed and ultra-processed foods are largely sterile, limiting dietary microbial exposure. Comparing a standard diet containing high microbial load to an identical diet with reduced microbial load in a double-blinded, randomised, controlled, crossover feeding study demonstrated transmission of live bacteria from food to gut and substantial diet-associated shifts in foodborne species and overall microbiome composition. This demonstrates that diets high in fresh foods can provide a source of health associated microbes, with the detrimental impacts of highly processed foods including reduced exposure to foodborne beneficial microbes.

Session 7: Microbiomes for mitigation of risks in the food system

S7-PL01 RESLIENCE thinking in management Salmonella spp in the pork supply chain

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Salmonella spp. control in pork supply chains has always been a challenging issue and insufficient control can lead to high social and economic consequences. Conventional risk management and risk management approaches and models are not sufficient to address potential food safety shocks caused by Salmonella spp., as they mainly focus on assessing measures to prevent or reduce Salmonella spp. contamination instead of developing the resilience capability (e.g., flexibility to adapt to sudden changes in the risks). A resilient supply chain that has the capacity to adapt and manage possible contaminations is more suitable and practical than trying to achieve a state of zero food safety risks.

In this study, the resilience concept will be applied into quantitative modeling of Salmonella spp. spread in the pork supply chain. The objective of this study was to explore the resilience performance of the pork supply chain under different food safety shocks caused by Salmonella spp., and to investigate the effectiveness of interventions on reducing the impact of these shocks on the resilience performance of the chain. Scenario analysis indicated that the effectiveness of the investigated resilience strategies or interventions depended on the risk profile (i.e., default, minimum, maximum level of Salmonella spp. contamination) of the pork supply chain. For pork supply chains with minimum and default risk profiles, more attention should be paid to increasing resilience of pigs towards Salmonella spp. infection. For supply chains with maximum risk profile, the focus should be on improving the performance of the slaughterhouse, such as careful evisceration, logistic slaughtering. To conclude, enhancing resilience performance of the pork supply chain can contribute to a safe pork supply.

S7-ST01 The ecology of persistence: How community complexity and composition shape *Salmonella*'s survival in the food chain.

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Salmonella is the third most costly foodborne pathogen in the UK, imposing an annual economic burden of £200 M. It persists in the food chain within complex microbial communities. Very little is known about how interspecies interactions influence its ability to survive and adapt under stress, posing a significant threat to food safety.

My research investigates how community context and composition impact *Salmonella* survival in food chain-relevant environments. To achieve this, we simulated food-processing microbiomes of varying ecological complexities using a Synthetic Community (SynCom) approach, coupled with an established biofilm evolution model. These SynComs were exposed to subinhibitory antibiotic concentrations reflecting real-world antimicrobial pressures and repeatedly passaged as biofilms. Through metagenomic analysis, we tracked community dynamics and *Salmonella* population changes over time. Whole-genome sequencing and SNP identification further mapped *Salmonella*'s evolutionary trajectory within these synthetic microbiomes versus single-species biofilms.

Our findings revealed that community composition and complexity significantly influence *Salmonella*'s survival, with higher pathogen recovery rates observed in more diverse microbial communities. However, this came with a trade-off: increased community complexity also heightened *Salmonella*'s susceptibility to subinhibitory antibiotic concentrations compared to single-species biofilms, suggesting a distinct community-mediated effect under antimicrobial exposure.

This research provides valuable insights into how foodborne pathogens survive and adapt within food-chain-relevant communities. It highlights the importance of microbiome structure and diversity in shaping pathogen evolution and antimicrobial resistance. Understanding how antimicrobials influence microbiome-pathogen interactions offers valuable information for designing targeted interventions that leverage beneficial microbial communities to outcompete pathogens, reducing pathogen resilience and enhancing food safety in real-world settings.

S7-SF01 Identifying prognostic microbiome biomarkers to predict post weaning diarrhea (PWD) in piglets and disentangling the effects of confounding factors

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Introduction: Post-weaning diarrhoea (PWD) is one of the major causes of piglet death in pig production. After weaning, PWD in some piglets commonly leads to antibiotic treatment in all co-housed piglets to prevent PWD spreading, even though not all piglets would develop diarrhoea.

Objective: Identify a pre-weaning intestinal microbiota signature to predict antibiotic-treatment requiring PWD disease in piglets.

Method: From a large prospective cohort study including approximately 2500 piglets, rectal swabs were post hoc selected for 72 piglets for six time points (days 1 till 32 after birth) for three phenotypic classes, namely (i) Robust (RO; no PWD) (ii) Resilient (RE; self-resolving PWD) (iii) Antibiotic treated (AT; antibiotic treatment requiring PWD). Time-resolved microbiota composition was determined by rectal-swab 16S rRNA gene profiling (N = 432), and multivariate statistics and machine learning techniques were used to identify pre-weaning microbiota signatures associated with the phenotypic classes.

Results: Initial analysis revealed microbiota signatures that discriminate AT animals from RO and RE animals on day 18 of life (7 days before weaning). Moreover, although overall birth-weights were similar across the different phenotypic classes, AT piglets displayed reduced relative weight in the pre-weaning period. Relative weight was furthermore negatively correlated ($p=0.0052$) with maturity of microbiota for AT piglets at day 18. Importantly, relative weight associated microbiota signatures were detected that in combination with preweaning supplemental feeding could confound the detected signature on day 18, and current analyses aim to disentangle the effects of these covariables.

Significance: Pre-weaning microbiota-based identification of AT-class piglets could translate to a prognostic toolkit that would enable timely implementation of (dietary) interventions to ameliorate PWD risk and lower antibiotic usage in the pig industry.

S7-SF02 Genomic characterization of persistent *Listeria monocytogenes* in European food processing facilities

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Listeria monocytogenes is a major public health concern as the causative agent of listeriosis. It is widely distributed in freshwater, soils and urban environments. Its ability to inhabit diverse ecological niches makes it highly adaptable to environmental stressors. This adaptability becomes problematic when this opportunistic pathogen enters the food processing environment, where it can persist for months or even years at specific hotspots. This poses a serious risk of food product contamination and listeriosis outbreaks.

Persistence - defined as the repeated isolation of genetically similar strains from the same environment over time - is not very well understood. Several factors may contribute, including the presence and absence of stress related genes (e.g., *qacH*, *bcrABC*, *cadA*, *cadC*, *SSI-1*, *SSI-2*, *clpL*), and phenotypic adaptations such as dormancy, biocide tolerance, and biofilm formation. Moreover, interactions with co-occurring bacteria – such the formation of multispecies biofilms – may further support long-term survival. A major challenge in persistence research is lack of a standardized definition. Moreover, studies often differ in sampling strategies, laboratory protocols, and analytical methods, making overall comparability difficult.

In the European Project FoodSafeR, we aim to investigate persistence from a holistic perspective. We conducted coordinated samplings in food production facilities across Greece, Spain, and Austria, over two years using a unified protocol. We collected 1194 swab samples from meat (n=4), fish (n=1) and dairy (n=6) facilities. Overall, 26% of swab samples were positive for *L. monocytogenes* strains. We selected 280 isolates for whole genome sequencing. First, we characterized the diversity of isolated strains, including identification of 64 distinct core genome multilocus sequence types across the facilities, including 21 potential persister types. By analyzing the whole-genome SNP differences and correlating them with our metadata, we selected persister strains and examined gene presence/absence patterns to better understand the genomic basis of persistence. Second, we analyzed the co-occurring microbial community to investigate the overall microbial ecology in the persistence hotspots.

Through this unified, large-scale study, we aim to deepen our understanding of the factors that are enabling persistence, supporting the improvement management strategies in the food industry.

S7-PL02 The microbiome of biofilms in real food systems

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Microbiomes shuttle through food systems in a complex manner. They form either transient, free-living communities or can be organized in biofilms. Yet, less understood is the role of biofilms in food systems. Biofilms, defined as multispecies biological structures embedded in a self-produced extracellular matrix (EPS), hamper the cleaning and sanitation in the food processing environment and can cause hygiene problems if they harbor pathogens or spoilage bacteria. Our studies in diverse food producing environments showed that 9-12% sampling sites harbored biofilms. Biofilms were frequently found on conveyor belts, drains and water hoses. Moreover, we could confirm the presence of *Listeria* in a biofilm in a frozen vegetable producing environment. An intriguing question is how pathogens react with the microbial microbiome in a biofilm. Using a multispecies biofilm model, we showed that *Listeria monocytogenes* was able to colonize and hide within the biofilm. The presence of *L. monocytogenes* did neither change the biofilm community, EPS production nor gene expression. An interesting question is how a microbiome of transient bacteria flows through the food system. Especially in meat processing where no decontamination step is included in the slaughtering and meat trimming process, microbial communities from the raw meat side encompass the majority of the microbiome in the final product. There the physico-chemical and storage parameters define the fate of the microbiome that usually loses diversity and enriches for spoilers that outgrow other bacteria in the final state of raw meat storage.

S7-ST02 A novel risk assessment framework to address antimicrobial resistance in the Australian and Asia-Pacific vegetable supply chain

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Antimicrobial resistance (AMR) is a growing global threat that undermines human, animal, and plant health. In Australia alone, AMR contributes to over a thousand human deaths annually and poses significant risks to agricultural productivity, food safety, biosecurity, and environmental sustainability. Of particular concern is the emergence of resistance in plant pathogens, which affects crop yields and market access. Although antimicrobial and pesticide use is subject to regulatory oversight, the complex links between usage patterns and resistance development in agricultural systems remain insufficiently understood. This knowledge gap increases the risk of overuse or misuse of antimicrobials and other chemical inputs, with potential consequences across the food system. Here, we investigate the risks and impacts of AMR in the vegetable supply chain across Australia and the Asia-Pacific region, focusing on food security, production practices, and safety. We present a novel, fit-for-purpose relative risk assessment framework tailored to the horticulture industry, specifically the raw vegetable sector. This framework considers a wide array of factors across the supply chain, including seed sourcing, water quality, soil and pest management, agricultural inputs, and post-harvest handling. The framework incorporates both pre- and post-harvest conditions and is adaptable to diverse production systems, climate conditions, and regulatory environments. By systematically analysing practices related to import/export, on-farm management, and environmental pressures, the framework identifies critical control points and high-risk practices contributing to AMR selection and spread. Application of this tool has yielded valuable insights into AMR drivers in the fresh produce sector and highlighted areas for improvement in disease control, input management, and hygiene practices. These insights are now being used to inform guidelines and support decision-making by regulatory bodies and industry stakeholders across Australia and the Asia-Pacific vegetable industry. This work contributes a science-based approach for integrating microbiome understanding into AMR risk mitigation strategies in food systems, offering a practical pathway to reduce AMR risks while supporting sustainable and safe vegetable production.

S7-SF03 The effect of climate change on food-borne disease outbreaks in the Netherlands

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Aim: Temperature plays an important role in food-borne pathogen contamination risk and indoor temperatures are expected to increase along with rising outdoor temperatures. However, how indoor climates are affected by outside conditions can vary greatly. This project aims to determine relations between environmental conditions and illness occurrence and to predict how weather conditions may affect microbial growth and thereby food-borne disease outbreaks in the light of climate change.

Method: As a first step, a literature review was done to examine the effect of the predicted change in indoor climates on specific food-borne pathogens on different foods. Subsequently, the registration of food-related outbreaks in the Netherlands provided by the National Institute for Public Health and the Environment and the Netherlands Food and Consumer Product Safety Authority were combined with climate data and geographic and demographic data. Poisson regression was used to examine the effect of climatological variables on outbreak occurrence.

Results: Poisson regression analyses showed that food-borne disease outbreak occurrence was associated with higher temperature (Incidence Rate Ratio (IRR) = 1.014, $p<0.001$) and lower humidity (IRR = 0.994, $p<0.001$). We then examined whether the degree of urbanity affected this relationship and found that in urban areas there was a larger effect of temperature on food-borne illness outbreak than in rural areas (IRR = 0.995, $p<0.001$). In addition to the linear effects of temperature and humidity, we examined the effect of the occurrence of heatwaves on food-borne illness outbreaks. Here, we found that there food-borne illness outbreaks are more frequent during heatwaves (IRR = 1.372, $p<0.001$). The relationship between heatwaves and food-borne illness outbreaks was again stronger in urban than in rural areas, although this was further qualified by humidity (three-way interaction: IRR = 1.019, $p<0.001$).

Conclusion: Temperature, humidity and heatwaves were related to food-borne illness outbreaks in the Netherlands. In urban areas increased temperatures and the occurrence of heatwaves were related to an increase in food-borne illness outbreaks, but this relationship was weaker in rural areas. This indicates that the effect of climate change on food-borne illness outbreaks may be more pronounced in urban areas than in rural areas.

S7-SF04 Assessment of a microbiome engineering strategy using Lactic Acid Bacteria as bioprotective cultures to delay the spoilage of Gilthead Seabream (*Sparus aurata*) fillets

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The Mediterranean gilthead seabream (*Sparus aurata*) is a widely consumed seafood product, with global production reaching 354,920 tonnes in 2022, primarily from aquaculture (FAO, 2024). However, seabream is microbiologically sensitive and highly perishable, which leads to significant food waste. Following slaughter, seabream flesh becomes vulnerable to microbial colonization, leading to the development of a specific endogenous microbiota. Some bacteria play a role in spoilage, degrade the product quality by generating metabolites that alter its sensory characteristics. Biopreservation is a soft preservation technic which seeks to modulate the microbiota of food product to slow down spoilage or pathogen growth. This technic involves inoculating the product with microorganisms or metabolites that exhibit antimicrobial activity (Passerini *et al*., 2021). In the frame work of the European project Foodguard, five protective lactic acid bacteria (LAB) were tested on seabream fillets stored under modified atmosphere packaging at 8°C during 11 days. During these shelf-life experiments, LAB strains effects on the microbial community and seabream quality were assessed on 110 samples using: classical microbiological enumeration techniques, 16S amplicons sequencing approach, biochemistry analysis and sensory evaluations conducted by an expert panel. Results show that three LAB strains significantly reduced the presence of seabream spoilage-associated bacteria such as *Brochothrix*, *Pseudomonas*, and members of the *Enterobacteriaceae* family. Sensory analyses confirmed the beneficial effects of these strains, which helped maintain the fillet quality for up to 8 days of storage. Multi-omics analyses were conducted to correlate microbiota composition and dynamics with biochemical profiles, as well as sensory scores and attributes, thereby revealing biologically relevant and robust molecular signatures.

Session 8: Novel microbiome concepts, applications and technologies

S8-PL01 Deciphering the chemical language of the microbiome using computational omics

Marnix Medema

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Microorganisms produce a wealth of specialized metabolites, which play important roles in microbiome ecology and provide a rich resource for natural product drug discovery. Genome sequence data has revealed that only a tiny fraction of the chemical diversity of these natural products has been unearthed. Here, I will highlight recent work performed in my research group and with the wider community on developing and applying computational and artificial intelligence approaches to chart the chemical diversity of microbial secondary metabolism and elucidate the mechanistic roles of metabolites in microbiomes using omics data. Specifically, I will highlight how such algorithms can be applied in combinations of culture-dependent and culture-independent approaches to identify specific genes responsible for microbiome-associated phenotypes of interest.

S8-ST01 The neglected side of the microbiome: Hotspots in food production and the fungal resistome

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The advances in (meta)genome sequencing and in the subsequent bioinformatic analyses are allowing us to unravel the microbiome function in the food chain with an incredible level of detail. While many investigations focus on the presence of potential pathogens and spoilers in the surfaces associated in food production, we developed a bioinformatic pipeline focused on investigating how the different surfaces contribute to the final product with antimicrobial resistant (AMR) determinants. As expected, most surfaces carried AMR genes that were naturally inoculated to the food product, being particularly critical in those ready to eat. However, we found that the greatest carriers of AMR in the food production environments were non-ESKAPEE species that are usually associated with food and production, and sometimes with beneficial properties, such as *Staphylococcus equorum* or *Acinetobacter johnsonii*.

While many bioinformatic software exist nowadays, there is a bias towards bacterial pathogens of human origin. The complexity of eukaryotic genomes (with the presence of exons-introns, ploidy, etc.) limits the usage of *de novo* prediction tools. Moreover, AMR in fungi is not mostly due to the presence of ARM genes but to mutations in proteins that are the target of the fungicides, what hinders their investigation. With that regard we developed FungAMR, an online resource that contains the greatest repository of AMR in fungi to date, with more than 50,000 entries after manual curation of > 500 scientific papers. Additionally, we developed the open-source software *Chromosome Query Targets* (ChroQueTas), that allows the screening of mutations causing AMR in more than 50 fungal species and 200 target proteins, by using as input either fugal genomes, proteomes or annotation files.

