SeedCon

The seed microbiome conference

5–7 May 2026

The First International Conference on Seed Microbiome and Microbial Inheritance

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Abstract Book

Leibniz Institute for Agricultural Engineering and
Bioeconomy (ATB), Potsdam, Germany

www.seedcon.org

Welcome to SeedCon 2026

It is our great pleasure to welcome you to SeedCon 2026, the first international conference dedicated to the seed microbiome and microbial inheritance. This conference brings together researchers from diverse disciplines to explore the origin, transmission, and function of plant-associated microbial communities across generations.

Understanding how microbiomes are assembled, maintained, and inherited is essential for advancing both fundamental plant science and sustainable agriculture. Seeds represent a critical interface between generations, and their microbiome plays a key role in plant health, adaptation, and productivity.

Throughout the conference, these topics will be explored through keynote lectures, invited talks, and contributed presentations, as well as poster sessions and discussions. We hope that SeedCon will foster new collaborations, stimulate new ideas, and help shape this rapidly emerging field.

We thank all speakers, participants, and partners for their contributions to this event and to the advancement of this field.
We wish you an inspiring and enjoyable conference.

Ahmed Abdelfattah
Conference Chair, SeedCon 2026
Leibniz Institute for Agricultural Engineering and Bioeconomy (ATB)

SeedCon
The seed microbiome conference

Program Overview

Day 1 – Structure and Transmission (May 5)

Opening Remarks
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers
Session 2: Microbial Inheritance: Routes and Mechanisms
Session 3: Dynamics of Microbial Transmission Across Plant Compartments
Poster Session & Coffee
Conference Dinner

Day 2 – Function and Intervention (May 6)

Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance
Session 5: Shaping the Seed Microbiome: From Intervention to Design
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science
Poster Session
Roundtable: Translation, AI, and Future Directions
BBQ & Social Evening

Day 3 – Evolution and the Future (May 7)

Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes
Session 8: Toward a Framework for Microbial Inheritance
SMWG World Café
Conference Synthesis & Awards

Funding and Support

Funded by the German Research Foundation (DFG)
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Host Institution
Leibniz Institute for Agricultural Engineering and Bioeconomy (ATB)

Our Gold Sponsors

SeedForward is a German agricultural biotechnology company dedicated to advancing sustainable and resilient agriculture through science-driven solutions. Based in Osnabrück, the company develops and markets biologically based seed treatment technologies designed to support plant health, improve growth and yield stability, and reduce reliance on synthetic chemicals.

Bejo (Bejo Zaden B.V.) is a globally recognized, family-owned Dutch company specializing in the breeding, production, and sale of premium vegetable seeds. With over a century of history and operations in over 30 countries, Bejo focuses on continuous innovation, organic breeding, and developing resilient crop varieties for sustainable global agriculture.

e-nema (e-nema GmbH) is a German biotechnology company recognized as the global leader in producing beneficial nematodes for biological plant protection. Founded in 1997, the company specializes in industrial-scale fermentation to create natural, chemical-free pest control solutions. They also provide contract biomanufacturing services for the agricultural, cosmetics, and food industries.

Our Silver Sponsors

KWS (KWS SAAT SE & Co. KGaA) is a globally operating German plant breeding company founded in 1856. The company specializes in developing and producing high-yield seeds for agricultural crops, including sugarbeet, corn, cereals, oilseed rape, and vegetables. By continuously improving crop genetics and offering expert digital consulting services, KWS aims to support sustainable agriculture and help feed a growing world population.

Supporting Societies

The New Phytologist Foundation is a not-for-profit organisation committed to the advancement and dissemination of knowledge and research in plant science. The Foundation currently fulfils this objective by publishing the scholarly journals *New Phytologist* and *Plants, People, Planet* and by funding a wide range of activities, such as the international New Phytologist Symposia and Workshop series, awarding grants, and the sponsorship of awards such as the Tansley Medal, named after *New Phytologist*'s founder Sir Arthur Tansley.

The International Society for Seed Science (ISSS) is a professional organisation dedicated to advancing research, education, and communication in seed biology. The Society supports the dissemination of scientific knowledge through its official journal Seed Science Research, the organisation of international conferences and workshops, and the promotion of collaboration within the global seed science community. ISSS also fosters education and training in seed biology and recognises excellence in the field through awards and honours.

MiCropBiomes (COST Action CA22158) is a European research network supported by the European Cooperation in Science and Technology (COST). The initiative focuses on exploiting plant-microbiome networks and synthetic microbial communities to improve crop fitness. They facilitate collaboration, organize international conferences, fund short-term scientific missions, and provide specialized training for researchers.

Day 1 – Structure and Transmission (May 5)

08:00–10:30
Registration & Coffee

10:30–10:45
Opening Remarks – Ahmed Abdelfattah

Session 1 – Seeds as Microbial Niches: Assembly, Filtering, and Barriers

10:45–12:45

10:45–11:25	Keynote – Gerhard Leubner
11:25–11:45	Featured talk – Massimiliano Cardinale
11:45–12:05	Featured talk – Marco Incarbone
12:05–12:45	Contributed Talks

12:45–13:45
Lunch

Session 2 – Microbial Inheritance: Routes and Mechanisms

13:45–15:45

13:45–14:25	Keynote – Matthieu Barret
14:25–14:45	Featured talk – Carolina Lobato
14:45–15:05	Featured talk – Thomas Chadelaud
15:05–15:45	Contributed Talks

15:45–16:15
Coffee & Poster Session I

Session 3 – Dynamics of Microbial Transmission Across Plant Compartments

16:15–18:15

16:15–16:55	Keynote – Seth Bordenstein
16:55–17:15	Featured talk – Marta Robledo
17:15–17:35	Featured talk – Cristian Andrés Salinas Castillo
17:35–18:15	Contributed Talks

18:15–19:30
Pre-dinner Reception

19:30–22:00
Conference Dinner

Day 2 – Function and Intervention (May 6)

Session 4 – Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

09:00–11:00

09:00–09:40	Keynote – Tomislav Cernava
09:40–10:00	Featured talk – Birgit Wassermann
10:00–10:20	Featured talk – Stéphane Compant
10:20–11:00	Contributed Talks

11:00–11:30
Coffee & Poster Session II

Session 5 – Shaping the Seed Microbiome: From Intervention to Design

11:30–13:30

11:30–12:10	Keynote – Marie Simonin
12:10–12:30	Featured talk – Daniel Garrido-Sanz
12:30–12:50	Featured talk – Davide Gerna
12:50–13:30	Contributed Talks

13:30–14:30
Lunch

Session 6 – From Data to Application: Prediction and Translation in Seed Microbiome Science

14:30–16:30

14:30–15:10	Keynote – Gabriele Berg
15:10–15:30	Featured talk – Alexandre Jousset
15:30–15:50	Featured talk – Kabiru Muhammad
15:50–16:30	Contributed Talks

16:30–17:00
Coffee & Poster Session III

17:00–18:00
Roundtable – Translation, AI, and Future Directions

18:00–19:30
BBQ

19:30–00:00
Social Evening

Day 3 – Evolution and the Future (May 7)

Session 7 – Global Patterns, Drivers, and Data in Seed Microbiomes

09:00–11:00

09:00–09:40	Keynote – Manuel Delgado Baquerizo
09:40–10:00	Featured talk – Hamed Azarbad
10:00–10:20	Featured talk – Natalia González Benítez
10:20–11:00	Contributed Talks

11:00–11:30
Coffee & Poster Session IV

Session 8 – Toward a Framework for Microbial Inheritance

11:30–13:30

11:30–13:00	SMWG World Café
13:00–13:15	Conference Synthesis & Awards

13:30
Official end of SeedCon 2026

COST Action CA22158 Workshop (by invitation only)

14:00–16:00

Toward a Framework for Seed Microbiome Research

S1-K01 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

The seed and its microbiome: how morphological and physiological seed traits shape interactions and environmental adaptation

***Gerhard Leubner-Metzger*[1]**

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Plant seeds represent complex entities providing reproduction and dispersal through time and space. An impressive diversity in morphological and physiological seed traits evolved to ensure plant survival, fitness and adaptation to prevailing environments and climate change. Most plant species disperse desiccation tolerant “dry” seeds in which the reduced moisture content (<10%) imposes a metabolically inactive state called quiescence (which does not equal seed dormancy). Upon imbibition the seed moisture content increases leading to the resumption of full metabolic activity during the seed germination process. Seed-transmitted microbes which persist through this quiescence passage in desiccation-tolerant seeds in a “dry” “viable-but-nonculturable (VBNC)” survival state are reactivated during germination. Seed desiccationion tolerance, quiescence and VBNC are established during seed maturation drying on the mother plant and are reversed with the completion of germination and transition to subsequent seedling growth. Very little is known about the mechanisms underpinning this seed-microbe interaction during seed quiescence. In most species the dispersed seeds consist of the embryo encased by living endosperm tissue (storage compartment with maternal dominance) and the seed coat (testa, maternal tissue). Many other species disperse dry fruits in which the seeds are encased by the fruit coat (pericarp); seed and fruit coat properties determine germination behaviour. Other key seed traits established during seed development are seed vigour, longevity, defense and - in many but not all species - seed dormancy. Seed dormancy is distinguished from quiescence in that it is an active state which blocks germination in the imbibed (hydrated) state under favourable environmental conditions. It is a highly adaptive seed trait which defines the germination responses to the environment. While we know quite something about the morphological (biophysical, biomechanical) and physiological (biochemical, hormonal) mechanisms underpinning many seed traits, almost nothing is known about the associated seed-microbe interactions leading to the observed responses of the seed holobiont. In the case of pericarp-imposed dormancy beneficial microbes are involved in facilitating the dormancy release. It is proposed that mechanistic knowledge about microbe-seed interactions is essential for developing better seed priming technologies and other applications which support the sustainable intensification of agriculture.

S1-FT01 Oral presentation

Day 1 – Structure and Transmission
Session 1*:* Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Sowing more than plants: the seed microbiome legacy

Massimiliano Cardinale[1]
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Presenting author: Massimiliano Cardinale, massimiliano.cardinale@unisalento.it

Historically, only phytopathogenic microorganisms were believed to be capable of colonizing the internal tissues of plants; similarly, seed were considered as sterile inside, been normally regarded as vehicles of plant genetic material, to generate new offspring; until recurring evidence fundamentally reshaped this view. Initially considered as annoying contaminants, microorganisms repeatedly retrieved as seed-associated were finally understood for what they actually are: well-structured microbial communities, actively assembled and then transmitted to the next plant generation. They indeed represent the co-inherited biological legacy, shaped by host genetics, environmental constraints and peculiar plant filtration mechanisms. The profound implications of this paradigm shift span from plant ecology and evolution to practical applications. Vertically transmitted microbiota influence seedling establishment and plant fitness, in ways that operate independently of (or parallel to) soil microbiome recruitment. This suggests that the seed microbiota constitutes one important component of plant adaptation and co-evolution with surrounding biota. From an applicative point of view, understanding the mechanisms of seed microbiota assembly and filtering can open new possibilities for sustainable crop management through microbiome manipulation. Harnessing the beneficial seed-associated microorganisms could reduce dependence on chemical inputs, while improving germination rates and early plant vigor in an environmental-friendly manner. Recent investigations started to shed light onto the cryptic nature of the seed microbiota: from tropical trees to mediterranean fruits, to staple food crops, all plant species investigated so far showed distinct compositions, which included both bacterial and fungal species. In future, the integration of observational studies and well-designed experimental trials, supported by multi-omic approaches, will be essential to unravel functional roles of seed-associated taxa, their transmission routes and interactions. A mechanistic understanding of how plants assemble, filter, and transmit microbial partners in seeds will be the key to unlock the full biotechnological and ecological potential of the seed microbiota.

S1-FT02 Oral presentation

Day 1 – Structure and Transmission
***Session* 1*:* Seeds as Microbial Niches: Assembly, Filtering, and Barriers**

AGO5 restricts virus vertical transmission in plant gametophytes

Marco Incarbone[1]
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Presenting author: Marco Incarbone, Marco.Incarbone@mpimp-golm.mpg.de

The propagation of a viral infection from a host parent to its progeny is known as vertical transmission, or seed transmission in plants. It allows viral infections to rapidly spread locally via pollen and worldwide through seeds. To be vertically transmitted to each progeny, a virus must pass through the tight bottleneck of at least one cell per parent – the gametes. Therefore, stopping infection during sexual reproduction is of vital importance to generate healthy offspring. Accordingly, vertical transmission of plant viruses often occurs at very low rates, if at all, suggesting the existence of highly effective – yet unknown – antiviral defenses in pre-meiotic cells, gametes and/or embryos. In this study, we show that AGO5, an RNA interference factor expressed specifically in shoot apical meristem (SAM) stem cells and the germline of A. thaliana, drastically reduces the vertical transmission of *Turnip yellow mosaic virus* (TYMV). Through a series of controlled pollination experiments leveraging different zygosity of ago5 knock-out, cell type-specific rescue of ago5 and TYMV detection in whole-mount reproductive tissues, we provide evidence that AGO5 acts in pollen and sperm cells to restrict virus transmission to progeny. We further show that triggering antiviral RNA interference specifically in sperm cells leads to a significant reduction in TYMV vertical transmission. In summary, this study provides the first description of a gamete-specific antiviral defense mechanism restricting virus vertical transmission, paving the way for new strategies to prevent the spread of pollen- and seed-borne viral epidemics.

S1-T01 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Heterosis Reconsidered: A Microbiome-Origin and Inheritance Perspective

Peng Yu[1]
[1]*Plant Genetics, TUM School of Life Sciences, Technical University of Munich, Munich, Germany*
Presenting author: Peng Yu, pengyu.yu@tum.de

Heterosis (hybrid vigor) is a central driver of crop productivity, yet its mechanistic basis remains incompletely understood beyond host genomic interactions. Increasing evidence suggests that plant-associated microbiomes contribute to heterosis; however, the origins, transmission, and inheritance of these microbial communities remain largely unresolved. Here, we propose that heterosis emerges as a heritable plant–microbiome trait, shaped by the integration of host genetics with microbiome assembly across environments. We examined how hybridization reshapes the microbiome recruitment, influenced by soil types and stress factors, leading to non-additive assembly patterns in hybrid plants. Importantly, hybrids may integrate and selectively filter parental microbiomes, resulting in microbial inheritance patterns that parallel, yet are not strictly determined by, host genetic inheritance. These processes are mediated by genotype-dependent root exudation, immune signaling, and metabolic reprogramming, which collectively define microbial colonization trajectories from bulk soil to rhizosphere, root, and reproductive tissues. We further highlight emerging evidence for microbiome transmission across plant generations, including vertical inheritance via seeds and transgenerational feedback through soil legacy effects. Such inheritance is linked to host regulatory networks, including hormone signaling, reactive oxygen species homeostasis, and secondary metabolism, which together modulate both microbial assembly and plant performance. These feedback loops enable the stabilization of beneficial microbial consortia, contributing to enhanced nutrient acquisition, stress resilience, and yield in hybrid crops. Collectively, this framework positions heterosis as a multi-layered inheritance phenomenon, integrating host genomic variation with ecological and evolutionary processes governing microbiome origin and transmission. Understanding these principles provides a foundation for microbiome-informed breeding strategies and the development of heritable beneficial plant–microbe interactions for sustainable agriculture.

S1-T02 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

A common garden experiment on 45 crop species reveals that plant species identity drives seed microbiota composition beyond phylogenetic relatedness

Tristan Lafont Rapnoui [1]*, Marie Le Guen*[1]*, Mathilde Brunel*[1]*, Augustin Latrompette*[1]*, Coralie Marais*[1]*, Marie Simonin*[1]

[1]*University of Angers, Institut Agro, INRAE, IRHS, SFR QUASAV, Angers, France*

Presenting author: Tristan Lafont Rapnouil, tristan.lafont-rapnouil@inrae.fr

Increasing efforts have been deployed over the last decade to characterize crop seed microbiota. These allowed identification of core members of the seed microbiota as well as of key drivers of seed microbial communities assembly (e.g., season, environment). Yet, past studies generally focus on few species, not always in a controlled production environment and on one generation. This prevents us from investigating plant species specific signatures, stability over generations and influence of host shared phylogenetic history (phylosymbiosis) on seed microbiota. We addressed these questions using a common garden experiment with 45 plant species. Characterization of greenhouse-produced seed (parent and progeny) and parental plants microbiota was conducted using ITS and gyrB metabarcoding (diversity) and colony counting (community size). We found a strong effect of plant species on microbiota ($R^2=0.51$ and 0.74 for bacteria and fungi respectively) but still with the dominance of members of the global core seed microbes (e.g., *Pantoea*, *Cladosporium*). This strong plant species signature was not explained by phylosymbiosis as previously reported for the root or leaf endosphere. This species effect with no higher taxonomic effect suggests that species-specific seed properties are driving microbial assembly rather than relationships with host evolution. Moreover, the characterization of original seed lots and parental plants (leaves) allowed the identification of ASVs shared across the whole plant lifecycle (seed to seed). We found that seeds from different species differed greatly in their cumulative relative abundance of these shared members. This was associated with striking differences between microbial kingdoms: shared bacterial ASVs represented 0.005 to 92.7% (median 7.64%) and fungal ASVs 6.1 to 94.1% (median 31%). Together, these results highlight that seed microbiota assembly is predominantly driven by species-specific traits rather than host phylogeny, with highly variable transmission potential across bacterial and fungal kingdoms.

S1-T03 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Host genome and bacterial taxa shape the *Arabidopsis* seed microbiome

Sabiha Parween[1], Naheed Tabassum[1], Kirti Shekhawat[1], Bruno Gnannt[2], Waad Alzayed[1], Rewaa Jalal[3], Heribert Hirt[1]

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[2]*Institut of Ecological Microbiology, University Bayreuth, Bayreuth, Germany*

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Presenting author: Sabiha Parween, sabiha.parween@kaust.edu.sa

Plant-microbiome interactions are crucial in shaping plant growth, stress resilience, and disease resistance. Among these, the seed microbiome plays a pivotal role in early plant development and eco-logical adaptation. However, little is known about the factors that determine the abundance and functions of the seed microbiome, as well as the role of the host genome in shaping the microbial diversity across different ecotypes. In this study, we investigated the diversity of the *Arabidopsis* seed microbiomes that originate from multiple geographical locations. High-throughput sequencing identified key bacterial taxa that govern *Arabidopsis* seed microbiota diversity. Distinct compositions of bacterial taxa were identified in *Arabidopsis* accessions sharing geographical location and similar soil features. Genome wide association studies (GWAS) revealed that both the abundance of key taxa and common functional traits are associated with specific host genetic loci such as the RNA-binding protein RPB47B, mutants of which showed altered physiological properties related to soil properties and microbial diversity. Overall, our study establishes that geographical, soil and genetic host factors shape the *Arabidopsis* seed microbiome.

S1-T04 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Seed-associated yeasts: diversity and beneficial effects on plants

Muriel Marchi[1], Anaïs Bosc-Bierne[1], Laurine Labourgade[1], Nathan Kavunu[1], Thomas Lerenard[1], Josiane Le Corff[1], Sophie Aligon[1], Aurélia Rolland[2], Marie Simonin[1], Coralie Marais[2], Martial Briand[1], Viviane Cordovez[3], Linda Gouka[3], Thomas Guillemette[1], Philippe Simoneau[1], Natalia Guschinskaya[1]

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Presenting author: Muriel Marchi, muriel.marchi@inrae.fr

A meta-analysis of seed microbiota defined 16 core taxa present in more than 20 plant species (Simonin et al., 2022). Among them, six seed core taxa were yeasts, belonging to the genera *Vishniacozyma*, *Filobasidium*, *Sporobolomyces*, and *Aureobasidium*, which are commonly detected in various environments (soil, root, shoot, air, litter from croplands, forest, deserts). However, within the seeds, yeast diversity and their functional roles remain poorly described. To fill this gap, we aimed to characterize the diversity of seed-associated yeasts across nine plant species (crops and non-cultivated species) using culturomics and microscopy and we evaluated 10 isolates for their antifungal activity and capacity to enhance plant growth. Our results showed that seed-associated yeasts predominantly belong to the Basidiomycota phylum, particularly the Tremellomycetes class. Our collection of 229 isolates covers 15 genera (2 of Ascomycota and 13 of Basidiomycota), with *Holtermanniella*, *Vishniacozyma*, *Filobasidium*, *Naganishia* and *Sporobolomyces* being the most frequently isolated. These dominant yeasts were isolated from multiple plant species (4 to 8), except for *Naganishia* only isolated from *Solanum lycopersicum* L. In vitro antifungal assays revealed that eight out of ten isolates significantly inhibited the growth at least one of six plant pathogens (*Fusarium graminearum, F. culmorum, F. oxysporum* sp. *phaseoli, F. oxysporum sp. lycopersici, Alternaria brassicicola, Globisporangium ultimum*). Both Aureobasidium isolates inhibited all plant pathogens growth, while other strains showed variable inhibition depending on the pathogen. In greenhouse experiments, most isolates slightly reduced bean seedling emergence and vigor under non-infected conditions, but *Filobasidium* and *Hannaella* improved seedling establishment when subjected to pathogen stress caused by G. ultimum. These results suggest that seeds represent a specific habitat that diverse Basidiomycota yeasts can colonize. Seed-associated yeast can compete with some plant pathogens and influence plant growth. To conclude, while yeasts are widely recognized as biotechnological resources, their potential in agriculture, particularly for plant growth promotion and protection remains underexplored and needs to be delved.

S1-T05 Oral presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Novel insights into the molecular control of seed development, inheritance, and quality from model to crops

Domenico Loperfido[1], Cecilia Zumajo-Cardona[1], Alice Casati[1], Marco Biancucci[1], Daniel Briceno[1], Ignacio Ezquer[1]
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Presenting author: Ignacio Ezquer, juan.ezquer@unimi.it

The Seed Development Team at the University of Milan has long applied integrated molecular biology, developmental biology, and plant cell biology approaches to generate fundamental knowledge in seed biology. Here we highlight our most recent advances obtained using *Arabidopsis thaliana* as a reference model to dissect the molecular and regulatory mechanisms governing seed development and inheritance. Our research focuses on genetic and hormonal signaling pathways that mediate the coordinated crosstalk among the seed compartments-embryo, endosperm, and seed-coat - during seed formation. We will present our recent discoveries of genetic regulators involved in hybridization and paternal genome contribution, with a specific emphasis on the molecular control of the triploid block. We will show how triploid block establishment and maintenance depend on tightly coordinated differentiation processes between the endosperm and the embryo. In addition, we will discuss cell wall-associated regulatory mechanisms that control seed growth, biomechanical properties, and tissue differentiation, providing key insights into fundamental developmental processes in seed biology. Finally, we will illustrate how this genetic and molecular framework is translated into crop systems such as rice and wheat to elucidate mechanisms underlying seed quality control, germination performance, and early seedling establishment, thereby contributing to the improvement of seed quality traits and crop resilience.

S1-P01 Poster presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Seeds as Microbial Niches: Ecology, Scope, and Future Perspectives

Bhavna Rajkumari[1]
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Traditionally seen as passive carriers of plant genetic material, seeds are now recognised as dynamic microbial niches that harbour diverse communities affecting plant health and development. Defined as ecological spaces for microorganisms, seeds provide unique environments rich in nutrients and selective pressures for microbial colonisation, including bacteria and fungi that contribute positively to plant robustness or may introduce pathogens. Microbial communities are transmitted vertically from parent plants and horizontally through various environmental vectors. This microbial presence within seeds is critical for promoting germination, enhancing stress tolerance, and protecting plants from diseases. The implications extend beyond individual plants, influencing population dynamics, ecosystem resilience, and agricultural practices via microbial seed treatments that foster sustainable farming by minimising chemical inputs. With recent advances in high-throughput sequencing and other methodologies, the characterisation of seed microbiomes is revealing their complexity and functional significance. However, challenges remain in understanding the stability of these microbiomes across generations and their response to environmental stressors. Ethical considerations regarding microbial manipulation and integration of this knowledge into crop breeding programmes are also essential for achieving sustainable food systems amid global agricultural challenges.

S1-P02 Poster presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

From single strains to microbiota, how biological resource centres can help research on seed microbiome?

Océane Fogliani[1], Céline Mirguet[1], Miguel Bonnin[2], Sara Pipponzi[3], Isa Hollopp[1], Clara Maire[1], Géraldine Taghouti[1], Cécile Dutrieux[1], Livio Antonielli[3], Matthew Ryan[2], Tanja Kostic[3], Perrine Portier[1]
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The French Collection for Plant-associated Bacteria was created in 1973 (CIRM-CFBP, https://cirm-cfbp.fr/) and preserves strategic resources for plant health. Among these resources, more and more bacteria are isolated from the native microbiota of many plant species, including strain isolated from seed microbiota. Biological resource centres have a long-standing tradition of being crucial for research, by preserving valuable and well characterized resources along with the associated data. The expertise held in collections is another key help for researchers. Beyond single strains, the preservation of complete microbiota or consortia could be critical for microbiota research topics, helping to have permanent access to these resources. However, to switch from single strains to complex communities can be challenging. CIRM-CFBP teamed up with other partners within the MICROBE project (https://www.microbeproject.eu/) in order to explore the preservation of native microbiota. We tested the microbiota preservation on bean seed microbiota. After extraction from the seeds, the microbial communities were preserved following nine different preservation modalities. The experiments were conducted jointly among three partners of the project (INRAE / AIT / CABI). The taxonomic composition had been assessed by metabarcoding (ITS/gyrB/16S rRNA markers) and the functional diversity by Biolog Ecoplates. This enabled us to measure effect of preservation and to determine the best ways to preserve these resources. Finally, this project will enable the collection to better preserve whole communities and pave the way to a new era for biological resources centres.

S1-P03 Poster presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

Germination Modulates Diversity and Network Connectivity in Tomato Seed Bacterial Endophytes

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Seeds are increasingly recognized not only as vectors of plant genetic information but also as reservoirs of vertically transmitted microbial communities that influence early development and plant performance. Seed borne endophytes are promising targets for sustainable crop protection, particularly through seed priming approaches leveraging beneficial microbes. In this study, we investigated the endophytic bacterial communities associated with commercial tomato seeds, aiming to assess shifts occurring during early germination. Following surface sterilization, seeds were examined either in their dry state or after pregermination on moist blotting paper at 25 °C under official germination testing conditions until at least 50% germination was reached. Eight commercial seed lots, each represented by five biological replicates and encompassing four tomato varieties (80 samples total), were examined. Bacterial communities were characterized using an amplicon based metagenomic approach targeting the 16S rRNA gene, and a parallel culture based analysis was conducted by plating seed extracts on standard bacteriological media. Across seed lots, Pseudomonadota, Actinomycetota and Bacillota dominated both seed endosphere and pregerminated samples, together accounting for at least 90% of the total bacterial composition. Overall, α diversity was higher in the seed endosphere than in pregerminated seeds, with differences influenced by seed origin (organic vs. conventional). β diversity analysis further indicated compositional shifts between the two sample types. Co occurrence network analysis revealed that endospheric communities had a more complex and interconnected structure, with more nodes and edges, higher cohesion, and a more articulated modular organization than the simpler, less connected networks of pregerminated seeds. Recovering the cultivable fraction proved challenging and required liquid medium enrichment, yielding higher recovery from pre-germinated seeds. A subset of isolates was screened for plant growth promoting traits and in vitro antagonism against major tomato pathogens, revealing substantial variability. When selected strains were used to inoculate tomato seeds, effects were heterogeneous, although some isolates consistently promoted seedling growth.

S1-P04 Poster presentation

Day 1 – Structure and Transmission
Session 1: Seeds as Microbial Niches: Assembly, Filtering, and Barriers

A Pilot Shotgun Metagenomics Exploration of Single *Capsicum annuum* Seed Microbiome and Functional Potential

Muhammad Kabiru Nata'ala[1,2], Denis Kiplimo[1,3], Daniel Höfle[1,3], Irda Pateriku[1], Marina M.-C. Höhne[2,4], Ahmed Abdelfattah[1]

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Seed-associated microbial communities play an important role in seed health and early development, yet their characterization using shotgun metagenomics remains challenging due to high host DNA contamination. Here, we present a pilot, genome-resolved metagenomic analysis of single *Capsicum annuum* seeds to assess the extent to which moderate sequencing depth (~10 GB per sample) enables characterization of seed microbiomes and their functional potential. We extracted DNA from three individual *Capsicum annuum* seeds using FastDNA™ Spin Kit and subjected to shotgun metagenomics. Samples were sequenced to approximately 10 Giga-Base pairs. Low quality sequences were filtered with Fastp, and the host sequences were removed by mapping to reference genome using Bowtie2. Remaining microbial reads were taxonomically classified with Kraken2 against the GTDB database. Metagenomic assembly and binning were performed using metaSPAdes, and MetaBAT2, respectively. Quality of recovered metagenome-assembled genomes (MAGs) was assessed using CheckM2 and taxonomy was assigned using GTDB-Tk. Across all samples, host-derived reads represented more than 98% of total sequences, resulting in 1.07 to 1.62% microbial reads per sample, corresponding to 0.12 to 0.19 GB. Taxonomic classification revealed a highly skewed community composition dominated by bacteria, accounting for more than 99.8% of non-host reads. The phylum Pseudomonadota comprised approximately 93 - 96% of microbial reads, with the genus *Pseudomonas* representing 88 - 92%, predominantly assigned to the lineage *Pseudomonas* sp002874965. Assembly and binning recovered two near-complete MAGs from this lineage, with estimated completeness of 100% and 99.97%. These results indicate that *Pseudomonas* population constitutes the dominant core of the *Capsicum annuum* seed microbiome. Overall, this study demonstrates that moderate sequencing depth is sufficient to resolve dominant seed-associated taxa and recover high-quality genomes from individual seeds, despite host DNA contamination. The ongoing analyses are directed at exploring functional profiling by characterising antimicrobial resistance genes (ARGs) and assess their potential association with assembled genomes and mobile genetic elements.

S2-K01 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

An overview of the genetic factors involved in the transmission of microorganisms to seeds

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The transmission of microorganisms from one generation of plants to another via seeds can be broadly divided into two stages: the first from the parent plant to the seed and the second from the seed to the seedling. The selective processes involved in these stages depend on the host plant and biotic interactions among microorganisms. This presentation will summarize the current knowledge of the molecular interactions that occur during these selective processes, from both the plant's and the microorganism's perspectives. Understanding the genetic factors involved in these stages of microbial transmission via seeds is essential for developing strategies to modulate the establishment of microorganisms that are either beneficial or harmful to plant growth and health.

S2-FT01 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

GENETIC CONTROL OF THE SEED MICROBIOME: IMPLICATIONS FOR SUSTAINABLE CROPPING

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The domestication of crops has been a cornerstone of agricultural success, enabling large scale production. However, breeding practices have largely overlooked the plant as a meta-organism, contributing to the uncertain conservation of beneficial relationships between plants and their associated microorganisms. Microorganisms shape nearly all ecological processes on Earth, and their interactions with plants are fundamental to nutrient cycling, pathogen suppression and stress tolerance. In the context of increasing climatic instability and soil degradation, these associations represent an underutilized component of agricultural sustainability, providing an additional layer of biological plasticity that can enhance plant performance under variable environmental conditions. Seeds represent a critical stage in plant-microbe interactions, as they serve as vehicles for the vertical transmission of microorganisms across plant generations. Through this process, seeds can perpetuate endophytic microbial partners that contribute to germination, early plant development and stress resilience. Understanding the ecological processes that shape the seed microbiome assembly is therefore central to explaining how plant-associated microbial communities are formed and maintained. In this talk, I synthesize current knowledge on seed microbiome assembly and present empirical evidence supporting a central role of plant genotype. Using *Cannabis* as a model system, I show that breeding has already significantly altered seed-associated bacterial communities, leading to reduced diversity, and highlight the potential of seed microorganisms lost during this process. This knowledge positions seeds as key vectors for the maintenance and transmission of beneficial microorganisms, opening new perspectives for sustainable cropping systems.