S8-ST02 Extending curatedFoodMetagenomicData(cFMD) for integrated analysis of food microbiomes

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The foods we eat have diverse and complex microbial communities. A deeper understanding of these food microbiomes holds potential ranging from enhancing food quality and safety to pinpointing their impact on human health. Despite this potential, comprehensive and accessible databases of food microbiomes are lacking in the literature. To address this gap, we developed curatedFoodMetagenomicData (cFMD) (https://github.com/SegataLab/cFMD), a metagenomic resource that catalogs microbial diversity across multiple food types.

In its current version (v1.2.1), cFMD comprises 3,310 metagenomically sequenced food samples from 85 datasets of 52 countries. It provides curated metadata, taxonomic and functional microbiome profiles, and metagenome-assembled genomes. The database includes 13,163 prokaryotic and 902 eukaryotic genomes, representing >1.3k microbial species, 287 of which are yet-to-be-isolated microbes discovered from food sources. This resource enables integrated and comparative analyses of food microbiomes across multiple applications. For example, the reconstruction of *Levilactobacillus brevis* from hundreds of samples facilitates exploration of its genomic diversity across food types. Additionally, cFMD supports investigations into microbial transmission from foods to humans, as evidenced by the identification of identical strains (e.g., *Streptococcus thermophilus*) in both food and human microbiomes.

As the largest publicly available resource of food metagenomes, cFMD is an important tool for advancing research in food science, agriculture, nutrition, and microbial ecology. Ongoing refinement of cFMD will continue to unlock the potential of food-associated microbes for developing safer and healthier food systems.

S8-SF01 Robust microbiome profiling with strain resolution using optical mapping

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Strain-level variation within the human microbiome is a major determinant of functional capacity, pathogenic potential, and host interaction. However, resolving such variation remains a significant challenge. Sequencing-based methods, while powerful, require deep coverage, elaborate bioinformatics pipelines, and time-consuming workflows to achieve strain-level accuracy—making them costly and impractical for large-scale or time-sensitive applications.

We present DynaMAP, a rapid, sequencing-independent microbiome profiling platform based on high-density optical DNA mapping. By directly imaging fluorophore-labeled high-molecular-weight DNA extracted from human stool and other complex samples, DynaMAP generates long, single-molecule optical maps that preserve structural features specific to individual strains. These maps are matched against a curated reference database of nearly 20,000 microbial genomes, enabling strain-level identification up to 99.8% average nucleotide identity (ANI) resolution.

We benchmark DynaMAP on mock communities, standardized microbial panels, and real human fecal samples, and show that it achieves taxonomic profiles highly concordant with shotgun metagenomics, but with reduced complexity, same-day turnaround time, and cost comparable to 16S amplicon sequencing. Crucially, DynaMAP avoids the need for genome assembly or computationally intensive strain-calling algorithms, enabling accessible and scalable microbiome analysis.

Our results demonstrate that DynaMAP enables same-day, strain-resolved profiling of gut microbiota, with potential applications in clinical diagnostics, antimicrobial resistance surveillance, and routine microbiome monitoring in research and healthcare settings.

S8-SF02 Phenotypic characterisation using BIOLOG: Microbial strains from cocoa and their novel application

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Yeasts associated with cocoa fermentation are critical for inducing biochemical changes, producing metabolites which are crucial flavour and aroma precursors for chocolate production. However, cocoa fermentation is highly variable, largely spontaneous and uncontrolled. In recent decades, research has focused on understanding this process more deeply—identifying the roles of specific microbes and linking their activity to the characteristics of the final product.

Beyond traditional cocoa, fermentation also offers promise in adapting novel, climate-resilient crop varieties to produce food products with comparable organoleptic qualities. As climate change increasingly threatens cocoa production in tropical regions, fermentation technologies can help preserve flavour profiles by tailoring processes to new ingredients. However, effective implementation of such novel product development requires careful strain selection— especially, strains that are not only metabolically active but also well-suited to the chemical composition of the raw material. Yeast strains behave variably based on the substrate composition, both in terms of growth and metabolite production. This strain-substrate specificity is critical for optimizing fermentation outcomes.

To this end, yeast strains isolated from cocoa plantations in West Africa were evaluated in this study for their ability to metabolise over ninety different carbon sources using OmniLog® FF technology to investigate the link between key fermentation characteristics and metabolite quality of the selected strains. The FF Microplate™ gives the phenotypic characterisation of the strains, which accurately represents their catabolic potential. The substrate-utilising ability of the strains was indicative of the uptake reactions for the carbon sources that enabled the growth of the strains.

By mapping strain-substrate synergies, this research contributes to the development of a rational strain selection framework. The results from the OmniLog® analysis served as a tool to guide the formulation of starter cultures tailored to specific, novel substrates as well as media optimisation. This supported the development of new products using the native cocoa microbiota, customising desired fermentation outcomes and supporting a more controlled, efficient, and high-quality end product.

S8-SF03 Conservation, evolution and recombination of tailocins in the genus *Pectobacterium*; and consequences for species and strain level interactions

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The *Pectobacterium* genus comprises globally prevalent phytopathogens, whose species are known to co-inhabit both symptomatic and asymptomatic plants. Extracellularly secreted phage tail-like bacteriocins, commonly known as tailocins, play an important role in shaping such bacterial communities. We applied a comparative pangenomics approach on 454 genomes to study the diversity and evolution of carotovoricin, a tailocin in the *Pectobacterium* genus. Firstly, the carotovoricin biosynthesis gene cluster is functionally retained and found in 94% of the strains. We detected both conserved and extremely variable regions within the carotovoricin gene cluster. In particular, the region encoding the tail fiber proteins, known to be important for the host range specificity, is extremely variable. We identified the local recombinational exchange of these tail fiber loci across the *Pectobacterium* genus. This process complements the existing DNA sequence inversion mechanism in the *Pectobacterium* species pathogens to achieve a polymorphic carotovoricin collection. We show that a pangenome approach can comprehensively capture polymorphisms in tailocins and help to understand the development of bacterial communities. Our approach can potentially aid the development of strain-specific antibiotics.

S8-PL02 New developments in studying food-microbiome-gut interactions

Paul Cotter

Teagasc, Ireland

There are many ways in which foods, including foods that contain live dietary microbes, can impact the gut microbiome. A variety of in vitro, ex vivo and in vivo approaches are available to study these impacts. Advances in the associated platforms, sample and data collection devices (including wearables) and multi-omics analyses are facilitating new insights into the study of food-microbiome-gut interactions. A number of advances and how they can and have been applied will be described during the course of this presentation.

S8-ST03 Evolution on autopilot: Engineering functional stability in synthetic microbial communities

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Synthetic microbial communities (SynComs), composed of intentionally assembled groups of microorganisms, offer exciting opportunities for controlled functional outputs in medicine, agriculture and industrial bioprocesses. However, environmental perturbations such as nutrient shifts, temperature fluctuations, pH changes, and microbial invasions threaten their consistent performance. Achieving long-term **compositional control and functional resilience** under such conditions remains a major challenge. Rational design of SynComs for stable functional outputs in bioprocesses in the face of biotic and abiotic perturbations requires moving beyond community profiling. There is an urgent need to move towards uncovering the mechanistic principles that govern long-term functional resilience. Crucially, there is a growing need for automated tools that can facilitate this discovery process.

To address this gap, we are developing a **fully automated**, **long-term evolution platform** that allows simultaneous real-time monitoring and environmental control. Our miniature bioreactor (pioreactor) currently allows precise control optical density, and stirring. We will extend the system with pH and fluorescence sensing. These upgrades enable continuous tracking of community composition and pH sensing without the need for frequent sampling. By automating long-term time-series experiments and coupling them with real-time modelling, we can systematically explore how different perturbation regimes drive compositional shifts and select for resilient traits. We use a minimal SynCom composed of *Saccharomyces cerevisiae* and *Lactobacillus plantarum* to investigate how communities respond to abiotic and biotic stress delivered in **pulse, press, and ramp** formats in our pioreactors. Preliminary trails with monocultures confirm that our system can effectively induce environmental shifts in temperature and nutrient availability.

This platform allows us to apply perturbations to shape community evolutionary trajectories and select for genetic features underlying functional resilience. Our low-cost, small-scale pioreactors enable dynamic measurement and precise environmental control. Overall, our approach paves the way for **predictive microbial engineering** and scalable, robust bioprocessing in the face of fluctuating environmental conditions.

S8-SF04 Leveraging advanced AI for enhanced food safety through pathogen analysis

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AlphaGenome, a powerful AI model from Google DeepMind, was developed to analyze and decipher the complexities of the human genome. Its advanced capabilities for the analysis of high-resolution DNA sequences and the prediction of genetic variant effects can offer significant promise for improving food safety by better understanding food pathogens, which is crucial to food safety.

AlphaGenome could transform how we identify and characterize microbial risks across the food chain. Its ability to analyze long DNA sequences and predict genetic changes at a detailed level could enable rapid pathogen detection, predictive risk assessment, and enhance genomic surveillance.

Applying AlphaGenome to food pathogens presents unique and interesting challenges. Unlike human genomes, food pathogen DNA is highly dynamic, characterized by frequent **horizontal gene transfer** and the critical role of **accessory genes** in traits like virulence and resistance. Furthermore, real-world data often involves **polyclonal outbreaks** (multiple strains in one sample) and inherent **biases** in existing microbial genomic datasets.

Using public benchmarking microbiome genomic datasets, our focus will be on assessing the impact of **uncharacterized mutations in known antimicrobial resistance genes** and **mutations in genes encoding antimicrobial targets,** from predicted gene expression patterns by the AlphaGenome model. This interdisciplinary effort aims to explore AlphaGenome's potential for a safer, healthier global food supply, fostering a new era of data-driven microbial food safety.

S8-SF05 Optimizing long-term storage and propagation strategies for the preservation and reuse of fermented sausage microbiome

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The preservation of complex microbial communities is essential for their future reuse in both research and food production. However, maintaining the structural and functional integrity of entire microbiomes over long-term storage remains a major challenge. This study aims to identify the most effective long-term storage conditions to preserve the viability and diversity of microbiomes associated with fermented sausages. An Italian fermented sausage, produced without the addition of starter cultures, was selected from a previous ecological study due to its high consumer appreciation and favourable organoleptic properties.

Three preservation methods were tested: a portion of fermented sausage directly stored under pure glycerol, a ten-folder dilution plus 30% v/v of glycerol, and the microbial cell pellet stored under 30% v/v glycerol. Samples were stored at -80 °C and analysed every three months for one year. Microbial load was assessed using culture-dependent methods, and microbiota changes were evaluated via amplicon-based sequencing. The best preservation method was determined by comparing microbial profiles at time zero and after 12 months. At each time point, microbiome was cultured in three broths (BHI, meat extract, and nutrient broth) with 24- and 48-hour incubations to evaluate the best propagation approach.

The results showed that fermented sausage portion covered with pure glycerol was the most effective strategy with minimal impact on microbial loads and diversity, while meat extract and BHI broths with 24-hour incubation were the most effective enrichment strategies for propagation purpose. These most promising preservation-enrichment combinations were then applied in a pilot-scale fermented sausage production to validate the selected strategy and assess its effectiveness in producing high-quality final products.

Samples from the pilot production were collected at day 0, and after 7 and 15 days of fermentation. A whole genome sequencing approach was applied to highlight species and gene-level differences in the microbial communities.

Closing Keynote Lecture

CL-KN01 The many faces of nitrification: From fundamental understanding to paths toward sustainable nitrogen management

Michael Wagner

Centre for Microbiology and Environmental Systems Science, University of Vienna, Austria

Food production for roughly half of the global population depends on synthetic nitrogen fertilizers, and their worldwide use continues to rise. However, the nitrogen-use efficiency of agricultural food production systems remains low, resulting in extensive release of reactive nitrogen compounds into the environment. The microbial conversion of fertilizers by nitrifying soil microbiome members - responsible for the oxidation of ammonia via nitrite to nitrate - leads to fertilizer loss, groundwater contamination, eutrophication of aquatic water bodies and production of nitrous oxide, a potent greenhouse gas and ozone-depleting compound. To enhance nitrogen-use efficiency, nitrification inhibition is gaining increasing attention. Notably, the diverse groups of nitrifiers—ammonia-oxidizing bacteria and archaea, complete ammonia-oxidizing (comammox) bacteria, and nitrite-oxidizing bacteria—differ markedly in their sensitivities to nitrification inhibitors and in their nitrous oxide production rates. In this talk, I will provide an overview of our current understanding of the diversity, ecophysiology, and niche differentiation of nitrifying microbes. I will also discuss emerging strategies to steer the composition and activity of nitrifying microbial communities in soils, aiming to improve nitrogen efficiency and advance more sustainable agricultural practices.

Poster Session 1: Interconnectedness of microbiomes across food systems

PS1-S1-PP01 Impact of carbon source and oxygen on volatile profiles of psychrotrophic food spoilage bacteria and human perception

Tanu Shree Hissaria, Per Johansson, Johanna Björkroth, Mari Sandell

Food chain and health, University of Helsinki, Finland

Microbial food spoilage poses a critical challenge to producers of perishable goods, with specific spoilage organisms (SSOs) contributing to as much as 30% of food loss and significantly degrading sensory attributes like taste, odor, and appearance (Bourdichon & Rouzeau, 2012; Gram et al., 2002).

This study investigates how oxygen availability (aerobic vs. anaerobic) and carbon source (glucose, pentose, raffinose) shape bacterial metabolism and volatile production. Emphasis is placed on key genera such as *Leuconostoc* and Pseudolactcoccus.

Using advanced analytical methods, including gas chromatography–olfactometry coupled with mass spectrometry (GC-O/MS), this research will characterize VOCs associated with spoilage and link them to specific microbial contributors. Additionally, human sensory evaluations will be integrated to account for individual variations in perception and acceptance, thereby offering a holistic perspective on how microbial dynamics translate into sensory changes.

By pinpointing specific VOCs and mapping their biochemical origins, this work aims to illuminate the mechanisms underpinning spoilage-driven sensory alteration. These insights will inform better detection, control strategies, and ultimately contribute to enhanced food safety, reduced waste, and improved consumer experience.

PS1-S1-PP02 Metagenomics and volatilomics portraying of traditional table olives from the Mediterranean area

Alessandra De Vivo[1], Vincenzo Valentino[1], Andrea Balivo[1], Chiara Maria Calvanese[1], Giuseppina Sequino[1], Alessandro Genovese[1], Annamaria Ricciardi[2], Eugenio Parente[2], **Francesca De Filippis[1]**

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Fermentation is among the earliest and most cost-effective techniques for food production and preservation. Beyond its economic and historical significance, fermentation naturally contributes to reducing the bulk of materials for easier transportation, eliminating harmful substances, improving the nutritional quality and visual appeal of foods, decreasing cooking energy demands, and enhancing overall food safety. Due to these characteristics, fermented foods (FFs) have always been an interesting field to be explored.

We characterized the microbiome and volatilome of table olives from the Mediterranean basin. More than 300 samples were collected from different Mediterranean countries - including Italy, Spain and Greece - with particular emphasis on the Oliva di Gaeta PDO variety. Shotgun metagenomic analysis was then performed, as well as volatilomics by GC/MS.

Results show that *Lactiplantibacillus pentosus* and *Lactiplantibacillus plantarum* are the predominant lactic acid bacteria species. Yeasts such as *Pichia membranifaciens*, *Candida boidinii* and *Wickerhamomyces anomalus*, closely associated with product spoilage, were also found. Among the regions studied, the natural table olive from Greece displayed higher microbiome variability.

These findings improve our understanding of the factors that influence final product quality and may help stakeholders identify microbial markers for olive varieties.

Acknowledgements

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PS1-S1-PP03 Species composition and phylogenetic diversity of acetic acid bacteria communities in homemade vinegars

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Despite their significance, the diversity of acetic acid bacteria (AAB) in homemade vinegars remains understudied. This study aimed to explore the species-level diversity of AAB in homemade vinegars and to assess their community structure to better understand this microbial niche. To investigate the diversity of these bacteria, we employed recently established customized 16S-23S rDNA ITS amplicon metagenomics to identify AAB at the species level. By applying Hill numbers, we calculated species richness, relative abundance, and dominance, providing a clearer understanding of the community structure of AAB in 11 homemade vinegars. Although species richness was relatively high, both relative abundance and dominance were considerably lower, suggesting a community structure dominated by a few highly abundant taxa, with most species being rare or low in abundance. The most dominant genera across most samples were *Komagataeibacter* and *Acetobacter,* both of which are known for their roles in oxidative fermentation. Several previously unreported, potentially novel species of AAB were identified, along with two potentially novel genera. This is one of the first studies to examine the diversity of AAB in homemade vinegars using a culture-independent amplicon metagenomic approach. Our findings suggest that microbiota of homemade vinegars remains an underexplored niche and a source for novel species with biotechnological potential. The results provide valuable baseline data for future microbial studies and may help in the development of novel, customized starter cultures for the improvement and standardization of vinegar production.

PS1-S1-PP04 Regrounding microbiomes across food systems: A conceptual framework for place-based interventions

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Microbiomes shape critical processes along the agriculture–food–health continuum, yet their contributions and complex interactions are often addressed in fragmented ways or remain correlational. Aiming to address this shortfall, this work proposes a systemic, place-based conceptual framework that links microbial dynamics across soils, food, and human health with broader societal dimensions, contributing to resilient food systems.

The framework is grounded in the understanding that microbial processes are highly dynamic, embedded in local ecologies, farming practices, dietary cultures, and human–environment interactions. As such, soil microbial communities are essential to nutrient cycling, plant health, and resilience to environmental stress. In turn, agricultural practices—such as crop diversity, tillage, and organic inputs—influence these networks and affect the nutritional quality and biochemical profiles of crops. As food is processed, microbial communities shift. Fermentation and preservation methods can sustain or suppress microbial presence, shaping dietary exposure and gut microbiota composition. Diets dominated by industrial processing are linked to low gut microbial diversity, immune impairment, and reduced metabolic resilience. Conversely, diverse soil microbiota and traditional food cultures are associated with improved gut health and systemic well-being. These linkages—from agriculture to food to health—are not linear but interactive, shaped by regional ecologies, governance systems, and cultural practices.

Transition efforts along the agriculture-food-health axis must therefore embrace the described complexity and be tailored, adaptive, and inclusive of local environments and actors. The proposed framework calls for interdisciplinary collaboration, integrated observation, and coordinated resource governance to develop context-aware and place-based interventions. It supports research designs, data infrastructures, and policy approaches that recognize microbiomes as part of dynamic, context-dependent food systems. Emphasizing the importance of local context, it underscores that microbial communities evolve with specific soils, climates, diets, and knowledge traditions contributing to the EU Green Deal, Farm to Fork, and Food 2030 agenda. Overall, it provides both a conceptual advance and a practical foundation for regenerative, health-promoting, and resilient food systems while remaining flexible and translatable to diverse global contexts.

PS1-S1-PP05 OneMicrobiome: Understanding of microbiomes across environments for sustainable nutrition

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Microbiomes play a pivotal role in promoting sustainable food production systems. Microorganisms inhabit plants, animals, and humans, where they contribute to host nutrition, and protection against biotic and abiotic stressors. It has been hypothesized that all components of the food production continuum are microbially interconnected. The objective of this study is to elucidate the extent to which interventions in primary feed and food production influence the health and resilience of animals and humans. Experiments are conducted using lettuce plants. The experimental design includes variation in growth substrates, combined with the application of a fungal pathogen of lettuce, *Fusarium oxysporum* f. sp. *lactucae*, at different spore densities. We hypothesize that disease incidence will vary across spore densities depending on the type of growth substrate. A multi-omics approach, combined with plant phenotyping, will be applied to assess the microbial and chemical composition of plants at different growth and disease stages. Compositional and functional differences in the lettuce plant microbiome are expected, depending on the substrate type and the presence or absence of the pathogen. The microbial and nutritional composition of harvested lettuce plants will further be examined in a fermenter system (Timothy), used as a proxy for the animal/human intestinal tract system. Through this approach, we aim to investigate how variation in agricultural production influences food safety and animal/human health.

PS1-S3-PP01 Isolation and characterization of linear low-density polyethylene (LLDPE) degrading *Brucella intermedia* strain from soil

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Introduction: Plastic pollution is a global concern due to widespread use and inadequate recycling, leading to plastic residues in the ecosystem and food web. Linear Low-Density Polyethylene (LLDPE), one of the most common plastics, is highly resistant to natural degradation due to strong C–C and C–H bonds. While chemical degradation methods exist, they pose environmental risks. Microbial bioremediation offers a safer, more sustainable alternative, as certain bacteria can secrete enzymes that break down plastic polymers into less harmful products. This study presents, for the first time, the whole-genome analysis of a *Brucella* species capable of LLDPE degradation, revealing novel enzymatic potential for plastic biodegradation.

Methods: Soil samples were collected from the Matuail sanitary landfill, Dhaka. Samples were serially diluted and spread on Minimal Salt Agar plates (No carbon source other than LLDPE). After 7 days of incubation, bacteria were isolated and cultured on nutrient agar media. These isolates were then incubated in minimal salt broth with LLDPE as the sole carbon source. After one month, bacteria were spread on NA and sent for 16S rDNA sequencing. Additionally, the one-month incubated LLDPE was sent for FTIR and Scanning Electron Microscopy (SEM). The best two isolates were then sent for whole-genome sequencing (WGS). Ultimately, the biofilm-forming capacity of these two isolates was assessed using the Congo red agar method.

Results: According to 16s rDNA sequencing, the two isolates were both *B. intermedia* and showed LLDPE surface degradation in SEM. FTIR analysis showed C=O, C-O, and O-H bond formation in incubated LLDPE. WGS data indicated that both isolates have expanded PEG-related dehydrogenase/aldehyde dehydrogenase, esterases, and laccases compared to other *B. intermedia* isolates. When compared to all sequenced *B. intermedia* (n=231), a statistically significant enrichment of 3HV_dehydrogenases and esterases for both isolates was observed. Biofilm test proved strong biofilm-forming strains.

Conclusion: This study identified two *B. intermedia* strains capable of degrading LLDPE, supported by SEM, FTIR, and genome analysis. Strong biofilm formation likely enhanced degradation. Findings reveal novel biodegradative potential in *Brucella* spp. Future research should explore enzymatic pathways and scale-up applications for sustainable plastic waste management.

Keywords: plastic pollution, *B. intermedia,* bioremediation

PS1-S3-PP02 Microbiomes for both food security and improved use of the bioresources

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So much more research and knowledge sharing are needed. Here are ideas, technologies and topics which can contribute to a better world, for food security and health, climate and biodiversity. 1. Integrating microbiome insight in breeding-efforts for more drought-tolerant crop plants; include specifically selected endophytic fungi in such microbiomes for improved drought-tolerance; and include also nutritional and health-potential of crop residues in such breeding of new climate adapted crop plants. 2. Tailormade fermentation-consortia (SynComs) to optimize valorization of crop residues; design the SynComs to include microbiomes with organisms of known nutritional value. 3. Optimize synergy between microbial fertilizers and the rhizosphere-microbiome of the crop plant. 4. For transition to mixed cropping, for improved food security, biodiversity and climate change adaptation, optimize rhizosphere-microbiome for faster growth of e.g. fruit trees or shading trees in horticulture. 5. Invest research, innovation and development efforts into Upscaling microbiome-derived products for improved food security and sustainability; Upscaling complex microbial products is not trivial; new research is needed. 6. Give priority to new research and development for product development of microbiome-derived products; much new knowledge is needed also regarding shelf life, safety etc. 7. Knowledge sharing is urgent in the total area of microbiome derived technologies and products; microbiome-derived solutions can contribute significantly to food-security and health as well as to socio-economy, job generation and rural livelihood.

PS1-S3-PP03 Exploring antimicrobial resistance in dairy farms: Multidisciplinary insights into AMR prevalence and diversity in neonatal calves and their environments.

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Antimicrobial resistance (AMR) is one of the biggest threats to both animal and human health, and requires a collaborative and multisectoral approach to overcome it. Here, we perform AMR surveillance within and across dairy farms by characterising the resistomes associated with neonatal calves, their feed, and their environments.

Ten dairy farms were surveyed for >90 parameters, including hygiene practices and antibiotic usage. Both culture-based and culture-independent techniques, including shotgun metagenomic sequencing, were used to characterise the resistomes present in calf faeces and calf housing environments, including feed equipment, concentrate feed and milk replacer. Samples were tested *in vitro* for phenotypic AMR against seven antibiotic classes: penicillins, macrolides, phenicols, aminoglycosides, tetracyclines, synthetic and polymyxins. Resistant bacteria were isolated and underwent 16S rRNA gene and whole-genome sequencing, and lab-based multidrug resistance (MDR) testing.

The study revealed high AMR diversity and abundance in calf houses, with metagenomics revealing high resistance gene abundances within faecal samples, while resistant bacterial CFU/mL reached 9.57×10^{8}. Phenotypic resistance to 6 antibiotic classes was detected on each farm, with the highest resistance levels reported for neomycin and trimethoprim. Of the 84 anaerobic AMR isolates 16S sequenced, 66 isolates (78.6%) were MDR, while 36.0% of the 75 aerobic isolates were MDR. Using metagenomic sequencing and a multi-tool read-mapping and alignment approach, we also identified SNP-level variations in AMR genes specific to different farms.

In summary, our multidisciplinary study in dairy farms reveals a highly diverse resistome in neonatal calves and their environments, emphasising the urgent need for targeted interventions to address this growing threat. Differences in resistome profiles were also observed both between and within farms, as well as across sample types. The high prevalence of MDR isolates underscores the complexity of the challenge and highlights the importance of mitigating AMR in dairy farming.

PS1-S4-PP01 Integrative analysis of plant growth-promoting and antifungal mechanisms in rhizosphere bacteria and their contribution to abiotic stress adaptation

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The application of inorganic fertilizers and chemical fungicides to meet the rising food demands has led to environmental impacts and contributed to the emission of greenhouse gases. This underscores the urgency of sustainable agriculture innovations. Plant growth-promoting bacteria (PGPB) support a bio-based approach to enhance crop resilience and reduce environmental impacts. This study towards a multi-national project aims to i) identify bacterial strains to promote maize growth and control maize pathogens, and ii) to characterize their mechanism of action for the mitigation of abiotic and biotic stresses. Twelve bacterial strains from South Africa, isolated from the rhizosphere of indigenous fynbos species *Aspalathus linearis* (rooibos), were evaluated for plant growth promotion (PGP) traits, antifungal activity, and abiotic stress tolerance. PGP activities of bacterial strains were characterized *in vitro*, such as in ammonia production, indole-3-acetic acid production, nitrogen fixation, protease activity, 1-aminocyclopropane-1-carboxylate deaminase activity, and siderophore production. Among the bacterial strains tested, *Streptomyces* sp. 44W showed the strongest PGP potential (six PGP traits), while *Streptomyces* sp. 72S and *Streptomyces* sp. 116W exhibited five positive traits. Antifungal screening against *Fusarium graminearum* and *F. verticillioides* revealed strong antagonistic activity of *Streptomyces* sp. 104W, *Streptomyces* sp. 41W, and *Brevibacillus* sp. 56W, highlighting their potential as biocontrol agents to suppress stalk/ear rot and blight disease in maize. Bacterial strains were evaluated for abiotic stress tolerance under heat (35°C), drought (10% polyethylene glycol), and combined (10% polyethylene glycol at 35°C) stress conditions. Although most of the strains tolerated individual stress, only *Streptomyces* sp. 133W tolerated combined stress conditions. These results highlighted the multifunctionality of some bacterial strains (e.g., *Streptomyces* sp. 104W), which combine PGP traits, antifungal activities, and stress tolerance. Bacterial strains will be further characterized as pure inoculum and consortium on maize plants under controlled and field conditions to reduce chemical inputs and enhance yield stability under adverse climatic conditions.

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PS1-S4-PP02 Evaluation of plant-microbe interactions in Introgression lines (ILs) of *Oryza rufipogon* X *Oryza sativa cv* Vialone Nano

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Rice (*Oryza sativa*) is a monocotyledonous plant and it represents the staple food for more than half of world population. Rice **domestication and varietal selection** in Europe (ssp. *japonica*) and in Asia (ssp. *indica*) improved desirable agronomic traits but also lead to lose different genetic traits, while the wild progenitor of cultivated rice, *O. rufipogon,* is considered a donor of genetic variability. Besides that, rice cultivation is facing different problems worldwide, such as the **loss of soil fertility**, the massive use of agrochemicals, especially nitrogen fertilizers that cause environmental degradation, and decrease in **soil microbial diversity**, with also negative impact on **human health**. In addition, also **drought stress** represents one of the main concerns, which can have an impact on crop growth and causes significant loss in productivity. One of the solutions to achieve sustainable rice cultivation is the exploitation of the **genetic variability** of the wild relatives and of **rhizosphere/root microbiota** to improve plant tolerance to abiotic stresses. The microbiota associated with wild relatives represents a resource for **low-input agriculture**. In particular, the wild rice ***O. rufipogon*** showed an aptitude to associate with RCA25, an endophytic nitrogen-fixing strain, more than **Vialone Nano** (*O. sativa* ssp. *Japonica*). Our research aim is to identify genomic regions of *O. rufipogon* involved in the root-PGPB association by using introgression lines (ILs) obtained from crossing Vialone Nano with *O. rufipogon*. 150 ILs were screened to detect their **capability to associate with RCA25**. Phenotyping for the association aptitude was conducted by counting CFU obtained from roots homogenate. Analysis of the phenotypic data with respect to SNPs generated by the sequencing of the ILs is currently underway for the identification of genetic regions possibly affecting the root colonization. Preliminary results show an outstanding variability in the association with RCA25, thus reflecting a genetic variability, probably involved in immune response or microbe recognition mechanisms, which will be further characterized through **transcriptomic analysis** of ILs showing contrasting association aptitude and grown in drought condition. Finally, **morpho-physiological evaluation** of these ILs in drought stress and inoculated with selected **Syncom** is currently ongoing.

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Poster Session 1: Microbiomes for circularity/sustainability

PS1-S5-PP01 Inoculated chickpea genotype and P-fertilization influence rhizosphere microbiota which drive symbiosis efficiency and growth performance under low-P conditions

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Co-inoculation of grain legumes, including chickpea, with nitrogen-fixing and phosphate-solubilising bacteria (PSB) improves symbiotic efficiency and plant productivity under low-P availability. However, the extent of chickpea's responsiveness to inoculation and their reliance on symbiotic nitrogen (N) fixation remains intricately influenced by plant genotypic diversity and the associated rhizosphere microbiome under different P levels. This study evaluated the agro-physiological, symbiotic and microbial traits of two Moroccan winter chickpea (Cicer arietinum) varieties (Arifi and Bochra) under low-P conditions represented by three rock-P levels (0, 25, 50 and 75 kg P_2O_5 ha^{-1}) and co-inoculation with *Mesorhizobium cicer*i and *Rhanella aceri* (PSB). Results showed that inoculation at rock-P levels ≥ 50 kg P_2O_5 ha^{-1}, significantly improved symbiotic traits, plant biomass and nutrient uptake in both varieties, with Bochra exhibiting superior performance. At 75 kg P_2O_5 ha^{-1} of rock-P, Bochra exhibited a strong correlation between root morphological traits and P-related rhizosphere traits. Results further highlighted Bochra's robust response to inoculation under 75 kg P_2O_5 ha^{-1} rock-P, driven by its ability to shape the rhizobacterial community composition, where *Mesorhizobium* dominated and significantly influenced plant and rhizosphere traits. More notably in Bochra than Arifi, rhizobacterial species richness and community composition correlated strongly with nodule traits, plant traits and rhizosphere P-related parameters. These findings elucidate the significant contribution of the rhizosphere bacterial community to the symbiotic performance of Mesorhizobium-inoculated chickpea, which remains both genotype- and P-dependent.

PS1-S5-PP02 Unravelling the microbiota of disease-resistant berry grapes

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The development of interspecific hybrid varieties (IHVs) resistant to diseases such as powdery mildew and downy mildew enables a reduction in chemical inputs in vineyards. Due to their resistance to these diseases, the microbial balance on IHVs is altered, potentially allowing the establishment of non-fermentative fungi or yeasts, including emerging phytopathogens or spoilage organisms. As a result, it is crucial to identify and characterize the microbial communities present on the surface of IHV grape berries.While many studies describe the biodiversity of microorganisms on traditional grape varieties, there is a lack of data on IHVs. In this context, the present study aims to characterize the diversity of the grape berry microbiota of IHVs, and to identify the biotic and abiotic factors that shape its composition.To achieve this, 23 grape varieties—including 12 IHVs—were collected from four experimental vineyards in the the south of France across 2023 and 2024. Some varieties were sampled from more than one location, resulting in a total 35 unique sample conditions. The grape microbiota were extracted by rinsing and analyzed using metabarcoding, targeting the ITS1 region as a taxonomic marker.The explanatory variables considered were: vintage, vineyard location, grape variety, disease resistance, and the presence of agroforestry components. Among these, the most significant factors influencing microbiota composition were vintage and vineyard location. In the Cazes vineyard, a clear distinction between IHVs and traditional varieties microbiota was observed in both vintages. A similar pattern was found in Pech Rouge (Clape area) in 2024. Agroecological components showed an influence in microbiota in both vintages. Across all samples, the majority of identified microorganisms were filamentous fungi, with yeasts less abundant. In IHV grapes higher abundance of species of filamentous fungi of the genus *Penicillium* were observed for the vintage 2023 in Pech Rouge, while the genus *Cladosporium* was more observed in the traditional grapes. In 2023 the presence of the genus *Erysiphe* (powdery mildew) was detected in expressive abundances only in the traditional grapes. This is the first study describing IHV grapes microbiota and provides insights of the dynamic of IHV's berries microbiota in contrast to traditional species. (Acknowledgements: G. P.M. would like to thank the Occitanie region and the INRAE MetaBio metaprogramme for funding her PhD.)