S2-FT02 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Exploring the transmission routes of bacteria to the seeds during plant development

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The seeds harbor a vast array of bacteria, some of which are beneficial, commensal, and pathogenic. Three main routes of seed transmission are described for pathogens: floral route, internal route via the vascular system and external route by contact with fruit tissue (Maude, 1996). Nevertheless, the relative importance of each route in the seed transmission of bacterial members of the microbiota is poorly understood. In the present study we investigated these transmission routes of 12 bacterial strains to bean seeds (*Phaseolus vulgaris*). These strains belong to the main bacterial populations of the bean as well as the phytopathogenic bacterium *Xanthomonas citri* pv. *fuscans* (Xcf). Although Xcf can be transmitted via all three routes, the vascular route was the most efficient with 30% of contaminated seeds with an average of 3 X 106 CFU per seed. In contrast, commensal strains were rarely found in seeds following lone inoculation or in a SynCom context (five contaminated lots out of 200). We examined the capacity of bacteria to colonize the plant via the vascular system and identified two bottlenecks for the transmission to seed: the passage from the stem to the pods and the passage from the funicle to the seed. A type III secretion system mutant of Xcf was able to colonize the vascular tissues of the stem but not early pods, suture, funicle or seeds no matter the route used. This gives us new insights on the implication of the plant's immune response in the transmission of bacteria to seeds. Plant/bacteria molecular dialogue and potential functional complementation between strains to bypass the plant immunity are the next focus for the understanding of the transmission of bacteria to seeds.

S2-T01 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Seed Microbial Inheritance Shapes Microbiome Assembly in Date Palm (*Phoenix dactylifera*)

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Seeds represent critical interfaces where plant development, microbial inheritance, and environmental selection converge. In desert crops such as the date palm (*Phoenix dactylifera* L.), seed-associated microbiomes may play a key role in early establishment and stress adaptation. Here, we investigated the assembly, transmission, and functional potential of bacterial and fungal communities across the seed–plant continuum of Ajwa date palm, with emphasis on seed microbial inheritance and compartmental filtering. Using 16S rRNA and ITS2 amplicon sequencing integrated with ecological and network analyses, we profiled microbiomes across seed- and plant-associated compartments, recovering over 18 million high-quality sequences and identifying 11,197 bacterial and 6,285 fungal non-singleton ASVs. Bacterial communities exhibited strong compartment-specific structuring, with diversity progressively declining from external environments to internal tissues, reflecting pronounced host filtering. In contrast, fungal communities showed greater compositional continuity across compartments. Seeds emerged as distinct microbial niches, harboring conserved fungal assemblages dominated by *Rhodotorula*, *Penicillium*, and *Hanseniaspora*, alongside dynamic bacterial taxa, particularly *Pseudomonas*, enriched during germination and early root development. SourceTracker analyses revealed contrasting transmission strategies: fungal communities were predominantly vertically inherited, whereas bacterial communities combined vertical transmission with substantial environmental recruitment. Functional profiling indicated enrichment of stress response, secondary metabolism, and defense-related pathways within the seed microbiome, supporting its role in early developmental priming. Together, these findings establish seeds as active microbial reservoirs shaping microbiome inheritance and plant adaptation in arid environments.

S2-T02 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Capsaicin Shapes Microbial Diversity and Transmission Across *Capsicum* Fruit Tissues

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Plant-associated microbiomes are shaped by complex interactions between host tissues and plant-derived chemical compounds. Capsaicin, a key secondary metabolite in *Capsicum* fruits, is widely recognized for its antimicrobial properties. However, it remains unclear whether capsaicin acts solely as an antimicrobial agent or plays a more complex role in structuring microbial diversity and transmission across plant tissues. This study investigates whether capsaicin concentration influences bacterial transmission and diversity across different fruit related tissues (peduncle, placenta, and seeds) in multiple *Capsicum* varieties. Microbial communities were analyzed using V4 16S rDNA amplicon sequencing. Despite technical limitations due to host DNA amplification, consistent patterns were observed. Bacterial community composition varied significantly with capsaicin levels, particularly in the placenta, where differences correlated with pungency. Seed-associated communities aligned along the capsaicin gradient, suggesting a potential filtering effect during microbial transmission. Taxonomic analysis revealed increased relative abundances of Firmicutes and Bacteriota in high-capsaicin varieties, while Actinobacteriota increased from peduncle to seed. Although bacterial diversity decreased along the tissue gradient, higher pungency levels were associated with increased diversity across all tissues, contradicting the expected antimicrobial filtering effect. Overall, the results indicate that capsaicin plays a complex role in structuring microbial communities in *Capsicum* fruits, potentially influencing microbial transmission and diversity. These findings provide new insights into plant-microbe interactions and highlight the need for further research on the ecological and agricultural implications of capsaicin.

S2-T03 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Soil microbial diversity loss impairs plant performance but not seed microbiome assembly in *Setaria viridis*

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Plant-associated microorganisms play essential roles in plant nutrition, stress tolerance, and overall host productivity. Although soil microbial communities are a major reservoir of plant-associated microbes, the mechanisms governing seed microbiome assembly and stability under environmental perturbations remain poorly understood. Here, we investigated the combined effect of soil type, microbial diversity, and heatwave stress on *Setaria viridis* development and seed microbiome assembly. We hypothesized that reduced soil microbial diversity would decrease plant productivity, exacerbate heatwave-induced stress responses, and alter associated prokaryotes; however, the functional diversity of seed endophytes would remain stable. Across three complementary plant growth experiments, plants were grown in soils with reduced microbial diversity, established using a dilution-to-extinction approach by mixing agricultural soil with γ-irradiated soil. Plants were grown through a full life cycle, and plant productivity, physiological responses, and microbial communities were assessed using 16S rRNA gene amplicon sequencing and metagenomics, together with physiological, metabolomic, and proteomic analyses. Reduced soil microbial diversity consistently impaired plant performance, leading to significant declines in plant height, biomass, root development, and yield. These effects were accompanied by elevated physiological stress indicators, including malondialdehyde, proline, and anthocyanins. Heatwave exposure further altered plant metabolic and proteomic profiles, including the upregulation of small heat shock proteins. Despite pronounced differences in soil microbial communities and plant responses across treatments, the seed microbiome remained remarkably stable. Seed endophytic communities exhibited highly similar taxonomic and functional compositions across soils and microbial diversity gradients, with a substantial proportion of putative diazotrophic bacteria consistently detected. Moreover, the functional diversity of seed endophytes remained comparable to that of the parental seeds. These findings indicate that *S. viridis* assembles a consistent seed microbiome largely independent of soil microbial diversity. Together, our results suggest strong host-mediated microbiome assembly that may help preserve plant reproductive success across generations under contrasting environmental conditions.

S2-T04 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Fungal endophytes as heritable microbial resource for plant resilience

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Fungal endophytes are symbionts that inhabit plant tissues without causing visible disease and often enhance host fitness. Among their ecological strategies, vertical transmission i.e., inheritance from parent plants to their offspring via seeds or reproductive tissues, plays a critical role in shaping endophyte persistence, plant–microbe coevolution, and the stability of beneficial traits across generations. Here, we present a collection of more than 2,000 fungal endophytes isolated from multiple host plant species. Of note 17 % of the fungal strains correspond with genera reported to be potentially vertically transmitted *Epichlöe* (142 strains), *Fusarium* (128 strains), *Alternaria* (22 strains), and *Nigrospora* (8 strains). These genera were mainly isolated from perennial grasses such as *Festuca rubra, Lolium perenne*, *Celtica gigantea*, and *Holcus lanatus*, growing in limiting or extreme environments. Each isolate was characterized using culture-based methods and ITS sequencing for taxonomical identification. For many of them, functional characterization based on plant growth-promotion data is also available. This collection provides a foundational resource for understanding vertical transmission and for identifying fungal features required to function as seed inoculants for sustainable agriculture and plant resilience.

S2-T05 Oral presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Beyond Environment: Host Genetics' Role in Shaping Seed Microbiomes

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Early research looked at the seed microbiome through the lens of plant pathology. This stance has since changed due to increasing evidence regarding the crucial role of the seed microbiome in plant health. However, there is limited knowledge regarding the factors influencing the composition and assembly of the seed microbiome, particularly in economically important crops like tomato (*Solanum lycopersicum*), but also less-studied African indigenous vegetables. Here, we examine host and environmental factors influencing seed microbiome structure. By using predictive modelling, we also show the influence of various plant inherent traits on the seed microbiome, such as insect resistance, yield, seed weight, number of ovaries, berry colour, berry taste, etc. We hypothesized that the heterogeneity in plant genetic background is reflected in the seed microbiome and that it not only depends on the region of production, but also on certain host traits. We detected high effective bacterial diversity in the range 20 to 150 amplicon sequence variants (ASVs); with host genetics, more than geographic region of tomato production contributing towards shaping the tomato seed bacterial community (R2=56% vs. 11%). Indigenous Nigerian Vegetables Harbour Plant Species-Specific Seed Microbial Signatures for Bacteria and Fungi. The core seed microbiota was comprised by potentially plant-beneficial taxa such as those categorised in bacterial genera *Methylobacterium*, *Bacillus*, *Paenibacillus*, *Stenotrophomonas*, *Pseudomonas*, *Serratia*, *Pantoea*, *Shingomonas*, and *Lactobacillus*; fungal genera *Aspergillus* and *Fusarium*; as well as archaeal genus *Methanobrevibacter*. This research highlights the crucial role of plant genetics in shaping the seed bacterial community, uncovers the plasticity of the seed microbiome, and provides a basis for seed microbiome engineering approaches, including the use of unique African germplasm in the search for novel bioproducts.

S2-P01 Poster presentation

Day 1 – Structure and Transmission
Session 2: Microbial Inheritance: Routes and Mechanisms

Arabidopsis seed microbiome and its effects on seed germination

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The seed endophytic microbiome is selectively conserved within seeds by the mother plant and transmitted across generations, playing a crucial role in early plant development, particularly during germination. The composition of seed endophytes is primarily influenced by host environment. In this study, we examined how different environments affect the seed endophytic bacterial communities of *Arabidopsis* by analyzing seeds from wild populations collected across various locations in Spain, as well as seeds from greenhouse populations cultivated under controlled conditions with both microbiome-enriched and low-diversity substrates. Seeds were surface-sterilized to remove epiphytic bacteria, and the endophytic bacterial communities were assessed using targeted 16S rRNA gene sequencing. Significant variation in seed endophytic bacterial communities was observed among wild populations, likely due to diverse environmental conditions, soil microbiomes, and plant-microbe interactions specific to each habitat. Conversely, no substantial differences were found within greenhouse populations, suggesting that controlled environment conditions contribute to a more homogeneous microbiome. A comparative analysis of wild and greenhouse populations revealed distinct microbial compositions. However, certain bacterial families, such as Carnobacteriaceae, Lachnospiraceae, Helicobacteraceae, and Muribaculaceae, were present in both, forming the *Arabidopsis* seed core microbiome. In addition, bacterial endophytes isolated from wild *Arabidopsis* seed populations significantly enhanced germination under osmotic stress.

S3-K01 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Winds of Change: Holobiont Biology, Phylosymbiosis, and Biology's Shifting Disciplinary Matrix

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The newly appreciated complexity and relevance of host-microbe associations has reached a critical inflection point, necessitating new layers in core biological principles. Consequently, bridging the micro- and macrobiological scales has become a fundamental requirement for modern plant science and general biology. The synthesis of biological processes across microscopic and macroscopic scales has spurred the rise of holistic terms and tools to significantly enhance biology's wider lens on the causes and consequences of trait variation, microbial flow through ecosystems, and evolutionary dynamics. Beyond theoretical frameworks, this unification provides a scaffold for One Health initiatives, translating basic science into tangible advancements in crop resilience, sustainable food production, and human health. In this presentation, I will examine these overarching themes, illustrating how an integrated biological perspective can address complex divisions in biology.

S3-FT01 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Seed-Bottleneck Dynamics and Transmission Pathways Shape the Diversity and Persistence of Endophytic Bacterial Lineages

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Intraspecies diversity in seed associated microbes remains one of the least explored dimensions of plant–microbe ecology. As seeds function as key vehicles of vertical microbial inheritance, they also act as evolutionary filters that narrow microbial populations and influence which lineages persist across generations. Yet, the broader principles governing how seed bottlenecks and transmission pathways shape endophytic bacterial diversity remain poorly understood. In this talk, we present a conceptual framework for exploring how population level patterns, genomic signals and ecological behaviour converge to reveal the long term trajectories of seed borne bacterial lineages. By examining bacterial isolates from seeds belonging to the same species and integrating genomic information with phenotypic characterisation, we uncover consistent signatures of seed associated specialization. These signatures point toward strong population bottlenecks during seed formation and stable transmission across plant generations as key structuring forces. Across seed samples from varied geographical origins, we observe the emergence of a single, highly similar bacterial lineage that persists within seeds yet shows distinct ecological limitations in other plant microenvironments. These include reduced performance in niches that demand greater dispersal capacity or rapid environmental responsiveness. Such patterns suggest that adaptation to the protected, stable conditions of seeds may impose trade-offs that shape the ability of this lineage to succeed across other environments. Overall, this work highlights the central role of seed stage constraints and transmission pathways in directing the diversity, specialization and persistence of endophytic bacterial populations. Understanding these dynamics provides a foundation for predicting how microbial lineages are inherited, maintained and filtered through plant life cycles and across agroecosystems.

S3-FT02 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

The impact of domestication and selection on seedborne microbiomes in tomato

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Plants transmit a diverse assortment of microbes within their seeds, many of which can be beneficial for plants. However, the understanding of how plant genetic factors influence these dynamic relationships is still unclear, which limits the capacity to harness these microbiomes for crop productivity. Plants evolved alongside their beneficial microbial symbionts in natural systems where plants and microbes were dependent on each other to acquire resources and withstand biotic and abiotic stress. Over domestication and subsequent selection in high-input agricultural systems, plants may have become less dependent on these beneficial relationships. Hence, by going back to the wild ancestors, it may be possible to uncover these lost traits. To investigate this hypothesis, this study is quantifying the composition and functional capacity of seedborne microbiomes in tomato, one of the world's most important vegetable crops. The study is being conducted in a set of genotypes that spans the domestication gradient and includes wild relatives, landraces, heirloom, and modern genotypes selected under organic and conventional systems. For this study, plants were grown under standard greenhouse conditions, and collected seeds were germinated in axenic conditions for later study of the microbiome in two-week-old seedlings using 16S next-generation amplicon sequencing and functional prediction. Results to date indicate that domestication alters the abundance of seed-transmitted *Bacillus* and seedlings host bacteria with metabolic pathways for resource allocation under scarcity. Results of this study will provide new insights into how anthropogenic selection can influence seedborne microbiomes and help pave the way for microbiome-informed breeding and management strategies.

S3-T01 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Effects of plant identity and pollination strategies on seed microbiomes

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The seed microbiome is shaped during plant reproduction and can be transmitted across generations, yet the relative importance of host traits versus phylogeny remains unclear. Because seeds arise from reproductive tissues, mating systems and pollination strategies may influence microbial assembly by altering microbial exposure and dispersal. Alternatively, these effects may largely reflect host species identity. Here, we conducted a meta-analysis of seed microbiomes from 52 angiosperm species to test how mating systems (autogamy, allogamy) and pollination syndromes (wind, insect) relate to microbial diversity and composition, and to compare their effects with host identity. We integrated 16S V4 amplicon data from the Seed Microbiota Database with trait data from the TRY Plant Trait Database and assessed their influence on bacterial communities. Preliminary analyses show higher bacterial diversity in self-pollinated and insect-pollinated plants, with distinct community composition across pollination strategies. However, these effects become non-significant when accounting for host species identity, indicating that plant identity is the dominant driver of seed microbiome structure. These findings highlight the need to disentangle trait-based and phylogenetic effects when interpreting seed microbiome patterns and emphasize the importance of multi-species frameworks across evolutionary gradients.