PS1-S5-PP03 Temporal and functional profiling of wheat rhizoplane biofilm-forming bacterial communities reveals core traits for designing SynCom-based biofertilizers

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Root-associated microbial biofilms are emerging as key drivers of plant performance under variable environmental conditions. This project investigates the ecological assembly, genomic potential, and functional role of biofilm-forming bacterial communities in the wheat rhizoplane, with the overarching goal of engineering synthetic microbial consortia (SynComs) to enhance plant growth and resilience. Using a plant-trap experimental design, two wheat cultivars were grown in soils with contrasting land-use histories (with or without prior wheat cultivation history) to dissect the dynamics of early root colonization. Time-resolved microbial community profiling analyses revealed soil-driven community shifts and microbial succession from initial colonizers (e.g., *Pantoea*, Acinetobacter and *Promicromonospora*) to later taxa (e.g., *Exiguobacterium*, *Asticcacaulis* and *Cellvibrio*), independently of the host genotype, alongside a shift in relative abundancies of the genera *Pantoea* and *Pseudomonas* over the time course. Shotgun metagenomics data uncovered temporal changes in KEGG pathways and COG functional categories, reflecting evolving microbial functions during biofilm formation within this time course. Up to 120 strains from the core bacteriome were isolated and sequenced. *In silico* analyses uncovered genetic traits linked to biofilm formation, nutrient solubilization, siderophore biosynthesis, and auxin production. *In vitro* biofilm analyses using epifluorescence microscopy showed that most of the tested isolates efficiently colonize rhizoplane and form biofilms. Functional validation demonstrated their ability to promote wheat growth *in planta*. Together, these findings establish a genomic and ecological framework for the rational design of synthetic microbial consortia (SynComs) tailored to enhance plant performance. By integrating *in silico* and *in planta* analyses, this work contributes to the development of microbial biofertilizers that align with climate-resilient and low-input agricultural strategies.

PS1-S5-PP04 Resolving viral, microbial, and antimicrobial resistance networks in the rumen: A Hi-C metagenomics framework for sustainable livestock microbiomes

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The rumen microbiome plays a critical role in livestock digestive processes, and which have an impact on feed efficiency and greenhouse gas emissions. Microbial fermentation within the ruminant gastrointestinal system produces hydrogen, which methanogenic archaea convert into methane, linking microbial ecology to climate outcomes. Bacteriophages (bacterial viruses) are increasingly recognized for their role in shaping microbial communities and influencing fermentation dynamics. In this study, we applied Hi-C metagenomics to resolve microbial genomes, phage–host interactions, and antimicrobial resistance (AMR) gene linkages in the cattle rumen with varying dietary compositions.Twelve rumen samples from cows consuming four distinct diets (grass; grass and concentrate; grass and clover; and grass, clover, and plantain) were analysed using Hi-C proximity ligation. From this, we reconstructed high-quality microbial, viral and plasmid metagenome-assembled genomes (MAGs). Viral genomes were clustered and taxonomically annotated using a network-based approach. AMR genes were identified and putatively linked to bacterial genomes, plasmids, or left unassigned based on Hi-C physical linkage, allowing direct insights into potential vectors of resistance dissemination.Preliminary observations reveal variable host–phage association patterns across the different diets, with viral load per cell differing among feeding regimes. Ongoing work will include CRISPR spacer matching to compare historical and current virus–host associations.In parallel, functional annotation of viral genomes is being explored to identify putative auxiliary metabolic genes (AMGs) that may influence host metabolic potential and ecosystem function. These genes, if present, could reveal how viruses contribute to the modulation of microbial processes relevant to feed utilization and methane production.This work demonstrates the utility of proximity-guided, genome-resolved metagenomics in complex microbial ecosystems. It contributes to global efforts in climate mitigation, sustainable livestock microbiomes, and functional microbial ecology, providing a framework for tracking mobile elements, resistance genes, and viral impacts on host metabolism.

PS1-S5-PP05 Integrative metagenomic and metataxonomic analysis of biofilm formation in the wheat rhizoplane as a model system

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Rhizoplane biofilms promote plant development by protecting beneficial microorganisms from environmental stress, improving nutrient uptake, nitrogen fixation, and defense against pathogens. In this study, due to the lack of knowledge about the process of formation and stabilization of biofilms by a complex community of microorganisms, we analyzed the composition and functional dynamics of bacterial communities during early stages of biofilm formation in the wheat rhizoplane.

We conducted a trap-plant experiment with two wheat varieties grown in four different soils that differed in cropping history, including one with associated metal toxicity. Rhizoplane samples were collected at 15 and 30 days after planting, and we analyzed the bacterial communities using both 16S rRNA gene amplicon sequencing and shotgun metagenomics.

Both approaches revealed a temporal shift in the dominant taxa and functions: *Pantoea* was enriched at 15 days, during the initial stage of biofilm development, while at 30 days, the bacterial communities became more complex and metabolically diverse. Shotgun metagenomic analysis identified differentially abundant genes between the two time points, including genes (KOs) related to biofilm formation (e.g., matrix production, quorum sensing, stress response), reflecting functional transitions during the biofilm stabilization process. Moreover, a total of 327 high-quality bacterial metagenome-assembled genomes (MAGs) were recovered, providing a genomic reference for the rhizoplane microbiota.

Overall, our findings reveal a coordinated shift in both the taxonomic composition and functional traits of bacterial communities during early biofilm formation on the rhizoplane. This work provides a genomic framework for the rational design of bioinoculants that leverage successional microbial dynamics.

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PS1-S5-PP06 Trinity of piglet gut biogeography development: Age, organ and tissue

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Understanding the gut microbiome development during early life in healthy, non-diarrheic piglets is an important cornerstone to designing sustainable pig production systems and promoting animal health without reliance on antibiotics.

To map the microbial dynamics in the developing piglet gut, we profiled the luminal microbiome of non-diarrheic piglets across three locations: jejunum, proximal colon, and rectal swabs at five ages: days 4, 14, 25, 49, and 67 of life. Using 16S rRNA gene amplicon sequencing, we identified location-specific and age-related microbial shifts in the gut microbiome. Location-specific changes associated facultative anaerobes with small intestine and obligate anaerobes with colon, reflecting the progressively declining oxygen gradient along the gastrointestinal tract. Age-related dynamics were marked by the dietary transition from pre-weaning to post-weaning phases, when milk-based diet becomes plant-based.

Furthermore, we characterized the variation between lumen-resident and mucosa-associated microbes at given locations and timepoints. Characterizing mucosal microbiomes is important as microbes are hypothesized to interact with the host at the mucosal interface directly. Nonetheless, characterizing mucosal microbiomes, especially using state-of-the-art shotgun metagenomic sequencing is hindered by host DNA contamination. To improve mucosal microbiome characterization, we evaluated a Tween20/PBS based mucosa-adherent microbiome enrichment method, and characterized mucosal, luminal and mucosa-adherent microbiomes variation in jejunum and proximal colon of day 67 piglets.

Together, these findings improve our ability to study and understand microbial biogeography in the developing piglet gut.

PS1-S5-PP07 Effects of agro-management on soybean root and rhizosphere microbiome under field conditions

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Soybean is one of the most globally significant crops, valued for its high protein content and diverse applications, mainly in food and animal feed. Interactions between plants and microorganisms play a vital role in crop performance, and thus, a better understanding of the soybean microbiome is key to enhancing crop performance and quality. To investigate the influence of different agro-management practices on soybean microbiomes, plant growth, and seed quality, a field trial was established in Bologna.

The trial involves five soybean varieties with specific traits: EM Pura, NAV 555 (high protein content), OL996 (high oleic acid content), AMMA (low trypsin inhibitor content), and Bahia (low trypsin inhibitor content). These varieties were cultivated under three different management regimes. Sampling was performed at two growth stages: V2 (second trifoliate fully developed, onset of nodule formation) and R2 (full bloom with peak nodulation activity). Rhizosphere, bulk soil, and root samples were collected for 16S rRNA gene amplicon sequencing analysis. The different agro-management practices led to distinct patterns of bacterial diversity and richness across sample types, including notable differences observed between the two sampling points. Taken together, our findings provide new insights into how agro-management practices influence the soybean-associated microbiomes and modulate them during their development.

PS1-S5-PP08 Creating transition pathways for microbiome applications in the soyabean valuechain: Insights from the MICROBIOMES4SOY project

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Accelerating a shift to plant-based proteins requires change across the whole food value chain that can be supported by microbiome applications. Recent work on food system transitions highlights moving beyond linear narratives toward integrated pathways linking production, consumption, and governance.MICROBIOMES4SOY co-develops stakeholder-validated transition pathways to accelerate effective uptake of microbiome applications in European soyabean systems supporting healthy diets and advancing FOOD 2030 goals. Using a multi-actor, co-creation approach based on sustainability transitions literature we identify niches and leverage points from farm to fork. Structured pathway workshops combine four strands of work:

- training and education to build microbiome literacy among farmers, advisors, and industry;

- industry-oriented innovation for new business models and investments

- policy dialogues on regulation and product approval and use of microbiome products across food and aquafeed;

- comparative meta-analysis of microbiome "signatures" across plant, aquaculture, and human contexts to inform actionable interventions.

An initial catalogue of barriers, gaps, and opportunities in regulation, literacy, evidence requirements, procurement, and market integration has been assembled. Based on two multi-stakeholder workshops and systems analysis, three interlinked transition pathways and storylines were defined:

1. tackling the environmental impact of soybean production,

2. transforming soy for novel fish feeds, and

3. advancing microbiome-enhanced soy for gut health and sustainable diets.

These are linked through a shared system spine of regulatory, innovation, and market functions coordinating change across the food system. These pathways generate outputs linking research to operational actions, targeted education resources, innovation opportunities, and policy options to ease regulatory bottlenecks. This work has been conducted with the valuable input and collaboration of the MICROBIOMES4SOY Consortium, ensuring alignment across science, policy, and practice. At the poster, we present these early storylines and invite structured feedback to validate and refine leverage points, uncover missing barriers and gaps.

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PS1-S5-PP09 High-throughput exploration of microbial catalytic potential for AI/ML based prediction of sustainable hybrid fermentation outcomes

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Transitioning toward sustainable and nutritionally balanced food systems requires novel approaches that close resource loops while maintaining product quality. One promising direction is the valorization of plant and dairy side streams through microbial fermentation, supported by advanced biotechnological and computational tools. Plant-derived residues such as cereal fibers and legume proteins represent a vast, underexploited resource of fermentable substrates rich in carbohydrates and proteins. Yet, many plant-based alternatives fall short in essential amino acids and overall nutritional completeness. In contrast, dairy side streams offer superior protein quality and functional components but pose environmental challenges when underutilized. Combining these complementary resources into hybrid substrates provides an opportunity to create foods that are both nutritionally complete and environmentally responsible. This work aims to establish a high-throughput discovery pipeline that explores the catalytic potential of diverse microbial strains for transforming hybrid plant–dairy side streams into flavorful and functional fermented products. The approach integrates parallel microbial screening with advanced metabolomics to capture strain-specific conversion patterns and metabolite profiles. By coupling these large-scale datasets with chemometric and machine learning frameworks, the study will advance predictive models capable of identifying optimal strain–substrate combinations and forecasting desirable fermentation outcomes, including enhanced flavor development, nutrient bioavailability, and beneficial metabolite release. The project is being developed in collaboration with industrial partners Arla and Lantmännen, who will provide representative side streams from dairy and plant production chains. Hybrid mixtures of the side streams are currently being fermented with type strains in microbioreactors, and metabolome profiles will be analyzed. These results include values of microbial growth, changes in pH, comparative fingerprints of aroma, flavour, peptides, fatty acids, and oligosaccharides between the fermented and unfermented substrates. These results will later feed to the ML models, setting out a framework for integrating microbial bioprospecting, high-throughput analytics, and AI-driven decision-making to accelerate sustainable innovation in food biotechnology.

PS1-S5-PP10 From roots to results: Wheat control of soil microbial nitrogen cycling in living lab farms

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The interactions between plants and soil microbial communities in the rhizosphere play a crucial role in soil productivity and the resilience and nutritional quality of our food systems. In intensive crop systems, root traits that drive beneficial microbiome recruitment can turn the tide on soil degradation, supporting more efficient nutrient cycling, higher yields, and enhanced grain nutrient content. Crop landraces are an untapped source of genetic diversity for identifying advantageous root traits that enhance soil health, crop performance, and the nutritional value of food produced within sustainable agricultural systems.

Through its “living lab” and “research to practice” approaches, the EJP SOIL programme has connected innovations in soil management to improvements in food security, nutritional quality, and the long-term sustainability of agricultural systems across Europe. As part of the programme, the WISH ROOTS project (Wheat Improving Soil Health with Root traits) explored how wheat root traits influence soil microbial functions that regulate nutrient cycling and soil health. By integrating agronomy, breeding, and soil microbiology within Living Lab farms, the project aimed to identify root traits that enhance nitrogen use efficiency and contribute to more sustainable and nutritious food systems. The WISH-ROOTS screened 20 wheat genotypes (modern cultivars and historic landraces) in parallel field trials across seven countries, assessing two regimes of nitrogen (N)-fertiliser.

The TRUTH project (Thriving Roots Underpinning Total soil Health) in collaboration with BOFIN (British On-Farm Innovation Network), extends the WISH-ROOTS research from controlled field trials to real-world farm environments. We have explored the soil microbiome across conventional, organic, and regenerative farming systems across UK to assess how management practices shape nutrient cycling, soil health, and crop resilience. The 2026 season will trial four wheat landraces selected from the WISH-ROOTS panel to capture genetic variation in root traits that influence soil microbiome functions, particularly cycling of nitrogen and other essential nutrients. This integration of genetic diversity with real-world management will provide insights to guide breeding and agronomy for more sustainable, resilient, and nutritious food systems.

PS1-S5-PP11 Multi-component plant extracts outperform single compounds in mitigating intestinal antimicrobial resistomes in swine

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Excessive antibiotic use in livestock has led to intestinal antibiotic residues and resistant bacteria, prompting China's comprehensive antibiotic ban. Plant extracts are promising antibiotic alternatives with antimicrobial and anti-inflammatory activities, but their effects on intestinal antimicrobial resistomes (AMRs) remain unclear. This study examined how different plant extract compositions influence intestinal AMRs in two swine trials. In Trial 1, 90-day-old finishing pigs were divided into four groups: basal diet (control), basal diet with hesperidin, basal diet with rosmarinic acid, and basal diet with both compounds. Hesperidin alone showed upregulating trend on total ARG/MGE abundance, number of ARG/MGE subtype, abundance of core ARG/MGE compared to controls, whereas combination of hesperidin and rosmarinic acid reversed these trends, suggesting synergistic suppression of the resistome. In Trial 2, 25-day-old piglets were assigned to basal diet or basal diet plus Acalypha australis extract (a multi-component mix of flavonoids, terpenoids, and organic acids). The extract significantly reduced total MGE abundance, abundance of multiple classes of ARGs/MGEs, and number of ARG/MGE subtype, demonstrating its efficacy in mitigating intestinal AMRs. Collectively, these findings highlight the potential of multi-component extracts as superior alternatives to single-component extracts for controlling AMRs in gut.

PS2-S6-PP01 Flavour, odour and texture improvements of plant-based dairy products using microbial fermentation products

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DELICIOUS proposes a novel production technology to create affordable, tasty and safe plant-based dairy analogues (cheese and kefir) with high nutritional value, by combining microbial products with plant-based raw materials. The project has the ambition to accelerate the dietary shift, acting like a paradigm for the whole plant-based food sector. DELICIOUS contributes to a better nutrition for everybody by developing products with high protein content, rich in vitamins, fibres and probiotics. The project aims also to decrease the environmental footprint of food industry not only by replacing conventional dairy products in peoples' diets but also by introducing microbial products which acquire less fresh water, less land use and inexpensive residual raw materials. Having as starting point the perceptions of culinary experts (chefs), the project will improve the sensory characteristics of the current, commercial plant-based products in order to improve their placement in the market. To that end, we will use tailor-made microbial fat, produced via precision fermentation, yeast biomass and fibre-producing microbial strains to achieve the desired organoleptic properties without additives, artificial flavours and avoiding ultra-processing methodologies. To accelerate the commercialisation of the developed products, DELICIOUS will perform various analyses and evaluations: Safety assessments, nutrition simulations, consumers testing and technoeconomic evaluation of the processes combined with behavioural economics to define the profit and price margins for such products. Capitalising on the great capacity and experience of the consortium on High Throughput methodologies, the project has also the great ambition to empower fermentation industry with a bioinformatic tool to predict flavour, odour, and texture of a product, based on the initial raw materials and the microorganisms used in fermentation, significantly decreasing the costs of product development.

PS2-S6-PP02 Potential of donkey milk microbiota for the development of functional fermented products

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Interest in functional foods has increased in the last decade due to their nutritional and health-promoting properties. Within this context, donkey milk (DM) is recognized for its beneficial properties. DM is a nutritionally rich source of bioactive compounds, vitamins, and minerals. However, its probiotic and functional potential remains largely unexplored. This study aimed to investigate microbial dynamics during the spontaneous fermentation of raw DM and to isolate DM-associated lactic acid bacteria (LAB) suitable for developing functional dairy products.

Raw milk from Zamorano-Leonesa breed donkeys, raised under organic farming conditions in Salamanca (Spain), was spontaneously fermented at 37 °C without the addition of exogenous cultures until pH 4.6. Metataxonomic analysis revealed a shift from *Pseudomonas* and *Enterococcus,* which dominated the raw milk at the beginning, to an increased abundance of LAB (including *Lactobacillus*, *Lactococcus*, and *Streptococcus*) at the end of fermentation. A total of 34 bacterial strains belonging to nine genera and 14 species were isolated and identified by full-length 16S rRNA gene sequencing. From those, ten LAB isolates were selected for *in vitro* fermentation assays, where five *Lactococcus lactis* isolates exhibited the most promising functional profiles. Whole-genome sequencing analysis of these five *Lactococcus* isolates revealed genomic differences between some of the isolates and confirmed the absence of antibiotic resistance or virulence-related genes. Pilot-scale fermentation trials with the two most suitable isolates led to the selection of *Lactococcus lactis* subsp. *lactis* CECT 31096, which was integrated into DM fermentation due to its improved organoleptic and bioactive properties. The bioaccessibility of bioactive compounds increased after DM fermentation, especially antihypertensive capacity, enhancing the inhibition of angiotensin-converting enzyme (IC_{50} 3.17 vs. IC_{50} 7.23 in pasteurized milk). Moreover, *in vitro* gastrointestinal dynamic studies showed that, after digestion, this ability was doubled (IC_{50} 1.25 vs. IC_{50} 1.32 in pasteurized milk), suggesting potential benefits in hypertension management. Soluble free phenols and peptides also increased significantly, boosting the reducing power and antioxidant capacity of the final product. These findings highlight the native microbiota of DM as a promising natural source of probiotic strains for the development of innovative functional fermented dairy products.

PS2-S6-PP03 Lettuce be healthy: the influence of agricultural practices on the lettuce microbiome and metabolome, and its importance for human health

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Many plants have an intimate relationship with their microbiome. This relationship can lead to pathogen suppression, improve plant growth and cause changes in the plant chemistry. The composition of the plant microbiome is mainly influenced by the microorganisms that are present in the soil, but also by environmental factors. However, it is poorly understood which factors are most influential in the formation of the crop microbiome in an agricultural setting. Additions of fertilizer, pesticides, biostimulants or other additives, as well as the frequency and depth of tillage, or the use of cover crops, have all been indicated as possible influencers of the crop microbiome composition, yet no clear key factor has been indicated. In order to effectively steer the soil microbiome to improve the crop microbiome composition, it is important to first decipher the most influential agricultural practices.

In a multi-omics field study, we explored the link between agricultural practices, the soil and plant microbiome and the plant metabolome. We focused on lettuce grown on a series of farms across the Netherlands with different soil and crop management. As lettuce is often consumed raw, the microbiome present in the plant may be consumed directly, and could act as a source of probiotics. To exclude potential effects of pesticides, we focused on lettuce grown on organic farms and a hydroponics growing system. From seventeen farms, we collected lettuce heads, rhizosphere and bulk soil samples. We then determined the microbiome with 16S and ITS amplicon sequencing and carried out 1H nuclear magnetic resonance (1H NMR) spectroscopy on the plant samples. In-depth questionnaires with the farmers provided insight into their management practices.

The first results show that in lettuce plants grown on soil, approximately half of the bacterial ASVs and two thirds of the fungal ASVs were found also in the rhizosphere, indicating a strong link between the plant and soil microbiome. This link was absent in the hydroponics system. Furthermore, one bacterial species has been found almost exclusively inside the lettuce and seems to lead to a shift in the chemical composition. The bacterium has been found in different cultivars yet consistently leads to a similar shift in the metabolome. This finding could underline the importance of the plant microbiome for crop quality and human health.

PS2-S6-PP04 ILSI Europe perspective review: site-specific microbiota changes during pregnancy associated with biological consequences and clinical outcomes: Opportunities for probiotic interventions

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Pregnancy induces notable alterations in the gut, vaginal, and oral microbiota driven by hormonal, immune, metabolic, dietary, and environmental factors. During pregnancy, the gut microbiota is characterized by increased proportions of the genus Bifidobacterium and the phyla Pseudomonadota (formerly Proteobacteria) and Actinomycetota (formerly Actinobacteria). These changes occur alongside reduced alpha diversity and greater beta diversity, changes that influence maternal metabolism and fetal development. Shifts in gut and oral microbiota have been associated with complications such as preterm birth (PTB), pre-eclampsia, and gestational diabetes (GDM), though patterns are sometimes inconsistent. The vaginal microbiota remains Lactobacillusdominant during pregnancy, with reduced diversity leading to reduced risk of pathogenic infection and increased diversity has been linked with a higher risk of PTB. Hormonal changes also affect the oral microbiota, potentially increasing pathogenic species and contributing to adverse outcomes like PTB. Probiotic supplementation during pregnancy has significant potential to reduce adverse pregnancy outcomes; however, clinical studies are still limited. Probiotics may be effective in alleviating maternal constipation and lead to lower PTB risk, particularly by modulating the vaginal microbiota, but they have limited impact on GDM. In the context of maternal mental health, some studies suggest benefits of probiotics in reducing anxiety, but effects on depression are inconclusive. This perspective examines how pregnancy-related microbial shifts, both natural and probiotic-induced, affect maternal and fetal health and highlights potential opportunities for the innovative use of probiotics during the gestation period.

PS2-S6-PP05 Development of a kombucha metagenome catalogue including a one-year longitudinal sampling

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INTRODUCTION. Kombucha microbiome exhibits dynamic community structures that drive fermentation. While biofilm and liquid phases interact throughout fermentation, their temporal microbiome succession and functional relationships remain underexplored.

METHODS. High–throughput shotgun metagenomic sequencing was performed on samples collected longitudinally from kombucha biofilms and liquid phases over a year–long fermentation (n=73). To evaluate temperature effects, the first half of the fermentation was performed at 20 °C, then shifted to 30 °C. To explore alternative ways of production, various sugar sources were tested, including simple sugar, mashed beans, hydrolysed bread cream, and ground bread. The dataset was integrated with public data (n=53) and enriched with a metadata curation ($N_{metadata}$=14), collecting information like fermentation conditions, sugar source, and geographical origin.

RESULTS. Thus, a comprehensive catalogue of kombucha microbiome (n=126) was built. Our findings revealed differences in a– and b–diversity depending on the metadata considered, as well as different distribution patterns of microbes and key functional genes associated with cellulose production, flavours and health benefits. Explainable machine learning models classified microbiome across metadata, highlighting microbial markers of kombucha features. Additionally, phylogenetic analyses unveiled strain–level microbial diversity, while functional genomics linked taxa with functional metabolic pathways. Critically, our analysis yielded to 789 metagenome–assembled genomes, incrementing existing kombucha microbiome resources and highlighting previously undescribed taxa.

CONCLUSIONS. This first longitudinal catalogue of kombucha offers a comprehensive view of biofilm–liquid microbiome dynamics during one year of fermentation. Our findings enhance our understanding of microbial ecology in kombucha fermentations, offering new insights into microbial contributions to kombucha quality and potential health benefits, providing genomic-resolved resources for supporting precision fermentation approaches.

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PS2-S6-PP06 The effect of increasing wheat arabinoxylan on the gut microbiome

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The human gut microbiome comprises the collective genomes of all the microbiota within the gastrointestinal tract with the largest quantity predominantly in the large intestine. Fibres are non-digestible carbohydrates, resistant to human enzymatic breakdown, providing an important nutrient source to the gut microbiota.

The interaction of fibre within gut microbiota can produce beneficial responses to the hosts physiology, mainly known through short chain fatty acids (SCFA). However, not all fibres behave in the same way or are fermented in the colon equally and so it is important in finding each fibres role in shaping the microbial community and SCFA production. Arabinoxylan (AX) is the main fibre present in wheats starchy endosperm and is common in our diets. Wheat breeding programmes have developed wheat lines with ranges of AX content and solubility. Isolated AX has been shown to be beneficial via production of SCFA and microbial composition, but little is known about its digestion within bread flour.

We have developed and used a higher throughput digestion and colon model to stimulate AX flour digestion with a focus on the gut microbiota response in healthy people. Here I show that these wheat lines with increasing water extractable AX have an impact on the gut microbiome response with evidence of increasing butyrate production, a key SCFA. Individual responses are also seen, with one microbiome community responding particularly well in terms of SCFA's to the AX flour treatment with specific strain differences. This confirms a potential positive impact AX can have on our health and as a potential prebiotic within wheat flour.

PS2-S6-PP07 Optimizing Taggiasca table olives fermentation: Development of autochthonous microbial starter culture

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This study, conducted within the European DOMINO project, aims to develop an autochthonous microbial consortia to improve the fermentation of Taggiasca table olives. Strain selection followed an integrated pipeline combining Whole Genome Sequencing (WGS), Genome-Scale Modelling (GSM), physiological screening, and enzymatic assays. A total of 53 yeast autochthonous strains were isolated in 2021, sequenced and tested for growth under different NaCl concentrations (0–12%), temperatures (10–30 °C), and pH values (4.5–5.5). Growth kinetics were monitored over 7 days. β-glucosidase, lipase, and pectinase activity were also assessed. Whole Genome Sequencing (WGS), Genome-Scale Modelling (GSM), physiological screening, and enzymatic assays were combined to select a minimal communities. GSM analyses highlighted *Wickerhamomyces anomalus* as essential for all consortia. *Pichia membranifaciens* exhibited strong stress tolerance, while *Candida diddensiae* was included based on its predicted functional role in the community. Pilot-scale fermentations were performed using Taggiasca olives (*Olea europaea* L., cv. *Taggiasca*) harvested in Liguria (Oct 2024). Twenty-four fermenters (∼20 kg each) were set up using two brines (6% and 10%). Three yeast-based consortia were inoculated in triplicate (∼10^6 CFU), one of which also included *Lactiplantibacillus plantarum O2*. Uninoculated controls were included. Fermentations were monitored over 160 days. Preliminary results indicate that fermentation was primarily yeast-driven, consistent with the strain selection strategy. However, fermentation timelines remained comparable to traditional processes (5–8 months), suggesting no significant acceleration under current conditions. MALDI-ToF MS confirmed a predominance of the inoculated species, and metabarcoding analyses revealed that salt concentration strongly shaped the microbial community, with higher salinity reducing microbial diversity and competition.

PS2-S6-PP08 Studying interactions of foodborne xenobiotics and the human intestinal microbiome: An *in vitro* approach

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Foodborne xenobiotics, i.e. substances foreign to the human body and ingested through food (such as natural toxins and residues of plant protection products), can enter the body via dietary exposure. Depending on their toxicokinetics, these xenobiotics can reach and interact with intestinal microbiota. These interactions can be bi-directional. One way is when a substance is metabolized or degraded by the microbiota, thereby affecting its bioactivity or toxicity. The other way is when a substance affects the composition or function of the microbiota, potentially contributing to dysbiosis. Previous work showed chemical metabolism can be studied and quantified by using small batch *in vitro* fermentation approaches with human fecal material. In this project, we aim to further develop this approach to allow studying of the adverse and beneficial effects of foodborne xenobiotics on the function of the human intestinal microbiota. To this end, targeted, suspect, and non-targeted approaches using high-resolution mass spectrometry (HRMS) will be used to study functional outcomes in fecal incubations, and combined with genomic readouts. Fecal material of 27 healthy individuals was collected and processed in anaerobic storage buffer. Relevant microbial metabolites and markers of metabolic processes (N=43) were selected and used to develop and optimize an analytical method employing a Waters UPLC BEH C18 column coupled to a Thermo Scientific Orbitrap IQ-X Tribrid mass spectrometer, successfully detecting 21 compounds. Different concentrations of the target compounds (0.05-125 ng/mL) were tested in solvent and in varying concentrations of pooled human fecal material (0.0125-0.25 g/mL) to evaluate matrix effects. Most compounds could be detected at concentrations as low as 1 ng/mL, and a fecal concentration of 0.0625 g/mL provided the best compromise between detectability and minimal matrix effects. Additionally, a database of over 7,000 human fecal metabolites and *in silico* predicted biotransformation products of the targeted compounds was built and used to perform suspect screening, as well as to support compound identification in the non-targeted analysis. The next steps will involve conducting further *in vitro* experiments with foodborne xenobiotics, and genomically profiling the microbiome. Eventually, the suitability of the developed *in vitro* methodology based on functional readouts will be evaluated for its applicability in *in vitro* safety testing strategies.

PS2-S6-PP09 The impact of the intake of partly fermented infant formula with 2'-FL, 3'-GL and bovine milk fat on the composition and functional properties of infant gut microbiome: Preliminary results

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Introduction: Human milk contains a rich array of bioactive components, that supports microbiota development, including over 200 different human milk oligosaccharides (HMOs), such as 2'-fucosyllactose (2'-FL) and in much lower amounts galactosyllactoses (GLs). Bovine milk fat, naturally rich in sn-2-palmitate, like human milk, is increasingly added to infant formulas. High sn-2 palmitate as well as HMOs and scGOS/lcFOS have demonstrated bifidogenic effect. Their utilization and impact on the gut microbiota development is not fully understood. Therefore this research aimed to compare the composition and functional properties of gut microbiota in infants fed breast milk or infant formula with (T) or without (C) added 2'-FL, 3'-GL and bovine milk fat.

Methods: In a randomized, controlled, double-blind trial infants (30 in each arm) were assigned at birth to receive either control formula (C), the test formula (T) or were breastfed (BF). Both formulas contained prebiotics. Fecal samples were collected from 17 week old infants. Microbial composition was analyzed using metagenomic sequencing. Functional profiling was done using HUMAnN 3.0.1 pipeline and metaproteomic analysis using MaxQuant.

Results: BF infants had the lowest relative abundance of *Enterococcus* genus, including *Enterococcus casseliflavus* species and also *Bifidobacterium* genus (38.5 ± 31.9 %) comparing to C (68.0 ± 29.2%) and T (64.7 ± 23.6%). T group had the highest relative abundance of *Intestinibacter*, including *Intestinibacter barletti*. Fucose degradation pathway was enriched in the microbiome of BF infants.

Conclusion: This project will help elucidate the role of the combination of 2'-FL, 3'-GL and bovine milk fat in the establishment of microbiome composition and its activity in infants.

PS2-S6-PP10 Differential carbohydrate fermentation in children with severe malnutrition: Recovery stage influences *in vitro* inulin utilisation

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Malnutrition remains a serious public health concern in low- and middle-income countries and a major contributor to global childhood mortality. Currently used milk powder-based recovery strategies to treat children with severe acute malnutrition (SAM) show mixed outcomes with high mortality and readmission rates. Evidence suggests that children with SAM have a disrupted gut microbiome and altered gut barrier function. It is hypothesised that using appropriate dietary carbohydrate could enhance gut microbial health and consequently improve overall treatment outcome. Therefore, we tested the fermentability of commonly consumed carbohydrates using an *in vitro* batch model inoculated with faecal samples from SAM children. Four carbohydrate substrates were tested: (i) inulin–a commonly used prebiotic, (ii) chickpea–a locally grown and cost-effective ingredient, (iii) infant formula enriched with human milk-like oligosaccharides–to mimic human milk, and (iv) infant formula–to reflect the current treatment regimen. We demonstrated that while the milk powders and chickpea feed were fermented to produce short-chain fatty acids, inulin was only fermented to a very limited degree, suggesting that the latter is not suitable for SAM recovery. Further to confirm if poor fermentation of inulin is a result of a disrupted gut microbiome in SAM children, we examined the fermentability of inulin using a miniaturised *in vitro* batch system inoculated with paired faecal samples collected on day 7 and day 90 post-hospitalisation (representing sick and partially anthropometrically recovered cohorts, respectively). Samples from the partially anthropometrically recovered cohort exhibited higher microbial diversity and higher abundance of GH32 enzyme class, resulting in higher fermentation of inulin compared to the sick cohort. These findings will be of use for the design of future therapeutic feeds for the treatment of SAM by supporting the gut microbiome.