S3-T02 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Metagenomic analysis reveals seed lot effects and microbial filtering during parsnip seed to seedling transition

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The seed microbiome plays a critical role in early plant development, yet remains poorly characterised in parsnip (*Pastinaca sativa*), despite its commercial importance in North America, Asia and Europe (Jha et al., 2025). While seed microbiome studies have been reported for other Apiaceae crops, such as carrot, comprehensive microbiome analyses across seed compartments and developmental stages are lacking for parsnip (Kumar et al., 2023). Parsnip seeds are particularly affected by dormancy and seed-borne phytopathogens, which reduce seed viability, delay germination, and weaken seedling vigour (Chappell et al., 2024; Nakabayashi et al., 2025). In this study, we used amplicon-based metagenomics to characterise the parsnip seed microbiome across distinct compartments (epiphytic and endophytic) and developmental stages (seed and seedling) using seed lots originating from France and New Zealand. This approach allowed us to investigate microbial composition, transmission, and restructuring during early plant establishment. Our results show that whole-seed microbial community composition differed significantly between seed lots, with seed lot explaining approximately 50% of the variation in bacterial communities and 76% of the variation in fungal communities. In contrast, endophytic bacterial communities showed a more moderate but still significant seed lot effect ($R^2 = 0.36$, $p = 0.027$), while endophytic fungal communities did not differ significantly between seed lots ($p = 0.13$). Despite variation in harvesting time, geography, environmental conditions, storage practices, and storage duration, these findings suggest the presence of a relatively conserved core endophytic microbiome maintained within seeds. Transition from seed to seedling was marked by strong microbial filtering. Bacterial abundance increased by approximately 2–2.5-fold, while fungal diversity decreased by 36–68%, indicating a major restructuring of the microbiome during germination. Several microbial taxa detected at the seedling stage were absent or below detection limits in seeds, suggesting that rare seed-associated microbes flourish under favourable seedling conditions rather than being newly acquired from the environment. This filtering may be driven by seedling immune responses, microbial competition, and changes in microbe-specific nutrient availability during germination. Overall, this study highlights germination as a key ecological bottleneck shaping the parsnip microbiome and provides evidence for selective enrichment of specific microbes during early plant development. These findings open opportunities to identify beneficial seed-associated microbes, isolate them, and test their reinoculation potential to enhance parsnip germination, seedling establishment, and early growth, contributing to future seed microbiome engineering strategies.

S3-T03 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Maize seed endophyte microbiome assembly: from ear to field scale

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Exploiting vertical transmission in plants to enhance microbe-mediated crop resilience is a promising strategy for promoting sustainable agriculture. Despite this, little is known about what controls seed community assembly and to what extent this occurs across the plant Kingdom. Maize hybrid varieties present an attractive model for study in that they are widely grown, agronomically important, exhibit genetic identity and are primarily wind-pollinated by neighboring plants. In this study, we explored maize seed endophytic bacterial communities across a spatial gradient, from individual ears to adjacent plants and across fields, in order to explore the core seed microbiome and determine variability in community structure across a wide spatial scale. We sampled hybrid DeKalb 70-27 maize from two research plots in central Kentucky, USA during Fall 2023 at ~30% seed moisture. Sampling occurred along a transect at four different sites per plot, with ears collected from adjacent plants at each site, totaling 16 ears. Multiple kernels were aseptically removed from each plant, with 100 kernels sampled in total. Kernels were surface sterilized, macerated and resuspended in phosphate-buffered saline, with the resulting macerate used for cultivation on three different media types and for 16S rDNA amplicon sequencing. Total CFU count was determined, and unique colony morphotypes were taxonomically identified using full-length 16S rDNA sequencing. CFU count varied dramatically between kernels, with no observable trends across spatial scales. Bacillota, Pseudomonadota and Actinomycetota were the most highly represented phyla among the cultured isolates, with *Bacillus*, *Stenotrophomonas* and *Curtobacterium* the most common genera from these phyla, respectively. Amplicon data analysis validated core taxa across the two methodologies, with richness highly dependent on individual kernel. High variability between kernel communities was observed, with hierarchical variance partitioning analysis indicating that kernel-level heterogeneity predominates, suggesting stochastic processes were primary contributors to community assembly.

S3-T04 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Microbiome Assembly Differs in Selected Sugar Beet Varieties Depending on Tolerance Towards Fungal Pathogens

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Seed and soil microbiota contribute to the plant microbiome, whose composition is crucial for plant pathogen tolerance. Sugar beet (*Beta vulgaris* L.) is the main agricultural source of sucrose under moderate climatic conditions, and its cultivation is confronted with various pathogens causing severe agronomic damage. These damages are specifically impactful during the seedling stage, as the rhizosphere microbiome is formed. Sugar beet breeding efforts often aim to increase tolerance to pathogens; however, increased tolerance to one pathogen may sometimes lead to a trade-off, affecting plant tolerance to other pathogens. Here, we investigated the relative importance of soil and seed microbiomes as sources of sugar beet seedling microbiomes in the rhizosphere, rhizoendosphere, and phyllosphere of seed lots of six different sugar beet cultivars of varying pathogen tolerance using a metabarcoding approach. Results from in silico analyses were used to design follow-up greenhouse experiments to test the derived hypotheses regarding the correlation of seed- or soil-derived microbiota on pathogen tolerance. The proportion of microbes originating from seeds increases progressively from the rhizosphere to the rhizoendosphere and then to the phyllosphere, whereas soil-borne microbes exhibit an opposite trend. Seed-borne bacteria colonize the rhizosphere in high abundances, while seed-borne fungi appear less abundant in the rhizosphere. Fungi in the phyllosphere majorly originate from seeds, while the proportion of soil-derived fungi in the phyllosphere is cultivar-dependent. Depending on the cultivar, a high microbial species richness in seeds does not necessarily correspond to high species richness in the rhizosphere, rhizoendosphere, or phyllosphere. Artificially decreasing soil microbes in growth substrates affected pathogen tolerance in follow-up greenhouse experiments, confirming our hypotheses. We hereby present a summary of plant microbiome assembly processes in sugar beet seedlings, highlighting and discussing the importance of seed and soil microbial diversity for protection against plant pathogens.

S3-T05 Oral presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Exploring vertical transmission of maize embryo bacterial microbiota in local varieties of Northern Italy

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Local varieties of crops are a reservoir of valuable genetic resources for addressing challenges to agriculture such as climate change and soil degradation that threaten food security and agricultural sustainability. Italian maize varieties, that farmers have developed as open pollinated populations in diversified climatic zones, represent an interesting resource for their adaptative abilities to different local environments which could be related not just to their genome, but also to their microbiota. In the GEMMA project (GEnotipi di Mais lombardo e MicrobiomA – Regione Lombardia), four Italian maize varieties, maintained at CREA Bergamo Genebank, were cultivated for three successive years in four different locations in Lombardy to understand which components of the seed-associated microbiota are determined by plant genetic background, and which are influenced by the environment. After each year of cultivation, NGS analyses on 16S gene were performed on DNA extracted from the maize embryos to characterize their bacterial communities. The results show that seeds of most of the 16 landrace-location combinations had a homogeneous situation with over 90% of Pseudomonadota after the first year of cultivation. After the second multiplication year, higher biodiversity was found and more differences could be seen between the combinations of landraces and cultivation sites, highlighting a strong influence based on the latter. Embryos obtained from plants of different landraces cultivated in the same field still showed specific patterns, indicating that also the plant genotype played an important role in shaping the microbiota. Data from the third year of cultivation showed gradual enrichment in Bacillota and reduction in Pseudomonadota in seeds multiplied in one location, agreeing with previous data obtained from that field. Overall, our results show little direct vertical transmission of bacterial embryo microbiota across generations, but a strong selection that adapts the seed microbiota to the soil the plants are growing in.

S3-P01 Poster presentation

Day 1 – Structure and Transmission

Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Influence of agro-management on soybean seed and plant microbiomes and early plant development

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Soybean is one of the most globally cultivated legume crops. Soybean seeds serve as a major source of plant-derived oil and protein for both food and feed systems. Both seed quality and plant development are strongly influenced by interactions with associated microbial communities, underscoring the importance of investigating seed and plant microbiome assembly and function under field conditions. We conducted a field trial (Bologna, Italy), using five soybean varieties with distinct traits: EM Pura, NAV 555 (high protein content), OL996 (high oleic acid content), and AMMA and Bahia (both have low trypsin inhibitor content). Three different management regimes were applied, i.e., conventional (typical tillage), conservational (reduced tillage and mechanical weeding), and organic (typical tillage, with no synthetic agrochemicals). Rhizosphere and root samples at different growth stages, as well as bulk soil and seed samples, were analyzed using 16S rRNA gene amplicon sequencing. Agronomic data were recorded, and plant microbiomes were analysed by 16S rRNA gene amplicon sequencing. Additionally, early seed vigour and germination capacity were assessed. Agro-management practices significantly influenced bacterial diversity and richness across sample types, alongside plant performance. Overall, these findings demonstrate that management strategies shape soybean-associated microbiomes, with downstream effects on seed quality and early plant development.

S3-P02 Poster presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Seed-Derived Microbiome Recruitment in the Rhizosphere: Effects of Osmotic Stress on Microbial Community Assembly in *Brachypodium distachyon*

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The seed microbiome represents a reservoir of microbial taxa that has co-evolved with the host plant and is expected to support plant health and productivity. Seed-associated microbes can colonise emerging plant compartments, including leaves, stems, and roots, and contribute to the assembly of rhizosphere microbial communities. In this study, we used the model plant *Brachypodium distachyon* to investigate the recruitment and enrichment of seed-derived microbiota in the rhizosphere during early seedling development. To robustly track microbiome dynamics originating from seeds, plants were grown under both sterile (water agar) and soil-based systems, allowing comparison between controlled and environmentally complex conditions. We further examined how osmotic stress influences microbial community assembly. Using 16S rRNA gene profiling, we found consistent evidence that seed-associated microbes contribute to microbial communities across plant compartments, including the rhizosphere, in both systems. This process was selective and strongly influenced by environmental conditions. Notably, members of the genus *Bacillus* were the most abundant seed-derived taxa enriched in the rhizosphere of B. distachyon seedlings, while *Paenibacillus* showed greater enrichment under osmotic stress conditions. Overall, our findings highlight the important role of the seed microbiome as a source of rhizosphere-associated microbes and demonstrate that environmental factors, such as osmotic stress and growth substrate, shape microbial recruitment and community composition. These results provide new insights into early plant–microbe interactions and support future strategies to harness seed microbiomes for improving plant resilience and productivity

S3-P03 Poster presentation

Day 1 – Structure and Transmission
Session 3: Dynamics of Microbial Transmission Across Plant Compartments

Fruit function beyond dispersal: effect of fruit decomposition on the plant microbiome assembly

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The ecological role of fruits has traditionally been viewed through the lens of seed dispersal. Yet, their effects on soil and plant microbiomes after decomposition remain unexplored. We proposed that decomposing fruits modify the soil microbiome and subsequently influence the plant microbiome and performance. Using amplicon sequencing, we characterized bacterial communities in soil, rhizosphere, and phyllosphere of tomato and chili plants cultivated with or without their fruits. Fruit decomposition altered soil chemistry, increased bacterial diversity, and reshaped community composition. Members of Blrii41, Sandaracinaceae, and functions linked to methanol oxidation, nitrification, and mammalian/human gut metabolism were enriched. Decomposition also reduced germination rates and affected shoot growth, while root length remained unchanged. In the phyllosphere, diversity decreased, and both rhizosphere and phyllosphere communities shifted markedly. Plant-associated microbiomes exhibited higher functional potentials for ligninolysis, methanol oxidation, methylotrophy, and xylanolysis, among others. Overall, our results demonstrate that fruits exert post-dispersal effects on the seedling environment and early plant microbiome assembly, challenging the classical view of fruit function and highlighting opportunities to harness fruit-derived microbiomes.

S4-K01 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

What is shaping the seed microbiome?

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Research of the last years has provided evidence for the importance of the seed microbiota for plant health and resilience. Individual seed endophytes were not only shown to be crucial for the protection against highly devastating phytopathogens but also to protect against abiotic stress and support germination as well as early seedling development. A detailed understanding of factors that shape the seed microbiome could pave the way for targeted engineering approaches. So far, large-scale assessments within individual crop species have shown that the plant genotype is likely the main factor influencing the composition and structure of the seed microbiome. This provides opportunities to explore links between host genetics and individual members of the microbiota to define potential breeding targets in the future. On the other hand, it is also important to elucidate which genetic determinants are required in microbes to efficiently colonize seeds. Targeted analyses have led to the identification of a set of genes in the core seed microbiome member *Pantoea*. This provides the basis to understand how beneficial microbes establish a stable and long-lasting symbiosis with their plant host. In addition, agricultural practices such as pesticide and fertilizers use were shown to exert effects of varying degrees on seed endophytes. A detailed understanding of the underlying mechanisms would enable us to develop strategies for plant production that do not harm beneficial microorganisms or even promote them. Using the current momentum in seed microbiome research could allow us to close critical knowledge gaps in order to fully harness the potential of seed-associated microbes in driving more resilient, sustainable plant production systems.

S4-FT01 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Drivers of Seed Microbiome Assembly: Roles of Breeding, Fertilization, and Storage

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The seed microbiome of oilseed rape (*Brassica napus* L.) was investigated from multiple perspectives to understand how breeding, nitrogen fertilization, and storage-related processes shape microbial community structure and function. Breeding was identified as a major factor influencing the seed microbiome. Across multiple European field sites and cultivars, seeds consistently harbored diverse bacterial communities dominated by genera such as *Ralstonia*, *Serratia*, *Enterobacter*, *Pseudomonas*, *Pantoea*, and *Sphingomonas*. The cultivar explained significant variation in microbial diversity and composition, with specific bacterial taxa associated with improved germination and disease resistance. Analysis suggests potential vertical transmission, indicating that both parental lines contribute to microbiome inheritance and may influence offspring performance. Nitrogen fertilization also significantly shaped microbiome structure. Prolonged low nitrogen availability over two growing seasons enriched nitrogen-fixing bacterial taxa such as *Rhizobium* and other Rhizobiales, along with increased abundance of nifH genes in seeds. Storage-related stress was further examined using accelerated aging experiments to assess seed storability. Accelerated aging reduced microbial diversity, shifted communities toward Gram-positive taxa, and correlated with decreased germination and abnormal seedling development. Positive relationships between microbial diversity and germination suggest that microbiome composition may serve as an indicator of seed quality. In contrast to accelerated aging, long-term storage in seed banks provided insight into microbiome changes during archiving. Seed microbiome analysis of endemic alpine plant species revealed that prolonged storage homogenized microbial communities and reduced differences driven by plant genotype. However, active microbial communities persisted and shifted dynamically during germination stages, indicating the presence of a viable rare biosphere. Differences between storage facilities further demonstrated that storage conditions influence microbial diversity and composition. These findings highlight the importance of microbiome-informed breeding, sustainable fertilization strategies, and optimized storage practices for agriculture, seed conservation, and biodiversity preservation.