PS2-S6-PP11 Antioxidant characterisation of Murciano-Granadina goat milk kefir

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The Murciano-Granadina is a Spanish dairy goat breed, valued for its adaptability to arid Mediterranean environments and for producing milk of high nutritional quality. Despite its relevance for artisanal cheese and fermented milk production, there is limited information on the microbial composition and functional potential of its milk. In this study, raw milk samples were collected from six farms in the Campo de Cartagena region (Spain) and analysed using Illumina 16S rRNA sequencing to characterise bacterial diversity and composition. The milk was then fermented with commercial kefir grains, and changes in microbial structure and antioxidant capacity were assessed.

Kefir fermentation significantly modified the native microbiota, increasing overall bacterial richness and promoting the dominance of lactic acid genera such as *Lactobacillus*, *Leuconostoc*, and *Acetobacter*. These microorganisms are known to produce bioactive compounds that contribute to the health-promoting properties of fermented products. The antioxidant capacity of both raw and fermented milk was evaluated using FRAP (Ferric Reducing Antioxidant Power) and TEAC (Trolox Equivalent Antioxidant Capacity) assays. Both tests showed a clear enhancement in antioxidant activity following fermentation, indicating that kefir microorganisms increase the production or release of compounds with reducing and radical-scavenging properties. This work provides the first comprehensive characterisation of the microbial community and antioxidant properties of kefir produced from Murciano-Granadina goat milk, highlighting its potential as a functional dairy product with added nutritional value.

PS2-S6-PP12 Impact of green tea polyphenols on sourdough fermentation: Implications for gluten detoxification and microbial activity

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Celiac disease (CD) is a chronic gluten-triggered enteropathy for which a strict gluten-free diet remains the only treatment, yet its prevalence continues to rise. Microbial strategies—particularly food fermentation—have emerged as promising tools to detoxify gluten, modulate the gut microbiota and even dampen immune responses. Traditional sourdough fermentation, driven by lactic-acid bacteria (LAB) and yeasts, not only improves bread flavor and nutrition but can also enhance antioxidant capacity and promote partial gluten degradation.

Polyphenols add a second line of intervention: they possess antioxidant and anti-inflammatory properties, can bind gliadin and lower the accessibility of immunogenic peptides, and are known to influence microbial ecology. Combining sourdough fermentation with polyphenol supplementation therefore offers a novel, double-action approach for mitigating gluten toxicity.

Using the heritage wheat cultivar Caaveiro, sourdoughs were prepared with tap water, flour, and graded levels of a green-tea polyphenol-rich extract (GTE; 0–10% w/w). Fermentations were refreshed until pH stabilized; LAB were enumerated on MRS agar. Protein alterations were tracked via SDS-PAGE/Western blot, gliadin immunoreactivity quantified by competitive ELISA, antioxidant capacity by DPPH, and phenolic profiles by LC-MS/MS.

Rising GTE concentrations consistently lowered gliadin recognition in ELISA, indicating reduced immunogenicity, and boosted antioxidant capacity beyond fermentation alone. At the same time, very high polyphenol levels appeared to impede microbial gliadin breakdown, likely through polyphenol–protein complexes that restrict enzymatic access.

Moderate enrichment of sourdough with green-tea polyphenols synergistically reduces gliadin immunogenicity and elevates antioxidant activity, highlighting a promising dual strategy for developing bread better suited to individuals at risk for celiac disease.

PS2-S6-PP13 Snack your way to a healthier gut: Impact of dietary fibre accessibility on the gut microbiome

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Aim: A global shift towards low-fibre foods has contributed to declining fibre intake and a rise in gut-related diseases. Unlike digestible carbohydrates, dietary fibre reaches the colon intact, where it is fermented by the gut microbiome to produce metabolites that regulate appetite and support gut health. This research aims to develop vegetable-incorporated, fibre-rich snack foods using novel processing technologies in collaboration with our industrial partner, PepsiCo. We investigate how processing affects the molecular structure, digestibility, fermentability, and microbial metabolism of the fibre-enriched products, as well as the microbiome composition.

Method: Vegetable-incorporated snacks were produced using two processing methods: conventional oven cooking and microwave-assisted drying. Digestion assays were carried out mimicking the upper gastrointestinal tract, and the resulting digesta was then fermented in an in vitro colon model. Metabolomic analysis of the fermentation products was conducted, as well as the changes in gut microbiome composition associated with vegetable-incorporated snack consumption.

Results: Our results show that incorporating vegetables into snack foods reduces their digestibility, lowering the release of reducing sugars during in vitro digestion, suggesting a lower glycaemic response. Solid-state NMR revealed changes in starch and fibre crystalline structure following digestion and structural rearrangements within the food matrix. These structural modifications also influence colonic fermentation, resulting in distinct metabolite profiles and promoting a shift in the gut microbiome towards a healthier community structure. Notably, the novel processing method, particularly when combined with wheat flour, further reduces digestibility by altering the food matrix, enhancing fibre functionality and delaying carbohydrate breakdown.

Conclusion: We have explored novel processing techniques to incorporate large quantities of vegetable purées into snack foods, that not only improved nutritional quality but also positively influence gut microbial activity. These snacks also showed increased fibre content, supporting gut health and overall well-being. These findings highlight an innovative approach to designing healthier, more sustainable food products that support both human and environmental health.

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PS2-S6-PP14 Prebiotic potential of seed mucilages and their impact on the host (adult and toddler's) gut microbiome.

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This study examined the impact of seed mucilages on gut microbial communities and their implications for gut health in toddlers (6–24 months) and adults. Mucilages were extracted from chia, fenugreek, basil, mustard, and flaxseeds and assessed for prebiotic potential through an amylase degradation assay and their ability to stimulate probiotic growth (*Bifidobacterium* and *Lactobacillus*). Rich in non-digestible carbohydrates, the mucilages promoted probiotic proliferation. Their effects on gut communities were evaluated using an in-vitro fecal fermentation model combined with 16S rRNA sequencing and measurement of short-chain fatty acids (SCFAs; butyrate, propionate, and acetate). Mucilage-treated samples displayed significantly elevated SCFA production, a key factor in gut and systemic metabolic health. Microbiome profiling revealed increases ($p < 0.05$) in beneficial fiber-degrading and SCFA-producing taxa, including *Lachnospiraceae* and *Butyricicoccus*, alongside a reduction in pro-inflammatory *Escherichia–Shigella*. Mustard seed mucilage uniquely enhanced *Bifidobacterium* abundance in both adults and toddlers. In addition, mucilage exposure modulated microbial pathways related to growth and amino acid synthesis, strongly correlating with the altered microbial composition. Fenugreek and mustard seed mucilages were particularly effective at suppressing members of the *Proteobacteria* phylum and *Escherichia–Shigella* genera. Based on these findings, fenugreek and mustard seed mucilages were selected for further analysis. Their structures were characterized by scanning electron microscopy (SEM), and ongoing animal studies aim to elucidate their potential benefits against metabolic disorders. Overall, this work highlights seed mucilages as promising prebiotic agents for improving gut microbiome composition and related metabolic outcomes.

Keyword: Prebiotic, Seed mucilage, Gut microbiome, Obesity, Diabetes.

PS2-S6-PP15 *Lactococcus lactis subsp. lactis 1 TIP4,* a newly discovered lactic acid bacterium derived from fermented *Mesembryanthemum crystallinum*, boosts immunity and decreases inflammation in immune cells

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Introduction: Probiotics derived from plants are increasingly recognized for their potential health-promoting properties, including antioxidant and immunomodulatory functions. However, new candidate strains with robust gastrointestinal tolerance and immune-regulatory activity remain to be identified. This study aimed to isolate lactic acid bacteria from Iceplant (*Mesembryanthemum crystallinum*) and evaluate their probiotic properties, focusing on antioxidant capacity, gastrointestinal tolerance, adhesion ability, and immunomodulatory activity.

Methods: Three isolates were identified as *Lactococcus lactis subsp. lactis* by RAPD, Gram staining, and scanning electron microscopy (SEM). Carbohydrate utilization, antioxidant activity, gastrointestinal tolerance, and adhesion to Caco-2 intestinal epithelial cells were assessed. Immunomodulatory effects of the most promising isolate (TIP-4) were evaluated in RAW264.7 macrophages and murine splenocytes by MTT, LDH assays, qPCR, ELISA, and flow cytometry.

Results: TIP-4 showed no cytotoxicity toward murine splenocytes or RAW264.7 macrophages at the tested concentrations. In splenocytes, TIP-4 suppressed Th1 (IFN-γ), Th2 (IL-4, IL-5), Th17 (IL-17), and TNF-α responses at both protein and transcriptional levels. In macrophages, TIP-4 enhanced iNOS expression while downregulating COX-2, IL-1β, and IL-6 but not TNF-α, indicating a dual role in promoting antimicrobial defense and limiting excessive inflammation.

Conclusions: These findings demonstrate that TIP-4 exerts balanced immunomodulatory effects by dampening overactive T-lymphocyte responses while selectively modulating macrophage activation, suggesting its potential as a therapeutic candidate for inflammatory and autoimmune disorders.

PS2-S6-PP16 Yeast probiotic for gut health: From *in vitro* model to clinic

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The gut microbiome plays a crucial role in maintaining overall health in humans and pets. Dysbiosis (imbalanced microbial communities) is often associated with various gastrointestinal (GI) disorders characterized by recurrent abdominal pain representing a significant clinical challenge. Probiotics have emerged as a promising solution for restoring gut homeostasis.

Herein, we investigated the effects of *S. cerevisiae* based probiotic intervention on gut health, using advanced *in vitro* models to simulate both human and canine gut environments (CNCM I-3856 for human and CNCM I-5660 for dog). We employed the Simulator of Human Intestinal Microbial Ecosystem (SHIME) and the Simulator of Canine Intestinal Microbial Ecosystem (SCIME) to evaluate species-specific yeast probiotic formulation. We monitored microbial composition, short-chain fatty acid (SCFA) production, and intestinal barrier functioning. Then *in vitro* results obtained were further compared to existing clinical evidence conducted in IBS-C (Irritable Bowel Syndrome with constipation) patients or healthy dogs submitted to antibiotic challenge. The *in vitro* findings showed an increase in beneficial bacteria belonging to the families *Bacteroidaceae* and *Bifidobacteriaceae*. Especially, for the *in vitro* human studies, we observed an increase in the total SCFA, particularly butyrate.

Regarding *in vivo* studies, a significantly higher proportion of abdominal pain responders was reported in IBS-C patients taking yeast probiotics compared to placebo group. After 8 weeks of supplementation, the overall quality of life score was significantly higher in the probiotic group than in the placebo group. In our canine studies, following antibiotic-induced dysbiosis, dogs receiving the probiotic maintained a more favorable microbiota composition with higher abundances of beneficial bacteria compared to controls.

Our comprehensive *in vitro* and *in vivo* findings demonstrate that *S. cerevisiae* yeast probiotic effectively modulates gut microbiota composition in both human IBS-C patients and dogs with stress-related profiles. Additionally, IBS-C patients had improved GI symptoms and enhanced quality of life. The consistent results between the *in vitro* models and the clinical studies validate this preclinical strategy as valuable tool for probiotic research and support the *S. cerevisiae* yeast probiotic as a promising therapeutic agent for GI disorders linked to dysbiosis in both humans and companion animals.

PS2-S6-PP17 Impact of the wheat production system on its nutritional properties and the gut microbiome

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The TRIBIOME project aims to improve the wheat productivity and nutritional quality of wheat-derived foods through strategies based on soil and plant microbiome modulation. One of its key objectives is to evaluate the nutritional composition of wheat flour and its effect on the gut microbiota, as well as potential implications for animal and human health. This multidisciplinary project, involving collaboration among 13 institutions, is funded by the European Union under the Horizon 2020 programme. Its overall goal is to enhance the sustainability and quality of wheat production and its characteristics.

The first trials were conducted on potted wheat, using fertilisers and microbial modulators, to obtain preliminary results informing subsequent large-scale trials in fields. The effects of biostimulants have been evaluated by analysing the physico-chemical parameters of the resulting flours. Preliminary findings from pot trials indicate a significant increase in protein content following the application of fertilisers and modulators, along with higher levels of minerals such as calcium and phosphorus when a modulating microbial strain was used.

Subsequently, field trials have been carried out to validate these pot-based findings at a large scale. The nutritional properties of field-grown wheat and wheat-derived foods are being analysed, alongside assessments of their impact on the gut microbiota. For this, *in vitro* gastrointestinal models simulating human digestion are employed to evaluate microbiota composition and function through next-generation sequencing (NGS) and metabolomic analyses. Functional effects on immune and endocrine responses will also be investigated using in vitro cell models.

Wheat with improved nutritional profiles could have high added value, contributing both to human and animal health and to environmental sustainability by protecting the soil and mitigating climate change impacts.

Keywords: Improved food, wheat, modulators, gut microbiota, microbiome connectivity

PS2-S6-PP18 Simulating the impact of drinking water microbiomes on the human gut microbiome

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Microbiomes residing in different environments have been studied one at a time with little focus on the impact of microbiome transfer from one ecosystem to another. For example, drinking water is a vehicle of microorganisms to the human gut. It is widely known that the microorganisms colonizing the gastrointestinal tract, the gut microbiome, heavily influence human physiology and susceptibility to disease via their metabolic activities and host interactions. However, the impact of drinking water microbiomes on the human gut microbiome is largely unexplored. The microbial community in Dutch drinking water is predominated by low nucleic acid (LNA) bacteria, which are hypothesized to support the biostability of water. However, environmental conditions such as high temperature during drinking water distribution promotes the growth of high nucleic acid (HNA) bacteria accompanied by a significant change in the overall bacterial composition. This study investigates the impact of consuming LNA-rich or HNA-rich drinking water on the composition and function of the human gut microbiome. *In-vitro* simulated gastrointestinal digestion revealed that a portion of the drinking water bacteria can withstand the harsh conditions of the gastrointestinal tract, suggesting that certain drinking water bacteria may indeed reach the gut microbiome. An *in-vitro* batch fermentation model was used to simulate drinking water consumption and monitor changes in the human gut microbiome composition and function. Overall, the results of this study may further guide efforts of improving water treatment and distribution methods by better understanding how certain drinking water microbiomes impact human health via the gut microbiome.

PS2-S6-PP19 "Missing microbes": Systematically understanding gut microbiome compositional and functional differences across populations

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The microbiome is a key driving factor of health and disease, connecting all life ecosystems from soil to plants to humans. In the last decades, human environmental and lifestyle factors (e.g., diet, hygiene, delivery mode, exposure to pollutants) have undergone notable changes, resulting in a loss of microbiome diversity, which has been linked to the rising prevalence of non-communicable diseases (NCD). Conversely, indigenous populations have a low incidence of NCD and higher microbiome diversity, suggesting that environmental exposure plays a key role in human health. Restoring microbiome diversity may potentially contribute to alleviating NCD pathogenesis. Probiotic administration could be one of the solutions to restore the microbiome. Applying metagenomic technologies and meta-analysis methodologies, which enable systematic identification of microbiome alterations and its functionalities across cohorts could help improve the development of new probiotic formulations. Recent meta-analyses identified microbiome signatures across various diseases. However, most studies did not consider microbiome gene functions, included few diseases and samples, and did not consider indigenous populations. As such, the objectives of this project are: 1) to systematically study composition and functional alterations across diseases from a wide range of human gut metagenomes, and 2) to understand whether diseased depleted microbiome signatures ("missing microbes") are associated with a Western lifestyle. We collected more than 4000 publicly available human gut metagenomes, including immune-mediated diseases, metabolic disorders, healthy Western and indigenous cohorts from diverse studies, population groups, and geographic locations. We analyzed microbiome taxonomic and functional diversity between cases and controls, identifying species and functional traits associated with both health and disease. Overall, we found significant differences in diversity between cases and controls for some diseases, with Crohn´s disease and Non-alcoholic fatty liver disease showing the strongest effects. Furthermore, several species and ortholog genes were significantly associated with disease in most cohorts, and many features overlapped multiple disorders. Overall, this work provides a systematic analysis of microbiome composition and functional features linked to human disease that may be useful to identify potential targets for probiotic research.

PS2-S6-PP20 Model-based insights into the potential probiotic role of *Flavonifractor plautii* for gut microbiota modulation

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Flavonifractor plautii is a prevalent gut commensal with the unique ability to degrade dietary flavonoids while producing beneficial short-chain fatty acids (SCFAs), notably butyrate and propionate. Despite its widespread presence, its metabolic capabilities and ecological functions remain underexplored. To investigate its probiotic potential, we developed a genome-scale metabolic model (iFP655) using automated reconstruction, deep-learning-assisted gap-filling, thermodynamic constraints, and transcriptomic integration. Compared to previous models, iFP655 showed improved predictions of growth rates and SCFA outputs. Simulations revealed that *F. plautii* primarily uses acetyl-CoA pathways for butyrate production, while the energetically costly lysine pathway remained inactive despite strong gene expression. Propionate synthesis was mediated mainly via the methylmalonyl-CoA pathway. Community modeling with representative taxa of a Western minimal gut microbiota highlighted *F. plautii*'s role in enhancing butyrate levels, supporting amino acid metabolism, and participating in diet-dependent syntrophic interactions. These results underscore the ecological relevance of *F. plautii* and support its potential use as a probiotic to promote gut health through targeted dietary interventions.