S4-FT02 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

The Seed Microbiome: From Research to Field Applications

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Global research on the plant microbiome has enhanced our understanding of the complex interactions between plants and microorganisms. Considerable research has been conducted on the microbial diversity, structure, and composition of plant microbiota, as well as their functions and the sources and niches of colonization of specific microbial strains. In particular, the plant microbiome associated with the rhizosphere and root endosphere, as well as plant organs such as flowers, fruits, and seeds, has been extensively studied. Microbial ecology studies have shown that seed microorganisms originate from different sources, including flowers and roots, and that specific microbiota become established within seeds. Studying the plant and seed microbiomes and the sources of microbial colonization has led to the development of various microbial applications aimed at improving crop productivity. Although gaps in research remain that limit the full utilization of plant and seed microbiome functions for sustainable plant production, certain microbial strains and emerging technologies have shown promise in enhancing crop performance. These include strains that increase seedling growth, promote plant health, and technologies designed to incorporate beneficial microbial strains into seeds, with demonstrated results ranging from laboratory to field conditions.

S4-T01 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

A semi-invasive method linking the seed microbiome to stress resilience in wheat

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Seeds harbor complex and diverse microbial communities that play a crucial role in plant development, health, and stress resilience. However, investigating seed-associated microbiota remains challenging, as most current methods require destructive sampling, preventing downstream phenotypic analyses of the same plant. In this study, we present a novel semi-invasive method for profiling the seed microbiome during early germination while preserving plant viability. Using wheat as a model plant, we evaluated multiple root excision strategies and identified the removal of two lateral roots as an optimal approach, yielding sufficient microbial DNA for sequencing without impairing plant growth under both standard and abiotic stress conditions. Applying this method, we examined microbiome dynamics under cold, drought, and salt stress by comparing best- and worst-performing plants. High-throughput sequencing revealed that while alpha diversity remained largely unchanged across conditions, microbial community composition was significantly shaped by stress type, sampling time, and plant performance. Core taxa, including *Pantoea* and *Paenibacillus,* were differentially enriched in the best-performing plants under salt and cold stress, respectively. Functional validation experiments demonstrated that inoculation with these taxa significantly enhanced plant growth under corresponding stress conditions (salt: 26.7%; cold: + 36.5%), confirming their role in stress mitigation. Our findings suggest that variation in seed microbiome composition contributes to differential stress tolerance in seedlings and highlight the potential of leveraging beneficial endophytes for crop improvement. Importantly, the presented semi-invasive approach enables direct linkage of microbiome structure to plant phenotype, providing a powerful tool for future studies on plant-microbe interactions and microbiome-assisted breeding strategies.

S4-T02 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Seed-Derived Diazotrophic Redundancy Associated with Belowground Taxonomic Identity of Sugar beet

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The seed microbiome is considered the primary inoculum for the plant holobiont, yet the transition from early seedling to mature communities remains poorly understood in agroecosystems. While lab-based studies suggest direct inheritance, moving this understanding to real-world field trials is critical for developing effective seed-based applications. In this study, we investigated the successional dynamics of the sugar beet (*Beta vulgaris*) microbiome between two distinct varieties with contrasting seed microbiota in a field trial. To move beyond culture-dependent functional assignments, we quantified nifH gene abundance via qPCR as a proxy for diazotrophic potential across seed and mature rhizosphere-root communities sampled at the 8-leaf stage and paired it with metagenomic data. Our results reveal that while bacterial communities in the seed, root, and rhizosphere were distinct and distinguishable by variety following a structured successional shift. We observed homogenous community dispersion between seed and mature root communities within varieties despite minimal taxonomic contribution from the seed. Furthermore, community divergence between the rhizosphere and root endosphere strongly covaried with nifH gene abundance, with each variety displaying distinct accumulation patterns. These findings suggest that genotype is the ultimate architect of microbiome composition, utilizing the seed not as a taxonomic source, but as a functional blueprint. By observing the seed-borne diazotrophic redundancy, we observed similar patterns in mature communities highlighting the effectiveness of functional molecular quantification. These findings provide a potential framework to assess seed microbiomes within variable conditions and highlights the importance of how functional redundancy from seed may be a genotype-dependent trait and influence later taxonomic identity.

S4-T03 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

From seed to seedling: cold plasma stimulates seedling growth without disturbing the seed microbiome of *Brassica napus*

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With growing legal restrictions on pesticide use under the European Green Deal, non-chemical seed treatments are becoming increasingly important. Cold atmospheric pressure plasma (CAPP) is a promising alternative because it can improve seed hygiene and stimulate plant growth without adding synthetic chemicals. However, its effects on the seed microbiome, especially possible long-term changes, are still poorly understood. Since seed-associated microbes are the plant's first inoculum, they may influence germination, seedling vigor, disease resistance, and stress tolerance, making them important for crop performance and food security. The study presented here investigated seeds from four *Brassica napus* genotypes, represented by six accessions, and the corresponding seedlings at 48 and 96 hours after germination. The aims were to assess: (i) how CAPP treatments of two exposure times affect seed vigor and seedling development; and by using 16S rRNA gene amplicon sequencing: (ii) how CAPP and germination stage influence bacterial communities; and (iii) to what extend does genotype/accession determine microbial composition. A short CAPP exposure of 3 seconds significantly increased radicle length and surface area in four of the six accessions, whereas a longer 10-second treatment had negative effects on seedling development. Microbiome analysis showed that CAPP had no significant effect on bacterial alpha diversity and only minor effects on beta diversity. In contrast, genotype/accession and germination stage were the main factors shaping the bacterial community. Notably, Firmicutes increased by 96 hours after germination. Five bacterial genera were detected consistently across all accessions and time points, indicating a stable, vertically transmitted core microbiome that was not altered by CAPP. Overall, the results show that short CAPP exposure can improve germination in B. napus without disrupting the natural seed microbiome, while longer exposure is harmful. Thus, CAPP appears to be a promising environmentally friendly seed treatment that supports plant development while preserving beneficial microbial communities.

S4-T04 Oral presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Seed coat mucilage regulates spermosphere microbiome composition, which influences root architecture of the emerging seedling

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Seed coats contain a diverse range of specialized structures and adaptations that presumably contribute to seed dispersal and survival. In particular, seed coats of many angiosperms synthesize a polysaccharide mixture known as mucilage, which absorb water, expand and encapsulate seeds when wetted. Despite seed coat mucilage being a fairly widespread occurrence, its biological relevance remains mostly unclear. Here we hypothesize that seed coat mucilage is involved in the establishment of microbiome community around the seed surface, i.e. spermosphere. Many soil microorganisms are known to associate with plant roots or seeds, and can have profound effects on the host plant's growth. Since mucilage extrusion drastically alters the spermosphere's physical properties, it presumably also changes the spermosphere microbiome ecology, which in turn may affect the host plant. To test this hypothesis, we compared the *Arabidopsis* spermosphere microbiomes of the wild-type (Col-0) with the mucilage extrusion-deficient mucilage modified 2 (mum2) mutant. Interestingly, Col-0 spermosphere contains a markedly higher proportion of bacteria in the genus *Paenibacillus* than mum2, suggesting *Paenibacillus* may preferentially interact with *Arabidopsis* seed coat mucilage. Although none of the spermosphere *Paenibacillus* strains we isolated significantly affect *Arabidopsis* seed germination, one particular strain (a3) was found to suppress main root elongation while enhancing lateral root formation. This *Paenibacillus*-induced root architecture shift appears to be regulated by a combination of auxin and nitrogen signaling, although the precise mechanisms remain uncharacterized. In summary, seed coat mucilage may have the biological function of regulating spermosphere microbiome community, which can continue to influence the growth of host plant after seed germination.

S4-P01 Poster presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

The Seed Microbiome and Its Role in Plant Health: What We Know and What Remains to Be Explored

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Seeds represent a critical stage in the plant life cycle, serving as both a vehicle for reproduction and a reservoir of microbial partners. The seed microbiome profoundly influences both plant health and productivity, as well as their ability to adapt to adverse environmental conditions. Despite a decade of intensified research into the functional roles of seed-associated microbes, the seed microbiome remains underexplored within the broader field of plant microbiome research. By assessing key studies of the last years, we synthesize recent advances in understanding diversity and composition, transmission pathway, and functional roles of seed-associated microbiota. Moreover, we highlight the most critical knowledge gaps that remain to be answered for a better understanding of seed microbiome assembly and functioning. Advancing this field will not only deepen our ecological and evolutionary understanding of plant–microbiome systems but also contribute to more sustainable crop production and improved food security under changing climatic conditions.

S4-P02 Poster presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Seeds, Microbes, and Drought: Linking Microbiome to Plant Performance

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The seed microbiome has gained increasing interest due to its influence on key aspects of plant development, including germination, seedling vigour, nutrient uptake, and stress tolerance, such as drought stress. However, the microbial functions and molecular mechanisms underlying these effects remain largely unknown. Drought stress is one of the most detrimental abiotic stresses reducing crop productivity and threatening food security, with particularly severe consequences on seed development and quality. Harnessing the seed microbiome offers a promising yet underexplored approach to mitigate these detrimental effects. Here, we present a novel seed-microbiome project, combining microbiome profiling, drought phenotyping, and molecular approaches to investigate how seed-associated microbes contribute to improved plant performance in watered-limited conditions. Specifically, we will address three main research questions which aim to: 1) determine whether plant genetics and seed traits shape seed microbiome recruitment and composition, 2) identify seed-associated microbes that enhance seed and plant performance under drought condition, and to what extent, and 3) understand the molecular mechanisms underlying these beneficial plant-microbe interactions. We will also present preliminary findings revealing a potential link between seed microbiome and plant drought tolerance.

S4-P03 Poster presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Interactive effects of soil and genotypes on pea spermosphere microbiome composition

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Seed contribution to a future plant health and its potential productivity is a major topic across many fields of study – including agriculture, food industry and medicine. Seed exudates influence the spermosphere microbiome from the moment of imbibition, and vice versa; the microbiome affects the seedling and enhances its growth into a healthy plant. We investigated the role of seeds, exudates and metabolites in relation to beneficial microbiome establishment and fungal diseases. We profiled both protein and metabolites in the seed exudates and conducted amplicon-based microbiome sequencing. In particular, selected phenolic compounds markedly suppressed mycelial growth, indicating their functional role in intrinsic seed defence. Concurrently, the presence of seeds promoted the enrichment of specific beneficial, soil-derived microbial taxa, underscoring a bidirectional relationship between exudate composition and microbiome structuring. Ongoing analyses aim to resolve the molecular determinants underlying these interactions, including the contribution of individual exudate metabolites, seed coat pigmentation, and polyphenol oxidase activity. By integrating metabolomic and proteomic profiling of seed coats and exudates with microbiome composition data, this work provides a systems-level perspective on the biochemical drivers of spermosphere dynamics. This study advances a fundamental understanding of how seed traits govern early-stage plant–microbe interactions. Such insights contribute to a mechanistic framework for interpreting the ecological and biochemical processes that underpin microbiome assembly during the earliest phases of plant development.

S4-P04 Poster presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

From Seed Microbiome to Seedling Success: Functional Role of Endophytic Fungi in Douglas Fir

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Seeds harbor various types of microbial communities, some of which play a significant role in the germination process. The favourable influence of plant growth-promoting (PGP) endophytes on host plant growth and development is due to their several plant-growth-promoting activities, such as indole-3-acetic acid production, phosphate solubilisation, nutrient acquisition, reduction in water stress, inhibition of plant pathogens and other influences. Understanding endophyte community assembly of seeds and their role in seedling establishment and survival may be key to designing effective conservation strategies. While seed inoculation with PGP endophytes is well established in agriculture, its application in forest tree species remains comparatively underexplored, although, there are several research demonstrating the positive effects of PGP endophytes on forest tree seed germination (e.g. *Pinus, Picea, Betula*). The aim of our study was thereby to investigate the seed-associated endophytic fungal community of Douglas fir (*Pseudotsuga menziesii*) with the aim of evaluating their functional potential and impact on germination. Seeds were collected from ten mature trees, followed by (i) characterization of seed-associated endophytic fungal community, (ii) isolation of culturable strains and screening for PGP traits, and (iii) assessment of their effects on seed germination. A total of ten endophytic fungal strains were isolated, of which six exhibited at least one PGP trait. These strains were combined into a consortium and applied to seeds via immersion prior to germination assays. Preliminary results indicate a positive effect of the fungal consortium on germination performance. Inoculated seeds exhibited a significantly reduced time to first germination compared to non-inoculated controls, suggesting enhanced germination dynamics. Our findings highlight the potential of seed-associated endophytic fungi as a biological tool to improve germination in forest tree species, with implications for reforestation and conservation strategies.

S4-P05 Poster presentation

Day 2 – Function and Intervention
Session 4: Functions of the Seed Microbiome: Ecology, Interactions, and Plant Performance

Effect of crop diversification on microbial diversity and product quality

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TheDCropS4OneHealth project aims to study the overarching effect of crop diversification on environmental biodiversity, crop health and human health, along the soil-plant-product-gut continuum. It is now well documented that a more diversified crop production is beneficial for the environment and crop health. However, less is known about the effects on plant-associated microorganisms and resulting quality of the harvested product. Indeed, plant-associated microbes are essential to the plant throughout all growth stages and can influence product quality through plant health and disease protection. Additionally, the seed microbiota is pivotal for product conservation, germination and seedling health. In this study we analyze the link between the diversity of rye cultivars and the resulting seed microbiota and metabolites. We have harvested 45 seed samples on-farm experiment consisting of rye cultivated as a single-cultivar (3 fields) or a mix of three cultivars (6 fields). We will then sequence full-lentgth 16S with Oxford nanopore technology and analyze secondary metabolites in the same samples. With this data we aim to uncover the benefits of crops diversification on product quality through microbial modulation.

S5-K01 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Rewiring the Seed Microbiome: From Chaos to SynCom Symphony

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The seed microbiome is emerging as a key lever for improving crop health, vigor, and resilience. Yet engineering remains challenging because seed-associated microbial communities are shaped by strong ecological filters and can display stability across generations. In this talk, we will present our different attempts to engineer seed microbiomes. First, I will review intervention strategies, including attempts to modify microbial inheritance by changing parental environments (drought and nutrient stress). I will then focus on inoculation-based strategies using synthetic communities (SynComs). Examples will include inoculation directly on seeds, where experiments demonstrated feasibility across diverse crops, as well as inoculation of parental plants through vascular, floral, or fruit-associated pathways that are still at preliminary stages. Second, I will discuss the move from intervention to design. The design of SynComs depends on the research question and objective, but in our case we aim to understand the assembly rules governing the microbial transmission from seed to seedling . I will highlight lessons learned from recent work on effective SynCom design and discuss how mechanistic understanding can guide more predictable microbiome manipulation. Overall, engineering the seed microbiome will require moving beyond trial-and-error inoculation toward hypothesis-driven design informed by environmental context, and community assembly principles.

S5-FT01 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

First come, first served? Seed-borne bacteria drive the assembly of the wheat rhizosphere microbiome

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The rhizosphere microbiome is a major determinant of plant health and productivity, yet the ecological processes governing its assembly remain poorly resolved. Soil has traditionally been regarded as the principal source of rhizosphere bacteria, whereas the contribution of heritable seed-borne bacteria has received much less attention. Here, we investigated the coalescence of soil and seed-derived microbiomes in wheat using a complex and reproducible natural rhizosphere community generated through sequential propagation in a microcosm system. By combining 16S rRNA amplicon sequencing with genome-resolved shotgun metagenomics, we found that while soil bacteria were enriched in traits characteristic of oligotrophic bacteria, rhizosphere and seed bacteria were enriched in functions characteristic of copiotrophic bacteria, as well as in traits consistent with efficient exploitation of the rhizosphere environment. Seed-borne rhizosphere bacteria surpassed native soil microorganisms as the dominant source of the early wheat rhizosphere microbiome. These results indicate that vertically transmitted bacteria are major ecological drivers of community assembly during early rhizosphere formation. Functional analyses further showed that seed-borne bacteria were enriched in host-associated traits linked to the degradation of key disaccharides, supporting a mechanism of niche partitioning in the rhizosphere. In addition, these bacteria displayed metabolic features consistent with facilitative interactions, including cross-feeding that supported partner strains. In vitro co-culture experiments confirmed that helper seed-borne strains promoted the growth of other bacteria on disaccharides as the sole carbon source. Together, these results show that seed-transmitted bacteria shape wheat rhizosphere microbiome assembly through both resource partitioning and metabolic facilitation [1]. This work highlights microbial inheritance as a central determinant of rhizosphere succession and provides a tractable framework for studying natural microbiome assembly.