PS2-S6-PP21 PROBIOGENOMIC approach to discover novel pro- and psychobiotic strains

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This study proposes that targeted psychobiotic dietary strategies and multi-omics approaches offer a holistic solution for cognitive impairment. A metagenomic analysis of 1185 food metagenomes, focusing on fermented foods, revealed that genes for neurotransmitter-related pathways were enriched, particularly in cheeses. Genomic screening of 74 Lactic Acid Bacteria (LAB) strains, informed by comparative analysis showing psychobiotic potential in species like *Levilactobacillus brevis, Lactiplantibacillus plantarum, and Limosilactobacillus fermentum*, confirmed species-specific genomic patterns for GABA, acetylcholine, serotonin, and catecholamine pathways. Four strains (*Lp. plantarum* (TO06), *Lm. fermentum* (TO24), *Lv. brevis* (TO10), and *Lentilactobacillus diolivorans* (B92)) were selected as the most promising candidates for mental health supplements after in vitro functional screening (LC-HRMS) and successful testing in a plant-based matrix. The efficacy of a psychobiotic composite (YL) containing these strains was tested in a M-SHIME® model simulating the gut microbiome of a depressed patient. Treatment significantly increased the relative abundance of Lv. brevis and *Lm. fermentum* in both the lumen and mucosa, with Lv. brevis demonstrating a capacity for mucosal persistence after washout. Crucially, the YL treatment significantly inhibited potentially harmful taxa (*Acidaminococcus intestini* and *Megasphaera massiliensis*) in both compartments, with the inhibitory effect persisting into the washout phase. These results suggest that the YL treatment can modulate and partially restore the dysbiotic gut microbiome, representing a key mechanism for improving the gut-brain axis in depressed individuals. This study successfully provides a comprehensive probiogenomics pipeline for identifying and validating novel psychobiotic strains.

PS2-S6-PP22 The food-gut microbiome axis: exploring the potential of fermented foods to restore gut microbiome diversity

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Over recent decades, the progressive Westernization of lifestyle, together with the decrease in overall microbial exposure linked to hygiene practices typical of industrialized societies, has profoundly reshaped the human gut microbiome. A consistent body of evidence indicates a marked loss of microbial diversity in industrialized populations compared to rural or traditional communities, associated with the global rise of diet-associated chronic diseases such as obesity, type 2 diabetes, and inflammatory disorders. Fermented foods (FFs) represent one of the most relevant and complex sources of live microorganisms in the diet. FFs harbour diverse microbial communities capable of transiently or permanently interacting with the host gut microbiome. The DOGMA project aims to elucidate the role of foodborne microorganisms in modulating the gut microbiome structure and functionality, exploring whether the consumption of FFs with high microbial diversity can restore gut microbial diversity and improve host health status. A multidisciplinary strategy combining metagenomics, metabolomics, and a nutritional intervention will be adopted. Three main activities are foreseen: (i) mapping the microbiome of traditional non-Westernized FFs and of their habitual consumers, to understand if the consumption of foods with higher microbial diversity is associated with a positive gut microbiome balance. (ii) In vitro gastrointestinal simulations will be employed to discriminate between the direct effects of viable microbial cells and the indirect, postbiotic effects of fermentation-derived metabolites, and to define the threshold dose of live microorganisms required to induce measurable changes in gut microbiome composition and metabolome. (iii) A randomized controlled trials in obese/type-2 diabetic subjects will be carried out to assess the impact of the consumption of a diet rich in FFs. DOGMA will clarify the extent to which dietary microbes contribute to the resilience and functional recovery of the gut microbiome and will provide a mechanistic framework to design evidence-based nutritional strategies aimed at counteracting the loss of microbial diversity.

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PS2-S6-PP23 Gut microbiota as a novel strategy to support fertility and hormonal equilibrium in endometriosis and polycystic ovary syndrome (PCOS)

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Introduction: The gut microbiota acts as an endocrine-like organ regulating metabolism, immunity, and hormonal balance. Dysbiosis alters estrogen metabolism, increases androgen excess, and promotes inflammation, which are mechanisms central to polycystic ovary syndrome (PCOS) and endometriosis. The estrobolome, encoding β-glucuronidase, controls enterohepatic estrogen recirculation; its hyperactivity may contribute to hyperestrogenism and endometrial proliferation. Modulation of the microbiota through diet, probiotics, and lifestyle is proposed to help restore hormonal and metabolic homeostasis.

Objectives: To assess the relationship between gut microbial composition and hormonal–metabolic dysregulation in PCOS and endometriosis, evaluate microbiota-targeted interventions, and propose an integrative therapeutic framework combining nutritional, physical, and psychological strategies.

Methods: A PRISMA-based review (2014–2024) of PubMed, Scopus, and Google Scholar identified 21 of 369 studies (12 on PCOS, 6 on endometriosis, 3 translational) analyzing microbiota diversity, hormonal and inflammatory parameters, and dietary, probiotic, and lifestyle interventions.

Results: Women with PCOS showed reduced microbial diversity, depletion of *Akkermansia* and Ruminococcaceae, and enrichment of *Bacteroides* and *Escherichia/Shigella*, correlating with higher testosterone and BMI. Probiotic, prebiotic, dietary, and lifestyle interventions improved insulin sensitivity, lipid metabolism, and hormonal balance while enhancing SCFA-producing bacteria and reducing inflammation. In endometriosis, an altered Firmicutes/Bacteroidetes ratio and Ruminococcaceae loss were associated with inflammation; animal models suggested that fecal microbiota transplantation (FMT) may alleviate pelvic pain and restore microbial balance. Dietary fiber, omega-3 fatty acids, vitamin D, and N-acetylcysteine increased SCFA production and supported hormonal equilibrium. Physiotherapy and psychotherapy modulated the gut–brain–hormone axis, reduced oxidative stress, and improved reproductive outcomes.

Conclusions: The gut microbiota is a key regulator of female fertility and endocrine health. Interventions that restore eubiosis through diet, probiotics, and psychosomatic support show strong potential for re-establishing hormonal and metabolic balance. Emerging approaches such as FMT and personalized microbiome-based therapies warrant further investigation as innovative strategies in hormonal and reproductive medicine.

PS2-S6-PP24 Unveiling the microbiome of PDO Halloumi cheese: A combined culture-dependent and metagenomic approaches

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Halloumi is a traditional and unique cheese produced in Cyprus for centuries and its popularity has significantly risen over the past years especially after granted a Protected Designation of Origin (PDO) status by the European Union. It has been produced locally from raw ovine milk or caprine milk and mixtures of these milks with bovine. Despite the PDO status of Halloumi, very few studies have addressed its properties, including its microbiology especially for the mature cheese. For this reason, the microbiome of PDO Halloumi cheese samples during their maturation period were investigated. In this study twelve samples of Halloumi PDO cheeses during maturation period for 90 days were analyzed, by microbiological analyses along with state-of-the art metagenomics. The identification and characterization of the Halloumi microbiome constitute an important approach for defining the typicity of this PDO cheese, providing a means of authentication to safeguard against fraudulent products, while simultaneously offering insights that can aid producers in enhancing product quality and ensuring consumer safety. Moreover, detailed profiling of bacterial communities in cheeses with protected designation of origin status is particularly significant, as these microorganisms play a critical role in shaping the final organoleptic properties, in ripening process, and shelf life. Furthermore, understanding the cheese microbiome is also essential from a nutritional and health perspective, as microbial communities can influence the bioavailability of nutrients, the presence of bioactive compounds, and potential probiotic effects that contribute to consumer well-being.

PS2-S7-PP01 Microbiological food safety: risk mitigation of foodborne pathogens by applying omics approaches within the food system

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Pathogenic microorganisms in food pose a risk to consumer health. Traditionally, to uncover outbreak routes and/or microbiological control measures, culture-dependent methods have been implemented routinely. However, the detection of pathogenic bacteria throughout the food chain is often limited by various challenges. In consequence, the integration of culture-independent methods, such as Next Generation Sequencing (NGS), into food safety practices has provided the improved resolution that was missed. Nevertheless, gaps related to detection limits, absolute estimates, and intraspecies dynamics must be addressed to refine effectively the integrated approach.To address these challenges, five serotype-source-diverse strains of *Listeria monocytogenes* were selected to create a cocktail master mix. Individual growth performance parameters were evaluated to avoid any bias when culturing together. Different selective enrichment cultures of raw minced meat inoculated with the cocktail mix were prepared, following the ISO 11290:1 standard method. Growth curves of the enrichment samples, comprising a 10-fold dilution inoculum, were established by counting colonies on selective agar to accurately determine the cell concentration and growth dynamics of each sample over the 48-hour enrichment period. The integration of DNA-based amplicon sequencing and metagenomics was conducted at three time points (T0, T10, T48) of the enrichment process. Preliminary results of shotgun metagenomics sequencing showed that *L. monocytogenes* was detectable in the sample with the highest inoculum concentration at T0 (10^6 CFU/g). By the end of the process, it was detected in all samples, with varying proportions that effectively reproduced the initial serial dilution inoculum. Additionally, to determine changes in the proportions of the different strains over time during enrichment and after culturing on selective agar, *L. monocytogenes* colonies were randomly selected from the plates along the whole enrichment process and fingerprinted by REP-PCR. A total of 558 colonies were analysed. There was a noticeable trend of higher presence of certain patterns at the beginning of the process, followed by similar proportions at the 24-hour mark, and a decrease in the most abundant ones during the final stage.Further analysis will be performed to assess intraspecies dynamics through metagenomics analysis and correlate viable counts with the sequencing-based data to elucidate the best approaches when integrating NGS into food safety protocols.

PS2-S7-PP02 Human-derived *Lactobacillus* postbiotics as biopreservatives in functional food development: antifungal efficacy and metabolomic profiling

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Food safety remains a global concern, particularly due to mycotoxin contamination, emphasizing the need for effective fungal control strategies in food processing. The growing demand for natural, clean-label preservatives and health-promoting products highlights the importance of identifying novel food biopreservatives.

The aim of this study was to evaluate the antifungal activity of human-derived *Lactobacillus* strains against major food-spoiling *Penicillium* species and to identify key metabolites contributing to their bioactivity using a metabolomic approach. Thirteen lactic acid bacteria strains were isolated from maternal-infant microbiota (saliva, feces, and areolar skin) and identified as *Lactiplantibacillus plantarum* (11 strains) and *Lacticaseibacillus paracasei* (2 strains). Antifungal activities were assessed by overlay assays, agar diffusion tests, minimum inhibitory concentration (MIC), and minimum fungicidal concentration (MFC) against ten *Penicillium* species (*P. roqueforti*, *P. chrysogenum*, *P. verrucosum*, *P. expansum*, *P. citrinum*, and *P. crustosum*, among others). Furthermore, an untargeted metabolomic analysis using HPLC-Q-TOF-MS/MS and GC-MS/MS was conducted on cell-free supernatants. Antimicrobial tests and fermentations were performed in MRS and Cultiply media (a food-grade fermentation medium) at 24 h and 48 h.

Despite the inherent resistance of *Penicillium* species, most bacterial strains demonstrated moderate antifungal activity, which was enhanced in Cultiply medium. Notably, *L. plantarum* FP10-CO8 and SP8-CO6 exhibited strong inhibition against *P. roqueforti*, *P. chrysogenum*, and *P. verrucosum*. SP8-CO6 completely inhibited *P. chrysogenum* and *P. verrucosum*. FP10-CO8 inhibited *P. roqueforti* and *P. chrysogenum* with inhibition zones of 6.7 mm and 18 mm, respectively. These effects correlated with high production of antifungal compounds, including lactic acid, acetic acid, 3-phenyllactic acid, 4-hydroxyphenyllactic acid, and phenolic acids. Metabolic profiles varied significantly between media, while fermentation time influenced profiles only in MRS. Additionally, the strains produced probiotic-associated metabolites such as short-chain fatty acids, vitamins, and indole derivatives (e.g., indole-3-acetate, indole-3-lactic acid).

These findings support the potential application of human-derived *L. plantarum* strains as postbiotics for food preservation, offering an alternative to chemical preservatives while enhancing the functional value of foods.

PS2-S7-PP03 Microbial composition and pathogen resistance in Sauerkraut: Effects of farming practice, potato peel, and fermentation stage

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Recent socio-economic conditions and the latest health and wellness trends have sparked a renewed interest in homemade fermented vegetables. Sauerkraut, a traditional spontaneously fermented food product, is popular among fermentation enthusiasts globally. Its microbial complexity and lactic acid bacteria (LAB) content are shaped by a variety of factors and can have an effect on the safety of the final product. In this study, we examined how conventional versus organic cabbage and the addition of potato peel influence LAB counts and microbial diversity at days 14 and 21 of the fermentation. All treatments were also tested for their susceptibility to the growth of Listeria monocytogenes, a human bacterial pathogen using a surrogate challenge test. Additionally, we tracked the presence of two key LAB species associated with early and late fermentation stages: Leuconostoc mesenteroides and Lactiplantibacillus plantarum. The potato peel addition slightly boosted LAB counts until day 14, while at day 21, conventional cabbage treatments with potato peel showed significantly higher LAB counts than their organic counterparts. The microbial community composition at day 21 differed notably between organic and conventional sauerkraut, whereas the peel additive did not affect overall microbiota structure. Distinct taxa such as Pediococcus in organic samples and Nissabacter and Bacillus in those with added peel suggest a strong influence of the starting material on the final microbiome. Furthermore, some microorganisms may remain below the detection limit in the starting material but can proliferate during fermentation, occupying newly formed ecological niches.

This work as part of project FoodSafeR has received funding from the European Union's Horizon Europe Research and Innovation Programme under Grant Agreement No. 101060698.

PS2-S7-PP04 The cell surface-associated rhamnose-glucose polysaccharide represents the receptor of *Streptococcus thermophilus* bacteriophage P738

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Streptococcus thermophilus is a key lactic acid bacterial species extensively used in dairy fermentations, where bacteriophage (phage) infections pose a significant threat to production efficiency. While the cell surface receptors for four of the five currently known streptococcal phage genera have previously been identified, the specific host-encoded receptor for the P738 phage group has not been elucidated to date. In this study, P738 bacteriophage-insensitive mutants (BIMs) of *S. thermophilus* UCCSt50 were isolated, and whole-genome sequencing revealed mutations in a glycosyltransferase-encoding gene within the *rgp* locus, responsible for biosynthesis of the cell wall-associated rhamnose-glucose polysaccharide (RGP). Compositional and methylation analysis demonstrated that loss of a terminal rhamnose residue from the RGP side chain underpinned the observed resistance to P738 binding and infection. Fluorescent binding assays validated the biological functionality of the predicted receptor binding protein (RBP) of P738, confirming the critical role of the RGP side chain in phage adsorption. These findings reveal a strict requirement for a complete tetrasaccharide side chain structure for P738 binding, contrasting with the less stringent requirements observed for the *Brussowvirus* SW13. This work bridges a key knowledge gap in dairy streptococcal phage biology and offers valuable insights to guide the development of phage-robust starter cultures, thereby supporting more sustainable and reliable dairy fermentation processes.

PS2-S7-PP05 Strategies for microbiome mapping in raw milk cheese: Findings from a pilot study

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In this pilot study, the microbiomes of 28 samples from the same cheese batch and 3 environmental samples were characterized. The cheese batch samples included raw milk (*n*=3), heated milk (*n*=1), curd (*n*=3), milk serum (*n*=3), brine liquid (*n*=1), post-stewing cheese (*n*=1), post-brine cheese (*n*=1), post-anti-mold cheese (*n*=1), and cheese after 7, 15, 30, 45, 60, 75 and 90 days of ripening, tested both internally (1 sample per time point) and on the rind (1 sample per time point). The three environmental samples were collected from floor drain swabs in the production area (1 pool of 5 swabs) and from the cheese ripening boards at 3 and 75 days. All collected samples were subjected to DNA extraction, library preparation and shotgun sequencing.

Lactococcus, *Pseudomonas* and *Acinetobacter* represented the dominant genera in the microbiomes of raw milk, while *Lactococcus*, *Streptococcus* and *Lactobacillus* in the curds and cheese during ripening. The microbiomes of the samples characterized during the production process were correlated with each other in varying percentages, with the exception of the brine liquid. The microbiomes identified in the floor drain swabs were correlated with those of raw milk and heated milk. Moreover, the microbiomes identified on the 75-day ripening boards were correlated with the microbiomes of the cheese rind seasoned at the same time point, with a clear presence of *Penicillium* in both samples. The microbiomes identified in the three sample units of milk serum and curd were found to be completely overlapping, whereas for the milk samples the overlap was not always observed.

The results of this study help to organize a microbiome mapping strategy in cheese making facilities and to set the number of sample units to test for each considered matrix from raw milk up to consumption.