S5-FT02 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Rethinking dormancy through a holobiont lens: inactivation and reactivation of seed-microbiome partnerships

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Desiccation-tolerant seeds are an extreme habitat that imposes severe constraints on microbial survival. From seed development to seedling establishment, desiccation-tolerant seeds undergo physiological fluctuations in water and nutrient availability. These fluctuations are accompanied by endogenous stresses, including desiccation, osmotic, and oxidative stresses, that together position desiccation-tolerant seeds as a model system for studying microbial dormancy, a reversible state of inactivation in response to stress. Water availability critically affects the metabolic quiescence of the seed host, while seed dormancy imposes an additional layer of environmental control over germination. This talk presents a conceptual framework to investigate the dormancy of the seed holobiont and outlines key open questions and opportunities for future research and mechanistic interpretations of seed microbiome dynamics. Focusing on bacterial responses to desiccation and rehydration, we emphasise similarities and differences between microbial and host dormancy within the seed holobiont. Pilot evidence suggests that microbial dormancy supports microbiome persistence throughout the seed life cycle. However, the signals triggering microbial reactivation and the potential interactions between seed physiological states (quiescence and dormancy) and microbial dormancy remain largely unknown. Understanding these dynamics could inform strategies to promote seed germination and seedling establishment by modulating seed-associated microbes, whether beneficial or pathogenic, thereby supporting seed quality.

S5-T01 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

From seed to solution: the sunflower seed microbiome as a source of growth-promoting and drought-resistant microbes

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Sunflower (*Helianthus annuus*), one of Europe's major oilseed crops, is generally considered drought tolerant, however, significant yield losses are registered annually due to frequent heat and drought events. These losses range from 4-10% at the European scale to over 50% in severely affected regions. Sunflowers are most vulnerable to drought stress during their early development, especially from seed germination to seedling establishment. To cope with drought stress and support seed germination, plant growth promoting microorganisms (PGPM) constitute a promising biological strategy, in particular when delivered via seed coatings that enable precise application and improved microbial survival. This project aims to develop microbial seed coatings that enhance early sunflower establishment and drought resilience. Candidate bacterial strains were identified through microbiome profiling of sunflower-associated compartments (seeds, seedlings, roots, and soil) across four Flemish fields using 16S rRNA gene amplicon sequencing. This was followed by targeted cultivation from seed and seedling compartments and functional screening for germination and early growth promotion. The bacterial community analysis showed a decreasing diversity gradient from soil to seed, with inner seeds harbouring a distinct microbiome enriched in plant growth–promoting genera, including *Pseudomonas*, *Streptomyces* and *Nocardioides*. However, these dominant taxa were underrepresented among cultured isolates, with seed derived isolates being dominated by genera such as *Bacillus*, *Corynebacterium* and *Pseudonocardia*. A selected PGPM collection consisting of 107 seed and seedling derived bacterial isolates, supplemented with 66 isolates from the research collection of the Laboratory of Microbiology at Ghent University, is currently being screened for drought tolerance, enhancement of germination performance, and promotion of early seedling growth. Promising isolates will be further characterized by whole-genome sequencing and incorporated into experimental seed coatings for greenhouse validation.

S5-T02 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Chickpea Seed Endophytes as a Source of Potent Bio-inoculants for enhancing Sustainable Agricultural productivity

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The chickpea seed microbiome represents a promising resource for developing effective bio-inoculants. This study represents the isolation and characterization of culturable bacterial endophytes from dry and germinating chickpea seeds (variety P-362) to assess their plant-beneficial potential. Presently, we identified twenty-nine bacterial strains through biochemical and molecular characterization. The potential seed endophytes and rhizosphere microbes were screened and identified as *Bacillus subtilis* BHUJPCS-24, *Brevundimonas* sp. BHUJPVCPR-1, *Brevundimonas naejangsanensis* BHUJPVCRS-1, *Enterobacter hormaechei* BHUJPCS-15, *Bacillus*, *Pseudomonas, Staphylococcus, Pantoea*, *Mixta* sp., for plant growth activity (PGP) testing such as production of Indole-3-acetic acid (IAA), ammonia, siderophore, ACC deaminase, hydrogen cyanide, solubilisation of phosphate and potassium, and suppression of fungal pathogens (*Fusarium oxysporum* f.sp. *ciceris* and *Rhizoctonia* sp.) under in-vitro assays. On the basis of PGP activities, we developed different treatment combination of single, duel, triple and tetra combination for testing their efficiency on chickpea seed under control, pot and field trials. The potential seed endophytes and rhizosphere microbial consortium of *Bacillus subtilis* BHUJPCS-24 + *Brevundimonas* sp. BHUJPVCPR-1 +, *Brevundimonas naejangsanensis* BHUJPVCRS-1 + *Enterobacter hormaechei* BHUJPCS-15 inoculated with chickpea seed (variety P-362) showed significantly increase plant growth, biomass, and yield under pot and field trials. Treated plants also exhibited increased seed macro and micro-nutrient content. Furthermore, inoculation improved soil health by increasing available nitrogen, phosphorus, and potassium, enhancing key soil enzyme activities, and enriching beneficial microbial communities. Our findings provide direct empirical evidence that the chickpea seed harbors a native, beneficial microbiome. These isolates are potent candidates for development as novel bio-inoculants to sustainably enhance crop productivity, nutritional quality, and soil fertility.

S5-T03 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Seed treatment with bacterial and fungal endophytes reshapes rice microbiome while suppressing bakanae disease

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Understanding how biological control agents (BCAs) modulate the plant microbiome is essential to characterise their modes of action and design effective consortia against seedborne diseases. The patented strain RS-ARS2 of *Sphingomonas yabuuchiae* and *Epicoccum catenisporum* RS-GAL41 were isolated from the rice seed endosphere and selected for their ability to suppress *Fusarium fujikuroi,* the causal agent of rice bakanae disease. These two BCAs also previously displayed induction of resistance in rice plants in response to *F. fujikuroi,* measured by increased phytoalexin production and expression of defence-related genes. This work aims to study how these BCAs reshape the rice microbiome when applied as seed dressings, either alone or after F. fujikuroi inoculation. Both BCAs significantly reduced disease severity and incidence, restored germination rates and total biomass relative to the inoculated control. Rice tissues were sampled at 1, 11, and 21 dpg for high-throughput 16S rDNA and ITS amplicon sequencing. Community composition was significantly restructured by both the BCAs and the pathogen. The healthy untreated control generally displayed the highest alpha diversity, though fungal Shannon diversity peaked under RS-GAL41 treatment in inoculated plants. LEfSe analysis highlighted *Kosakonia* as the dominant bacterial taxon enriched in RS-ARS2-treated healthy seedlings, alongside beneficial taxa like *Methylobacterium-Methylorubrum*, *Streptomyces*, and *Paenibacillus*. Concerning the mycobiome, *Humicola*, *Clonostachys*, and *Cephalotrichum* were prevalent, whereas *Fusarium* abundance in inoculated plants was strongly suppressed, particularly in RS-GAL41-treated seedlings. SpiecEasi co-occurrence networks identified structural hub taxa, including *Kosakonia*, Sphingomonadaceae, and Didymellaceae, suggesting how BCAs successfully integrated into the resident microbiome. Notably, targeted robustness analysis revealed that *F. fujikuroi* alone establishes highly resilient network structures, suggesting the pathogen actively remodulates the native microbiome to facilitate its own infection cycle. Together, these results demonstrate that RS-ARS2 and RS-GAL41 achieve disease suppression by reshaping pathogen affected networks and driving specific shifts in the seedling microbiome.

S5-T04 Oral presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Seed Microbes Affect Seedling Metabolism, Microbiome Assembly, and Phenotype in Common Bean depending on Host Variety and Conditions

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Seed microbiota, present from the earliest plant stages, influences germination, emergence, and seedling development - key aspects of seed vigor. Modulating this microbiota via microbial inoculation offers promising agricultural applications, yet early seedling-microbiota interactions and genotype effects remain poorly understood. To explore the functional effects of seed microbiota, we inoculated one *Phaseolus vulgaris* bean variety's seeds with four bacterial consortia of 8 strains each, representing seeds native microbial load. We tracked plant metabolome and microbiota changes from seed to seedling (7 days) in each compartment (cotyledons, hypocotyl-radicle axis and preleaves then cotyledon, stem, leaves, and roots). Inoculated seed taxa persisted mainly in above-ground tissues (> 60% relative abundance), with some taxa becoming prevalent depending on their biotic context (*Siccibacter turicensis*, *Kosakonia*, *Pantoea agglomerans*). The inoculation modulated seedling metabolome, especially in the hypocotyl-radicle axis and later in cotyledons and leaves. The four consortia showed varying impact on the seedling phenotype, from deleterious to neutral to beneficial. We explored the association between inoculated strains and each metabolite relative abundance, for single strain and strain combinations in a time-dependant analysis. We also analysed the delay between inoculation and metabolism shift between conditions. To assess the reproducibility of one consortia beneficial impact, we tested its effects across a panel of 8 diverse bean genotypes and in presence of cold stress. The eight varieties natively displayed a wide range of germination and emergence dynamics and capabilities. The consortia was efficiently transmitted to the inoculated seeds across bean varieties, but showed varying impact on seedling phenotype according to bean variety and condition. Overall, our results highlight the critical role of early plant-microbiota interactions and demonstrate seed inoculation as a tool to engineer seed microbiota to boost crop establishment.

S5-P01 Poster presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Engineering Biopolymer Microgels to Support Beneficial Bacteria for Seed Coatings

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Feeding a growing global population demands resource-efficient and sustainable agricultural technologies. Seed quality critically determines crop yield, and seed coatings offer a powerful platform to enhance seed performance while reducing chemical inputs and environmental contamination. However, many current commercial coatings depend on synthetic fertilizers and nutrients that are chemically persistent and contribute to environmental pollution. This work focuses on the development of biodegradable biopolymer-based microgels as functional seed coating and carrier for beneficial bacteria. By varying polysaccharide concentration and crosslinking density, we tune the hydrogel's mechanical properties, which influence Bacillus subtilis behaviour within the matrix. Using this model organism, we investigate how these material features affect survival, growth, motility, nutrient diffusion, and long-term stability, linking hydrogel design to microbial performance and offering insights for more effective, sustainable seed-coating systems. The goal is to create programmable, biodegradable coatings that support seeds and encapsulated bacteria under variable moisture conditions, providing a sustainable, microplastic-free alternative to conventional formulations.

S5-P02 Poster presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Next-Level Seed Coatings: Bio-Based with Thermo-Responsive Degradation and Microbiome Release

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Pumpkin seed oil is an important export product from Styria, Austria. While the weakly lignified seed coat of Styrian oil pumpkins (*Cucurbita pepo* var. *styriaca*) makes them suitable for producing high-quality seed oil, it also makes them vulnerable to mechanical damage and fungal infections. These challenges are intensifying with climate change due to shifts in the timing and conditions for cultivation. Hence, there is a need for solutions that are effective and safe for human consumption and the environment. However, current approaches, such as synthetic polymer coatings and fungicide seed treatments, raise health-related concerns and contribute to microplastic pollution. Therefore, we are developing sustainable concepts for bio-based seed coatings that provide mechanical and antifungal protection, release beneficial microbes, and allow efficient seed germination. The development of novel thermo-responsive polymers based on renewable resources will allow fine-tuning the seed resuscitation from dormancy for optimal germination under varying climatic conditions. This approach offers an eco-friendly and climate-ready alternative to current seed treatments. It aims to protect seeds, reduce health risks and environmental impact to help secure a sustainable future for pumpkin seed oil production and, furthermore, other sensitive seeds.

Multifunctional Microbial Seed Treatments: Synergy of Biostimulation and Biocontrol activity

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The need to reduce chemical plant protection products has shifted focus toward biological alternatives that not only stimulate growth but also actively protect plants during their most vulnerable developmental stages. This study, conducted as part of the SPIN-FERT project, evaluates individual rhizospheric bacterial strains as innovative seed treatments with a dual mechanism of action: enhancing mineral nutrition and mitigating the pressure of soil-borne phytopathogens. In the laboratory phase, strains were selected based on their biostimulation capacity (e.g. nitrogen fixation and solubilization of phosphorus). A crucial element of the selection was the evaluation of biocontrol potential against Rhizoctonia spp., a major cause of devastating seedling damping-off. In in vitro dual-culture assays, selected isolates demonstrated the ability to inhibit mycelial growth by 40,0–55,4%, which was associated with the production of extracellular lytic enzymes and lipopeptide antibiotics. The transition to the field allowed for the verification of these traits within a dynamic soil environment. The application of the studied strains as seed treatments resulted in an improvement in initial plant vigor and an increase in root system biomass. Importantly, under conditions of artificial soil inoculation with Rhizoctonia spp., microbially treated seeds showed an increase in plant biomass compared, proving the effectiveness of the "bio-shield" established around the seed. The analysis of plant tissues confirmed increased accumulation of nitrogen and phosphorus, indicating that the mechanisms identified in the laboratory effectively translate into improved nutrient uptake efficiency in the field. These results confirm that precisely selected microbial strains can potentially replace conventional fungicidal treatments while simultaneously acting as growth biostimulants in sustainable crop production. Research carried out as part of the SPIN-FERT project entitled “Innovative practices, tools, and products to increase soil fertility and peat substitution in horticultural crops,” funded under the European Union's Horizon 2020 research and innovation program, project no. 101157265.

S5-P04 Poster presentation

Day 2 – Function and Intervention
Session 5: Shaping the Seed Microbiome: From Intervention to Design

Harnessing halophilic yeast-mediated seed biopriming to enhance salinity resilience in Solanum lycopersicum: a genomic and transgenerational microbiome perspective

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Soil salinization poses a critical threat to global agricultural productivity, particularly affecting the germination and early establishment of glycoptic crops such as tomato (*Solanum lycopersicum*). This study evaluates the potential of two halotolerant yeast strains, *Aureobasidium pullulans* (AP1) and *Cystobasidium lysinophilum* (R5), as seed biopriming agents to mitigate salinity stress. Whole-genome sequencing (WGS) using an Illumina PCR-Free protocol (100X coverage) was performed to characterize the molecular mechanisms of biostimulation and stress tolerance in both strains. *In vitro* assays confirmed high halotolerance, with growth persisting up to 10-15% NaCl. Physiological trials demonstrated that biopriming significantly improves resilience: R5 increased total germination by 30% under saline stress and enhanced the leaf area of cv. Micro-Tom by 45% in soil amended with 150 mM NaCl. A central focus of this research is the ecological impact of biopriming on the plant holobiont and its transgenerational inheritance. Through a dual-metabarcoding approach (16S rRNA V4 and ITS regions), we characterized the microbial recruitment in the rhizosphere and phyllosphere, utilizing PNA clamps to minimize host DNA interference. Furthermore, comparative analysis between parental (G0) and first filial (F1) seed endospheres is being conducted to evaluate the vertical transmission of beneficial taxa and the long-term remodeling of the seed microbiome induced by biopriming. Our findings suggest that microbial seed priming, particularly with strain R5, establishes a robust plant-soil-microbe association that persists across generations. Beyond direct physiological benefits, these halotolerant yeasts act as key ecological modulators, actively reshaping microbial assemblages in the rhizosphere, phyllosphere, and seed endosphere. By influencing the recruitment of beneficial taxa, this work provides a comprehensive framework for using extremophilic yeasts as sustainable bioengineers to safeguard crop yields and restore multi-niche microbial synergy in salt-affected environments.

S6-K01 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Sowing the seed of success - translating the seed microbiome

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The seed microbiome, transmitting beneficial microbes across generations, is critical for plant germination, growth and health. Since its discovery, it has therefore been the subject of extensive research, particularly in relation to crops. However, crop plants have already lost much of their indigenous microbial diversity because of long-term domestication, breeding and intense agriculture and seed production at global scale. This microbial diversity loss is reflected in seeds as well, and has consequences for One health issues. To restore functional diversity, microbial seed treatments can be designed. Understanding seed microbiome assembly and specificity is important to develop seed treatments that have predictable and effective benefits for plant health and resilience. While bioactive inoculants can be harvested from the rich seed microbiome of wild ancestors or native plants, they can be designed as single strain inoculants containing key stone species or soterobionts, microbial consortia or whole microbiome transplants. Different successful examples will be presented, e.g. INITIO seed treatment for sugar beets. In addition, technological challenges and solutions for seed treatment by microbes will be discussed.

S6-FT01 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

AI-Driven Seed Microbiome Engineering

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Seed-associated microbes are increasingly recognized as heritable determinants of plant fitness, influencing germination, stress resilience, and agronomic performance. Despite growing adoption of seed microbial inoculants, product development remains largely a trial and error process dependent on costly and iterative field trials with limited predictive power about efficacy. A core bottleneck is the absence of computational frameworks capable of linking microbial genomic traits to functional outcomes and translating those relationships across soils and climatic conditions. We address this gap using artificial intelligence purpose-built for microbiome data. I will present the advances in the development of a microbiome world model that replays the ecological and functional logic of plant-associated microbiomes based on DNA sequences. This model unlocks three capabilities critical to product development: automated inference of microbial functional potential, in silico prediction of product performance under diverse environmental conditions, and generative design of novel microbial consortia optimized for target agronomic traits. Together, these capabilities transform seed microbiome R&D from a brute-force discovery process into a self-driving autonomous pipeline, translating DNA sequence into blueprint for field-ready products. I will discuss the model's architecture, validation against field performance data, and its integration into an end-to-end automated R&D workflow. This framework represents a scalable path toward rational, environment-aware microbiome engineering for seed health and productivity.

S6-FT02 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

PlantMetaBase: Harmonizing Public Plant Microbiome Metadata Reveals Taxonomic and Geographic Bias

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Public repositories, such as Sequence Read Archive (SRA), contain thousands of plant-associated microbiome datasets. However, large-scale comparative analyses are limited by fragmented, inconsistent, and poorly-standardised metadata. Key descriptors, including host identity, plant compartment, environmental context, and geographic origin, are unstructured, miss-annotated or missing, constraining reproducibility and cross-study integration. We present PlantMetaBase, a curated and standardised metadata resource for plant-associated microbiome studies derived from mining SRA. We retrieved metadata using SRAdb and identified plant-associated runs. The framework integrates curated plant taxonomic dictionaries with weighted evaluation of multiple metadata fields. We parsed unstructured sample attributes and harmonised them to standardise host taxonomy, plant parts, microbiome compartment, geographic coordinates, country names, environmental variables, and temporal descriptors using controlled standards. PlantMetaBase includes 252,734 plant-associated sequencing-runs from 2,185 BioProjects, representing over 600 plant species across 176 families and 64 countries. The datasets encompass diverse plant compartments, including root, leaf, seed and flower, with an imbalanced representation across taxa. Quantitative assessment reveals strong taxonomic skew toward economically important plant families, such as Poaceae and Brassicaceae. The skew creates a blind spot, narrowing our collective ecological vision and potentially leaving critical host-microbe interactions in understudied lineages undiscovered. As a result, key ecological processes and novel microbial associations linked to a majority of global plant diversity may remain obscured, constraining our ability to uncover generalizable patterns from existing data. Geographic distribution is similarly imbalanced, especially for studies originating from North America, Europe, and East Asia. This leverages structural biases in publicly available plant microbiome datasets. Furthermore, metadata completeness varies considerably among studies, particularly for environmental descriptors and plant compartment annotations. By harmonising fragmented public records and accounting for taxonomic and geographic bias, PlantMetaBase enables reproducible cohort construction and provides a foundation for large-scale meta-analyses aimed at quantifying and correcting these biases in plant microbiome studies.

S6-T01 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Stress reshapes microbiota inheritance in tomato, consistent with metabolic filtering and enhanced heat resilience

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Understanding how plants transmit beneficial microbiota across generations is critical for exploiting the seed microbiome under climate stress. Here, we investigated how maternal heat stress affects microbiota assembly and vertical transmission in Micro-Tom tomato (*Solanum lycopersicum*). Plants were grown under controlled conditions minimizing horizontal transmission, using natural soil as the primary microbial source. Heat stress applied during flowering significantly reduced microbial diversity in flowers, with marked decreases in Proteobacteria and Bacteroidetes, while Firmicutes remained stable. In contrast, seed-associated microbiota showed distinct compositional shifts, indicating intergenerational restructuring. Metagenomic analyses, complemented by culturomics, identified specific taxa consistently transmitted from flowers to seeds under heat stress, including *Dyella japonica* and *Neobacillus drentensis*, suggesting selective vertical inheritance of stress-associated bacteria. Metabolomic profiling of flowers revealed clear stress-induced changes, with increased levels of proline and glutamine and decreased levels of xylose, lactate, and gluconate. Correlation analyses between metabolites and microbial taxa indicated structured associations consistent with a metabolite-mediated filtering process influencing microbiota assembly in reproductive tissues. Functional validation was performed through comparative bioinoculation assays using isolates representing distinct transmission patterns. *Dyella japonica* was selected as a conserved vertically transmitted taxon, while the heat-enriched isolate *Neobacillus* drentensis was used as an adaptive treatment. Under heat stress conditions, these treatments revealed contrasting functional outcomes. While *Dyella japonica* supported general plant performance across conditions, *Neobacillus* drentensis conferred the strongest effect at the reproductive stage. Inoculated plants showed a reduction in heat-induced flower abortion of approximately 30–50%, resulting in a higher proportion of fertile flowers and increases in fruit set of ~20–40%. Additionally, treated plants displayed improved progression to fruit maturation under elevated temperatures compared to non-inoculated controls. GFP-based tracing confirmed that all tested strains were capable of transgenerational transmission from maternal tissues to the next generation. Together, these findings demonstrate that stress-selected seed microbiota contribute to reproductive stability and can be leveraged to enhance crop resilience under heat stress.

S6-T02 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Presentation of NordGen - Nordic Genetic Resource Center and Svalbard Global Seed Vault experiments

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NordGen, the Nordic Genetic Resource Centre, is the Nordic joint genebank and knowledge centre for genetic resources. We work in three sections (Plants, Farm Animals, and Forest), are the operational manager of the Svalbard Global Seed vault, and act as Secretariat for the Nordic Public-Private Partnership on pre-breeding. Part of our work involves maintaining a good and healthy gene bank, such as conservation, propagation, and distribution of seeds. This collection includes more than 33 000 samples from important crops, crop wild relatives, ornamental and medicinal plants, and continues to grow. As a knowledge centre, we are also involved in collaborations with Nordic and international partners. An overview of some of our resources in these projects is presented by highlights of ongoing projects such as "Next generation genebanking – unlocking the potential of plant genetic resources in the sequencing era", focusing on the protein crop collection, and "Nordic flax futures". In the "100-year seed storage experiment in Mine 3", the longevity of seeds stored in the permafrost at Coal mine no. 3 on Svalbard are monitored. Pathogen survival on the seeds has been assessed since the initiation of the project in 1986. The first results of the project, after 35 years of storage, are reported.

S6-T03 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Genomic and Functional Insights into an Artemisia-Derived Endophyte Enhancing Pea Growth and Disease Resistance

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Seed-associated and endophytic microbiomes play a critical role in plant development, stress tolerance, and resilience against pathogens. However, the functional mechanisms underlying these interactions and their potential for sustainable crop improvement remain insufficiently explored. This study investigated the plant growth promoting and biocontrol potential of an endophytic bacterium isolated from Artemisia absinthium, with a particular focus on its functional traits, genomic architecture, and performance under pathogen pressure. A collection of endophytic bacteria was screened for plant-beneficial traits, from which strain AR11 emerged as the most effective. Greenhouse experiments demonstrated that AR11 significantly enhanced pea (*Pisum sativum*) growth, biomass accumulation, and chlorophyll content under both normal and *Fusarium* stress conditions. Inoculated plants exhibited disease severity reduction and maintained higher physiological performance compared with non-inoculated controls. To elucidate the molecular basis of these effects, whole-genome sequencing was performed using PacBio long-read technology. The 5.49 Mb circular genome revealed extensive functional potential, including genes involved in nitrogen metabolism, phosphate solubilization, siderophore production, stress response, and secondary metabolite biosynthesis. Multiple biosynthetic gene clusters, CAZymes, and regulatory systems associated with plant–microbe interactions were identified, alongside CRISPR loci and methylation patterns indicative of adaptive potential. Importantly, no high-risk virulence or acquired antibiotic resistance genes were detected. The results demonstrate that *Serratia* sp. AR11 acts as a multifunctional endophyte capable of enhancing plant performance while suppressing disease, linking microbial genomic traits with host-level benefits. This study highlights the functional importance of seed and plant-associated microbiomes and supports their application in sustainable, low-input agricultural systems.

S6-T04 Oral presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

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Functional roles of seed endophytic bacteria in seedling development and biotic stress tolerance in maize

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Seed-associated endophytes possess significant plant growth-promoting (PGP) and biocontrol attributes. However, the precise molecular and biochemical mechanisms driving these benefits remain poorly understood. We investigated the functional roles of maize seed endophytic bacteria in enhancing seedling vigor and defense against fungal pathogens. First, 23 bacterial endophytes were isolated and identified via 16S rDNA sequencing. Functional profiling revealed robust PGP traits: all isolates fixed nitrogen, 74% solubilized phosphate, and 70% synthesized auxin. Eliminating the native microbiome via antibiotics compromised seedling growth, but re-inoculation with isolates ZM1 (*Lysinibacillus* sp.) and ZM2 (*Paenibacillus* sp.) successfully restored root and shoot architecture. Second, the mechanistic basis of ZM1 was elucidated. Confocal microscopy revealed extensive ZM1 root colonization. LC-MS and transcriptomic analysis demonstrated elevated auxin biosynthesis and accumulation in the roots of the ZM1 treated maize seedlings. Furthermore, ZM1 significantly enhanced nitrogen metabolism as evidenced by increased endogenous ammonium, upregulated GS/GOGAT enzyme activities and improved plant growth under nitrogen-deficient conditions. Finally, the biocontrol ability of ZMW8 (Bacillus velezensis) was evaluated. Application of ZMW8 lipopeptides conferred protection enhanced protection against *Fusarium verticillioides* and improved overall plant growth. This defense response was characterized by the upregulation of key defense response genes (including ZmPR-1, ZmPR-4, ZmSOD-2, ZmLOX, ZmPDF1.2, and ZmERF) and the accumulation of antifungal polyphenols (including p-coumaric acid, kaempferol, dihydrokaempferol, and dihydroquercetin). Ultimately, this study highlights the potential of specific seed-borne bacteria to modulate host auxin, nitrogen, and defense pathways, underscoring their potential as targeted biofertilizers and biocontrol agents.

S6-P01 Poster presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

The seed microbiome as a source of plant resilience: linking genetics, drought, and early growth

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Plants are associated with diverse microbial communities that influence growth, development, and stress resilience. The seed microbiome constitutes a key but understudied component of this association, enabling the vertical transmission of a subset of the maternal microbiota to the next generation. This inherited community is likely playing an important role during early plant life, improving seed germination and seedling establishment, and tolerance to stresses such as drought. However, the mechanisms governing seed microbiome assembly, transmission, and function, as well as the relative contributions of host genotype and environmental factors, remain poorly understood. In this project, we aim to address these knowledge gaps by investigating both how plant genetics and drought stress shape the seed microbiome in tomato and lettuce, and how the seed microbiome, in turn, influences seed germination and plant performance. We will conduct genome-wide association studies (GWAS) to identify plant genomic regions associated with seed microbiome composition and with the presence of beneficial microbial taxa. In parallel, we will evaluate the impact of drought stress on seed-associated microbial communities. Candidate beneficial microbes will be isolated from seeds and screened for their ability to enhance germination and improve drought tolerance under controlled conditions. Finally, multi-omics approaches will be employed to investigate the molecular mechanisms governing these plant–microbe interactions. By integrating host genetics, microbial ecology, and functional analyses, we aim to advance our understanding of the dynamics and functions of microbial inheritance in seeds.

S6-P02 Poster presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Automation and Streamlining of Risk Assessment for Potential Microbial Low-Risk Pesticides

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Seed coating with microbial low-risk pesticides (LRPs, or biopesticides) can offer a sustainable and effective strategy to enhance seed germination, provide early-stage protection against pests and diseases, and strengthen crop resilience to microbial pathogens. By reducing reliance on synthetic chemicals, seed coatings with microbial LRPs contribute to environmentally friendly and integrated pest management systems. However, LRPs go through the same registration and approval process used for synthetic pesticides without considering the needs and characteristics of LRPs. The increasing adoption of microbial LRPs in agrifood systems highlights the urgent need for transparent, publicly accessible tools that enable comprehensive risk assessment of these biological agents. Existing assessment platforms are often proprietary and predominantly focused on pathogenicity, neglecting critical factors such as gene transfer potential and the broader genomic context that may have environmental and human-health implications. The RATION project (https://www.ration-lrp.eu/) addresses this gap by developing an open-access, user-friendly risk assessment platform specifically tailored for microbial LRPs. The tool integrates genomic data to evaluate pathogenicity-related genes, horizontal gene transfer potential, and overall genomic context, providing a holistic risk assessment. Designed for accessibility by researchers, regulators, farmers, and consumers, the platform supports evidence-based decision-making while fostering transparency and public trust. By establishing a standardized, comprehensive, and scientifically robust framework, this approach enables an automated assessment of biopesticide safety and performance. Ultimately, the responsible, collaborative, and informed management of microbial LRPs use will contribute to advancing sustainable agricultural practices and accelerating the market introduction of safe microbial LRPs.

S6-P03 Poster presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Agricultural soils under restoration practices are a source of bacterial strains adequate to develop bio-inocula to support oat growth

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Intensively used arable soils are prone to degradation, demanding innovation in agricultural management in the face of global change and global food security. Soil restoration practices (SRP) such as reduced tillage and altered fertilization regimes can recover soil health and enrich bacteria potentially beneficial to plant growth in depleted soils. Bio-inoculation approaches need to be efficient across the heterogeneity of soils. We hypothesized that soils under SRP are a reservoir for bacterial strains, which can serve as effective inoculants in both degraded and fertile soils. Bacterial isolates were obtained from Uruguayan soils under SRP to determine their potential to promote plant growth and resilience. Bacterial hub taxa guiding microbial community structure in response to SRP were identified using cross-kingdom co-occurrence network analyses. Comparison of 16S rRNA gene sequences of amplicon sequencing variants and isolates allowed to select bacterial isolates corresponding to hub taxa. Selected isolates were characterized in vitro and in silico for plant-beneficial traits. Almost all isolates produced siderophores. Half of the isolates produced extracellular polymeric substances and indole-3-acetic acid and were capable of phosphate solubilization. The inoculation efficacy of four isolates with complementing traits was tested under greenhouse conditions. Single isolates were coated onto oat seeds using methylcellulose and planted in either degraded or fertile topsoil. Compared to non-inoculated plants, inoculated plants exhibited higher shoot biomass in fertile soils, finer root systems, and lower spectral stress proxies in degraded soil. A significantly different microbial community structure evolved in the rhizosphere of inoculated plants. Thus, inoculation may have initially influenced rhizosphere community assembly, but the inoculated bacteria were of low abundance six weeks after planting. To compensate for low fertility new approaches will be tested: inoculation with consortia of several isolates or inoculation combined with adequate soil management.