The activities of this project were financed by the MASAF project, Contratto di Filiera, Stalla Modello, DM no. 0673777 of 22/12/2021, V Avviso no. 0182458 of 22/04/2022 and subsequent amendments.

PS2-S7-PP06 Predicting biological haazards in raw milk cheese using microbiome data

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The composition of microbiome in foodstuffs during production can either support or inhibit the colonization and growth of foodborne pathogens. In this pilot study, raw milk cheese samples were tested for the presence of *Listeria monocytogenes* at 7, 45 and 90 days of ripening, both inside the cheese and on the rind, using the ISO 11209-1 cultural method. Moreover, the presence of this pathogen was investigated on drain swabs and sponges collected from cheese ripening boards. Raw milk and raw milk cheese samples were also tested for the presence of *Salmonella enterica* and *Campylobacter jejuni,* using the ISO methods 6579 and 10272-1, respectively, and for the enumeration of coagulase-positive *Staphylococcus* spp. In parallel to the cultural methods, all food and environmental samples, which belonged to the same production batch, were submitted to DNA extraction using a bead beating procedure and the DNeasy PowerFood Microbial Kit (Qiagen). The extracted DNA was then processed for library preparation and shotgun sequencing at 150 bp in paired ends, at a coverage >5 Gbp. *Listeria monocytogenes*, *Salmonella enterica* and *Campylobacter jejuni* were not detected in 25 g o ml of any sample by culture methods. *Staphylococcus* spp. was enumerated in raw milk and raw milk cheeses after 7, 45 and 90 days of ripening, both inside the cheese and on the rind, with reduction in colony-forming units over time. In microbiome sequencing data, samples where *Staphylococcus* was enumerated also showed representative reads counts for this genus compared to other tested pathogens. A high number of *L. monocytogenes* reads were quantified in cheese brine. Although the pathogen is likely to be inactivated in this matrix, its presence could represent a critical control point for potential cheese contamination. The results of this pilot study demonstrate that longitudinal microbiome analysis of raw milk cheese and environmental samples throughout the production process enables the simultaneous mapping of different foodborne pathogens. In the long term, these studies can help to predict the drivers promoting their colonization, persistence and growth.

The activities of this project were financed by the MASAF project, Contratto di Filiera, Stalla Modello, DM no. 0673777 of 22/12/2021, V Avviso no. 0182458 of 22/04/2022 and subsequent amendments.

PS2-S7-PP07 Microgreens microbiome: Impact of sanitation on microbial community shifts

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Sanitation practices are applied to reduce microbial contamination in fresh produce. However, their broader impact on the core microbiome of microgreen crops remains poorly characterised. In this preliminary study, we evaluated the effect of sanitation on the bacterial communities of *Lepidium sativum* (cress) and *Eruca vesicaria* (rocket), using both culture-dependent (colony-forming unit) and culture-independent (amplicon sequencing) methods. Microgreen samples were collected from sanitised, unsanitised, and farm-grown samples to assess microbial load, alpha and beta diversity, as well as taxonomic composition.

Shannon diversity indices revealed a consistent reduction in alpha diversity in sanitised samples, exhibiting significantly lower richness and evenness across both microgreen species. Beta diversity analysis using Bray-Curtis demonstrated clear segregation among sanitised, unsanitised, and farm samples, with farm samples exhibiting the highest microbial diversity, indicating distinct microbial community structures. Taxonomic profiling showed reductions in several dominant genera (e.g., *Pseudomonas*), while certain spoilage-associated taxa persisted, suggesting incomplete microbial removal and possible selection for persistent organisms.

These findings highlight the dual role of sanitation: while it effectively reduces microbial load, it can also disrupt the native microbiome of microgreens, potentially influencing shelf-life stability and food safety. Our results contribute to a better understanding of how microbiome-level shifts induced by sanitation may affect pathogen mitigation and spoilage risk in fresh produce systems.

Keywords:

Microgreens, microbiome, sanitation, microbial shift, 16S rRNA, sustainable fresh produce

PS2-S7-PP08 The leaf rust biocontrol mediated by an endophytic *Bacillus subtilis* strain

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The interest in biological control methods in agriculture has gained momentum as the limitations of chemical control become increasingly evident. One of the devastating diseases of wheat is caused by *Puccinia triticina,* resulting in significant annual yield loss [1]. The wheat leaf rust is impacting global wheat production and food security. It was estimated that 94.4% of global wheat production is vulnerable [2], severely affecting food supply chains and causing economic strain. There is an urgent need for sustainable alternatives to chemical fungicides, which pose significant environmental and health risks [3]. *Bacillus* species, known for their antimicrobial properties and ability to induce plant resistance, are promising candidates[1]. We have isolated a *Bacillus subtilis* SA82 from a Saudi Arabian desert plant, *Zygophyllum simplex* [4], and evaluated its antifungal activity against *Puccinia triticina* in vivo. The results revealed a significant decrease in the relative infection frequency (RIF) of the pustules/cm^2 of the infected leaves in the treated wheat plants compared to the non-treated plants (controls) before the artificial infection by the fungal spores (81%, $p < 0.0001$). The ability of *B. subtilis* SA82 to produce antifungal compounds was assessed through genome mining and in vitro biochemical assays, using *Magnaporthe oryzae* as a model system since *P. triticina* can't be cultured in isolation from its host plant. The effectiveness and mechanisms of action showed that antifungal compounds were optimally synthesized during the fungal pathogenesis. These findings will promote sustainable agriculture and reduce reliance on chemical inputs, contributing to leadership in agricultural innovation and ultimately aiding the achievement of food security objectives while safeguarding environmental and human health.

Keywords: Wheat Leaf Rust, *Puccinia triticini*, *Bacillus subtilis*, Biocontrol

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PS2-S7-PP09 Multi-omics profiling reveals microbial ecology of fish spoilage under different packaging conditions

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Introduction This study aims to investigate the fish microbial ecology during storage using a multi-omics strategy, which includes the evolution of the fish microbiome and its functionality in response to various packaging conditions.

Materials and Method The development of the fish (*Sparus aurata*) microbiome was assessed at 0, 4, 8 and 12 °C. Sampling was performed at several time points from the skin of the fish. In total, 104 skin samples were collected, with eight biological replicates per time point. The samples were analysed with shotgun metagenomics and untargeted metabolomics profiling. The resulting datasets were integrated to enable cross-omics analyses. Planned analyses include group comparisons, microbe–metabolite network construction, and candidate biomarker identification. These efforts aim to reveal key microbial and metabolic signatures associated with spoilage progression, ultimately supporting the development of early detection strategies based on robust spoilage biomarkers.

Results and Discussion Alpha and beta diversity analyses (KrakenUniq-based) revealed consistent and progressive shifts in microbial community structure occurred across all temperature conditions during spoilage, indicating (i) a loss in microbial richness and evenness as spoilage progressed, and (ii) a clear temporal separations of microbial communities, suggesting that microbiome composition became increasingly distinct at later spoilage stages. Untargeted metabolomics identified 3,617 metabolites across 24 Class I and 78 Class II categories. Principal Component Analysis revealed consistent separation of samples across timepoints analyzed at each storage temperature, indicating distinct metabolic trajectories under different temperature treatments (PERMANOVA, p = 0.001). These findings suggest that temperature and time jointly shape the metabolic landscape of the fish skin microbiota, providing a strong foundation for identifying spoilage-associated metabolic markers

The study was funded by the FoodGuard project No.1011136542

PS2-S7-PP10 From food to FASTA: Metagenomics for rapid foodborne bacterial pathogen detection

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Different bacterial pathogens can contaminate food and cause harm upon consumption. Traditional detection methods are dependent on selective culturing which is slow (often requiring a week), pathogen-specific and fail to capture the complete food microbiome.

Metagenomics, the study of genetic material in a given sample is a powerful molecular detection approach. It relies on the detection of pathogen-derived DNA and offers a view of the food microbial community and is thus not necessarily biased towards a single species.

However, implementing a practical metagenomic workflow presents multiple challenges that must be addressed: a reliable DNA extraction technique is a prerequisite; efficient removal of undesirable food-derived eukaryotic DNA is necessary to increase the sequence reads allocated to bacteria and finally the often limited concentration of bacterial DNA in food needs to be tackled as this is crucial for sequencing approaches.

The aim is to develop a metagenomic protocol which addresses these limitations to deliver a rapid and untargeted tool for foodborne bacterial pathogen surveillance from food.

PS2-S8-PP01 A complete pipeline for microbiome modulation – from simple high-throughput screening to well-conducted clinical trails

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At WFBR our experts have >25 years of experience in working on modulating the composition and activity of the gut microbiota using different expertise fields. Combining these fields in our gut microbiome proposition allows us to contribute significantly to (speed of) product development. The pipeline usually starts with proof-of-concept, high-throughput screening methods (batch and fed-batch; with single isolates, defined communities or faecal-donations) that allow for quick screening of various substrates, dose-finding studies, effect of combining substrates etc. Usually the screening-phase leads to subsequent experiments investigating mode-of-action in more dynamic *in vitro* models, such as SHIME [which is run in collaboration with our university colleagues] or TIMOTHI^{TM} [The Incredible Mimic Of The Human Intestine], which is under development at WFBR and which will have incorporated all positive aspects of currently existing *in vitro* models, and more. Next, as real proof of the observed effect, a well-conducted clinical trial can be performed. These are well-conducted, because they e.g., are carefully designed for longitudinal sampling, stratify volunteers beforehand, and/or are completely diet-controlled. Samples are taken for e.g., full-length 16S sequencing, metagenomics, CAZyme expression, remaining substrate, SCFA and/or other metabolites. Furthermore, in the *in vitro*/*ex vivo* experiments, pH and optical density can be traced. Sophisticated state-of-the-art bioIT and statistical tools are used to evaluate the data. This includes machine learning and artificial intelligence to get most out of the data, which is subsequently presented in an interactive manner, allowing the user to decide what is important in the dataset, by e.g. choosing the taxon of interest, or comparing two or more of the tested variables. These studies can be done in (microbiotas collected from) different populations, from infants to elderly and anything in between, or specific targets groups (e.g. sporters) or patients. Examples of 'substrates' that can be used: fibres, pre-, pro- and postbiotics, polyphenols, drugs (and means of how to mitigate the effects of these), novel proteins, sweeteners, emulsifiers and other food additives, etc.

PS2-S8-PP02 Bridging data and disease: A reproducible metagenomic workflow framework within MIRRI-IT's HPC Platform

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The Italian Node of the Microbial Resource Research Infrastructure (MIRRI-IT), coordinated by the Joint Research Unit MIRRI-IT, plays a central role in advancing microbial research and supporting microbiological services and innovation in Italy. To meet the increasing demand for microbiome research in Health Sciences, MIRRI-IT has developed a set of standardized and reproducible bioinformatics workflows aimed at enhancing data analysis, reproducibility, and interoperability.

In line with this mission, we have created a Collaborative Working Environment (CWE) platform that allows scientists to perform all steps of metagenomic analysis on a High-Performance Computing infrastructure.

On the CWE platform, we have implemented two dedicated workflows. The first focuses on metagenomic assembly, reconstructing longer contiguous sequences from microbiome samples, and performing gene and protein prediction to annotate potential coding sequences [10.3389/fbinf.2025.1632189]. The second is a novel, previously unpublished workflow for metagenomic profiling and functional analysis, which characterizes both the taxonomic composition and functional potential of microbial communities.

In the metagenome profiling workflow, researchers can perform raw read quality checks, followed by read alignment to remove host contaminants. Taxonomic classification of Bacteria, Archaea, and Eukaryotes is then carried out using three complementary approaches: a **k-mer-based approach** (Kraken followed by Bracken), a **marker gene-based approach** (MetaPhlAn), and an approach based on **MAGs identification** (Sylph).

Additionally, a run using HUMANn3 can be performed to infer enriched metabolic pathways. Post-processing includes sample normalization, supervised decontamination, prevalence filtering, abundance estimation, and calculation of diversity metrics. Metadata exploratory analysis and regression modeling are also integrated into the workflow.

These workflows were applied to shotgun metagenomic data from fecal samples of Multiple Sclerosis patients. This approach enables a comprehensive analysis of the gut microbiome and its potential role in the disease, linking microbial composition with genome-level insights.

The resulting genomic resources support further downstream analyses, including strain-level resolution, metabolic pathway reconstruction, and comparisons with reference databases, thus contributing to the growing body of knowledge on host-microbiome interactions in neuroinflammatory diseases.

PS2-S8-PP03 First Insights into soil microbiome preservation: Strategies, challenges, and future directions

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Microbiomes are complex communities of microorganisms that, together with their "theatre of activity", define a specific habitat and provide essential ecosystem services critical to the health of plants, animals and the environment. Among the use cases investigated by the EU-funded MICROBE (Microbiome Biobanking (RI) Enabler) project, the soil microbiome is particularly important because of its complexity and the wide range of functions and ecosystem services it provides. Furthermore, the soil microbiome plays a significant role in human health through the food system.The MICROBE project addresses the critical challenges of microbiome preservation and current challenges faced by culture collections and biobanks that need new approaches for sample preservation and metadata management. By establishing standardised protocols and optimising preservation methods, the project aims to ensure the long-term stability of microbial communities and their functionality, as well as, the storage of metadata associated with samples, to enable future scientific research and industrial applications.To this end, the project has conducted a comprehensive study evaluating different preservation strategies on well-characterised soil samples, including different storage temperatures, cryoprotectants and cooling rates. Preliminary results suggest that these methods successfully maintain bacterial and fungal culturability over time, while ongoing assessments explore their effects on community composition.The insights gained from these efforts will provide a blueprint for microbiome biobanking across different systems, fostering collaboration between academic and industrial stakeholders while promoting best practices for data sharing and long-term resource accessibility.

PS2-S8-PP04 Marine sponge microbiomes for sustainable food preservation

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Marine sponges are valuable components of ocean nutrient cycling, filtering dissolved organic matter at rates comparable to coral reef primary productivity. Due to their sessile nature, these animals have co-evolved with microbial communities to develop vast chemical defenses, with most bioactive compounds produced by microbial symbionts. Acidobacteriota represent a major component of sponge microbiomes, possessing a high number of biosynthetic gene clusters (BGC) [1]. However, these bacteria remain poorly understood.

We collected and analyzed 20,000 Acidobacteriota metagenome-assembled genomes from diverse environments, focusing on marine host-associated representatives. First, we discovered that host-association is a phylogenetic trait, with four families exhibiting facultative or obligate symbiotic lifestyles. We then found that symbiotic Acidobacteriota possess significantly more halogenase-containing BGCs than free-living relatives. Given that halogenation enhances antimicrobial potency, this halogenase enrichment suggests that symbiosis has driven the evolution of more effective chemical defenses.

Genomics screening of these halogenase-enriched BGCs revealed over 30 novel clusters containing halogenases embedded within core biosynthetic genes, indicating the production of new halogenated metabolites. Our analysis further revealed that these symbionts repurpose known biosynthetic clusters by incorporating halogenases into known BGCs. For example, alkylresorcinol clusters are found across many bacteria, but family UBA8438 is the only lineage we've seen that adds halogenases to this cluster. This strategy allows marine bacteria to create novel halogenated versions of common natural products.

These halogenated compounds represent a promising source of natural food preservatives, offering eco-friendly alternatives to synthetic chemicals. Marine sponge-associated Acidobacteriota thus constitute an important yet underexplored reservoir of biosynthetic diversity with significant potential for developing sustainable antimicrobial solutions in food preservation.

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PS2-S8-PP05 Ferme Scholen: A safe and engaging gateway to microbiology for the high school curriculum through fermented vegetables and their microbiome

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Recent curriculum changes in Flanders (Belgium) have introduced research skills and microbiological literacy into high school curricula across age groups and education systems. As a result, STEAM teachers are increasingly in need of safe, engaging teaching material and research projects. However, traditional microbiology demonstrations often rely on tests designed for pathogen identification. When asked to design a research project, most students -and even teachers- tend to default to plating samples from different surfaces or environments and comparing colony counts. This approach carries the risk of exposing untrained students and teachers to large numbers of unknown, potentially pathogenic microorganisms.

Vegetable fermentations offer a safer and more controlled alternative for unexperienced microbiologists. Even without the use of starter cultures, the fermentation environment is self-limiting, providing a safe space to explore physical parameters of the fermentations, colony growth, and even single-cell metabolism within a basic high school context.

The 'Ferme Scholen' project is a citizen science initiative designed to support this approach. Participating teachers are invited to set up fermentations with their students, supported by background material, essential hardware and online support to develop their own lesson plans. Participating classes send samples from their fermentations to the university lab for microbiome sequencing and receive individualized reports on the microbial composition of their fermentations. Additionally, these samples contribute to ongoing research on the microbial communities and dynamics involved in vegetable fermentations.

So far, the project has generated strong enthusiasm and engagement from both teachers and students, while also yielding valuable new insights into microbial communities present in home and classroom vegetable fermentations.

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