S6-P04 Poster presentation

Day 2 – Function and Intervention

Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Mitigating yield decline in wheat rotations – exploring the potential of seed inoculation with plant-growth promoting rhizobacteria

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Winter wheat is one of the most important staple and cash crops worldwide, but increasing its proportion in crop rotations has led to challenges related to self-succession. Continuous wheat cultivation often results in yield decline, increased incidence of soil-borne pathogens, and shifts in the rhizosphere microbiome, including the enrichment of potentially beneficial taxa such as *Bacillus* and *Pseudomonas*. Although these beneficial bacteria are not always highly abundant, they can exhibit important functional traits. In this study, key bacterial taxa were isolated using classical cultivation techniques and characterized in vitro with the aim to find promising isolates for inoculation to mitigate yield decline. The inoculant strain *Bacillus pumilus* proved efficient under greenhouse and outdoor conditions using vegetative cells, demonstrating root biomass increases of up to 40%, enhanced root traits and improved nutrient uptake. Genome sequencing showed that the strain harbors several genes involved in carbohydrate metabolism, siderophore biosynthesis and antibiotic resistance and enabled the development of a strain-specific qPCR to track its persistence after inoculation. To further assess field relevance, an outdoor lysimeter experiment examined yield parameters, root plasticity, and microbial community dynamics in response to *B. pumilus* spore inoculation and crop rotational position. As expected, rotational wheat (W1) exhibited higher biomass and yield compared to continuous wheat (W2). Seed inoculation with *B. pumilus*, unexpectedly, did not mitigate yield decline in W2. However, the inoculation influenced the rhizosphere microbial community composition to a minor but significant extent across soil depths at flowering. Additionally, inoculation influenced soil enzymatic activities, particularly β-glucosidase and leucine aminopeptidase, indicating effects on carbon and nitrogen cycling. Preliminary results from an ongoing field inoculation experiment similarly showed no significant early differences in plant growth between inoculated and control treatments. These findings highlight inconsistencies in inoculant performance and emphasize the need to better understand factors influencing the success of seed-applied beneficial bacteria under field conditions.

S6-P05 Poster presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

Cross-host endophytic diazotrophs drive biological nitrogen fixation in wheat-maize rotations

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Biological nitrogen fixation (BNF) offers a sustainable alternative to synthetic fertilizers, yet the mechanistic and ecological basis of associative BNF, especially investigation and application of cross-host-adapted endophytic diazotrophs in cereal crops, remains poorly understood. Integrating 16S rRNA and nifH amplicon sequencing with shotgun metagenomics, we characterized nitrogen-fixing microbiomes across wheat-maize rotation systems in North China, uncovering core diazotrophic microbiota subject to inter-host horizontal transmission. We isolated two keystone diazotrophics, *Klebsiella pasteurii* and *Kosakonia pseudosacchari*, exhibiting robust nitrogenase and plant-growth-promoting activities in both hosts. Under 30% nitrogen limitation, inoculation with either strain sustained plant growth comparable to full nitrogen supply in wheat and maize, while their combination achieved BNF rates up to 60%Ndfa. In situ fluorescence imaging demonstrated stable endophytic co-localization and structured micro-aggregate formation within root epidermal and intercellular compartments. These findings establish ecological principles of cross-host diazotrophic assembly and provide a biotechnological BNF framework for sustainable cereal production.

S6-P06 Poster presentation

Day 2 – Function and Intervention
Session 6: From Data to Application: Prediction and Translation in Seed Microbiome Science

The seed microbiome as a reservoir for seed treatment applications in oilseed rape

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The native seed microbiome of oilseed rape (OSR) offers a myriad of versatile seedborne microorganisms that can be of potential use even in industrial applications. Here it was utilized for targeted seed treatment applications to enhance field emergence and early growth performance of different genotypes of the same crop type (*Brassica napus* L.). This was tested 3 years in multiple field trials across different environmental conditions in Germany. The seed microbiome of low to high germinating seedlots of different OSR genotypes was characterized by 16S-RNA sequencing and according to their germination behaviour (Wassermann et al 2022). Then specific strains from high germinating seedlots were isolated. Solid and liquid raw formulations of the strains of interest were applied to different genotypes and tested in comparison to other gram positive and negative bacterial strains in vitro, in the lab, greenhouse and field trials. Growth promoting effects were first observed in laboratory-scale germination and vigour tests. Under field conditions the results have shown high variability depending on environmental conditions. The challenges for successful seed microbiome strain transfer is sufficient quality control of seed and root colonization, as well as durability. Since the predominant species used in this project were gram negative, regular analysis of colony forming units of the bacteria as measurement for on-seed survival and also formulations strategies are emphasized.

S7-K01 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Title TBC

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S7-FT01 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Seed microbiota mediate transgenerational drought adaptation in wheat

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Drought is a major constraint on crop productivity, yet the mechanisms by which plants adapt across generations remain poorly understood. Here, we investigated whether drought leaves a transgenerational imprint on the wheat seed microbiota and whether this microbial legacy influences plant performance under subsequent water limitation. Using a multi-year rainfall manipulation experiment, we showed that drought restructures seed-associated bacterial and fungal communities across generations. In the drought-sensitive wheat cultivar, these shifts were linked to yield: plants whose seed microbiota resembled drought-adapted communities showed more stable yields under future water stress. A transgenerational field test confirmed that daughter plants derived from drought-exposed parent plants maintained performance under water limitation, whereas those from wetter origins did not. Extending these findings, a greenhouse experiment in a distinct agroecosystem demonstrated that seeds derived from fields with water stress history produced plants with higher photosynthetic assimilation, increased water-use efficiency, and distinct root-associated microbiomes under controlled drought conditions. Together, these results indicate that microbiota serves as an ecological archive of the stress history of plants, with seed-associated microbial communities transmitting drought legacy across generations. These insights open new avenues for microbiome-informed agriculture. Identifying, preserving, or reintroducing stress-adapted microbial consortia into seed systems could enhance crop resilience under water limitation without the need for genetic modification or chemical inputs.

S7-FT02 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Seed Microbiota as a Driver of Plant Adaptation in the Current Context of Climate Change

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Climate change is one of the most significant global threats to biodiversity conservation. Its impacts are far reaching and often unpredictable, altering ecological processes across all biological scales. Species respond to climatic stress through mechanisms such as migration, phenotypic plasticity, adaptation, and evolutionary change. However, many organisms, particularly those with limited dispersal capacity, have increased vulnerability as the velocity of climate change moves faster than their natural ability to track suitable habitats. In this context, human mediated strategies have gained prominence as additional tools to support species persistence. Among these strategies, artificial selection aims to identify and promote phenotypes that confer advantages under climatic stress. This approach may target individuals that carry beneficial traits or those capable of forming advantageous associations with bacterial partners. Increasing evidence shows that plants exert selective pressure on their seed microbiome, driving co evolution and establishing reservoirs of beneficial microorganisms that persist across generations, ultimately enhancing survival in challenging environments. Seed associated microbial communities therefore play an increasingly recognized role in plant adaptation. By isolating, sequencing, and characterizing bacterial taxa with positive functional effects, it is possible to evaluate their influence through controlled inoculation experiments. This integrative perspective underscores the importance of plant–microbiome interactions as a complementary avenue for strengthening adaptive responses. Our research demonstrates that combining artificial selection with microbiome based approaches can effectively modify key phenotypic traits, such as flowering time, and identify microbial consortia associated with adaptive advantages. Together, these strategies provide valuable tools for improving the resilience and long term conservation of vulnerable or threatened plant species in the face of accelerating climate change.

S7-T01 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

A global analysis reveals biased exploration in flower microbiome research

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Floral microbiomes influence plant reproduction, pollinator interactions and microbial transmission, yet their global diversity and ecological drivers remain poorly understood. Flowers comprise distinct microhabitats, including stigma, nectar, petals and pollen, each imposing different filters on microbial colonization. Whether patterns observed in local systems scale across angiosperm diversity, however, remains unknown. Here we assembled a globally harmonized database of flower-associated microbiome studies by curating publicly available 16S rRNA gene and ITS amplicon datasets from more than 80 studies and thousands of samples. We standardized host taxonomy, floral organ categories and key ecological metadata to enable cross-study synthesis and trait integration. This synthesis shows that, despite rapid growth in study number, floral microbiome research remains strongly biased toward a narrow and phylogenetically clustered subset of angiosperms. Sampling is geographically uneven, concentrated in a few host families, and disproportionately based on whole-flower material, particularly in fungal studies, limiting organ-resolved ecological inference. Discovery analyses further show that host species accumulate faster than host families, indicating that new work expands sampling mainly within already represented lineages. We also developed an interactive platform for standardized exploration of curated datasets. Together, these results reveal structural biases that currently constrain general theory in floral microbiome ecology.

S7-T02 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Seed multiplication imprints seed-associated fungal communities in a farming system- and year-specific manner

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Seed-associated microbiomes are increasingly recognized as potential modulators of seed quality and crop establishment. However, the extent to which farm management systems and environmental conditions during seed multiplication shape these communities and their functions remains unclear. Here, we studied the fungal microbiota, vitality, and field establishment of winter wheat seeds harvested in 2022 (hot and dry season) and 2024 (wet season) from the long-term DOK trial, which compares organic and conventional farming systems over 45 years. In 2024, soil and root microbiota were also assessed. Our results show that the farming system influenced seed fungal alpha diversity in a year-specific manner, while harvesting year had a strong overall effect on Shannon diversity. Seed fungal community composition (beta diversity) was structured by farming system and harvesting year. The effect of the farming system (organic vs. conventional) on microbiota was stronger for seeds than for roots or soil. Seed fungal community composition correlated with germination rate in the field only in one of the two harvesting years, while root and soil fungal community composition showed no association with germination rate. Vitality assays under controlled conditions confirmed strong environmental context dependency. Under optimal conditions (20 °C), only the year of seed production affected germination. Under cold stress (3.5 °C) and in the field, germination responses were shaped by interactions between year and farming system or fertilization level, indicating that seed performance depends on both production context and environmental stress during germination. Overall, our results indicate that the farm management system during seed multiplication shapes fungal community structure, with increasingly pronounced effects from soil to root to seed. However, the context-specific correlation with vitality and field germination across harvest years and assay conditions highlights both the potential and limitations of seed microbiome-based indicators for seed quality in agricultural systems.

S7-T03 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Seed microbiomes change in the soil over time and predict seed mortality

Carolyn Lowry[1], Kara Eckert[1], Simon Delattre[1], Estelle Couradeau[1]
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Species of many ruderal weed species remain viable in the soil for years and even decades, enabling these species to continue invading crop fields even after years with perfect weed management. For example, *Amaranthus powellii* is a problematic weed species in the Northeastern region of the USA that can remain dormant in the soil for up to X years. Thus far, much of the research on seed microbiomes has occurred in crop species, and due to breeding efforts, these species have little to no seed dormancy. Because of this, we have a limited understanding of how seed microbiomes change over time in dormant seeds inhabiting the soil. To address this knowledge gap, we buried *A. powellii* seeds in the soil within a perennial forage diversity gradient and excavated seeds periodically over a 2.5-year time period and examined rates of seed mortality, as well as characterized the bacterial (16S rRNA gene) and fungal (ITS) community composition within seeds. We found that seed microbial communities changed within seeds in the soil overtime, and both seed bacterial and fungal communities predicted seed mortality. We identified specific bacterial and fungal taxa that may play a role in infecting dormant weeds seeds in the soil, thereby regulating populations of problematic weeds. Future research should focus on demonstrating a causal link between specific microbial taxa and seed mortality, as well as determine the management practices that may increase the abundance and activity of these microbial taxa so they can further contribute to decreasing the density of weeds in the soil seedbank.

S7-T04 Oral presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Seed microbiota as a functional driver of biodiversity benefits in mixed-cropping systems

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Mixed-cropping systems can outperform monocultures in terms of productivity, highlighting a substantial net benefit of biodiversity. These biodiversity-driven advantages tend to be stronger in wild relatives than in domesticated crops. However, the role of seed endophytic microbiota remains unknown, despite the potential as a key functional trait modulating plant-plant interactions shown to be beneficial. We hypothesize that seed microbiota directly contributes to the benefits of mixed cropping by mediating plant-plant interactions and enhancing the traits of species combinations that display higher complementarity. The common garden experiment was conducted with six annual crop species grown as individual plants, monocultures, and two-species mixtures: *Triticum aestivum* (wheat), *Avena sativa* (oat), *Lens culinaris* (lentil), *Camelina sativa* (*camelina*), *Lupinus angustifolius* (blue lupin), and *Linum usitatissimum* (linseed). The wild relatives are *Aegilops geniculata*, *Avena sterilis, Lupinus angustifolius, Lens nigricans, Linum bienne, and Camelina microcarpa*. From the results, we selected those two-species combinations that showed significantly higher seed weight under joint growth, as well as increased seed number and plant size. We are currently characterizing the seed endophytic microbiota taxa that act as heritable functional plant trait using seeds harvested from different crop combinations. We expect to identify specific endophytes associated with the most productive and complementary species mixtures (beneficial effects). Such insights can provide the way for microbiome breeding and the manipulation of vertically transmitted seed microbiota in crop mixtures to enhance productivity and resilience in mixed cropping systems, ultimately informing sustainable agricultural practices, guiding the selection of crop combinations, and promoting ecosystem services such as nutrient-use efficiency, stress tolerance, and disease suppression.

S7-P01 Poster presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Manipulation of seed dormancy in *Arabidopsis thaliana* promotes the maintenance of *Turnip Mosaic Virus* in natural populations

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Recently, it has been shown that an aphid-borne positive strand RNA potyvirus, *Turnip Mosaic Virus* (TuMV), has the ability to transmit vertically in A. thaliana. Vertical transmission through seeds may contribute to the viral maintenance in the natural populations by bridging across successive growing seasons. In this study, we show that while TuMV efficiently colonizes the reproductive tissues and represses stem elongation in A. thaliana, it does not prevent the seed development. Remarkably, following the seed maturation embryonic tissues are free of the viral RNA, as opposed to seed bearing tissues. We describe morphological and molecular consequences of systemic TuMV infection on seed development in A. thaliana, which eventually lead to physiological changes of resulting seed population, particularly in seed dormancy and longevity. Utilizing a mathematical model, we speculate that changes in the physiological properties of the resulting seed population contribute to the viral maintenance in natural populations by increasing the seasonal host availability. Lastly, we investigate potential molecular mechanisms through which systemic TuMV infection reduces the dormancy in A. thaliana seeds. We show that the activation of systemic acquired resistance (SAR) signalling reduces the expression of DOG1, one of the main regulators of seed dormancy. In conclusion, our results indicate that systemic TuMV infection reduces physiological dormancy in A. thaliana seeds through DOG1, which may contribute to viral maintenance in natural populations.

S7-P02 Poster presentation

Day 3 – Evolution and the Future
Session 7: Global Patterns, Drivers, and Data in Seed Microbiomes

Exploring the role of seed-borne bacteria in wheat rhizosphere microbiome assembly through metabolic modeling

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Despite the proven efficacy of plant-beneficial bacterial inoculants in promoting plant growth and suppressing pathogens, their establishment in the rhizosphere remains inconsistent under field conditions, largely due to competition with resident microorganisms. Heritable, seed-borne bacteria arrive first to this niche and are therefore likely to play crucial roles in assembling the early rhizosphere microbiome through priority effects. Previous studies have suggested that seed-borne bacteria may pre-emptively consume resources early in the development of the plant rhizosphere, thereby limiting the establishment of late arrivals [1]. At the same time, seed-borne bacteria may also release metabolites that facilitate the assembly of other bacteria. However, the metabolic interactions between seed and soil bacteria remain largely unexplored and could greatly impact new strategies for enhancing the establishment of plant-beneficial inoculants. In this study, we sequenced a collection of around 40 bacterial isolates obtained from wheat seeds, the wheat rhizosphere, and soil. We constructed genome-scale metabolic models and predicted the utilization of common carbon sources found in the rhizosphere. These analyses provide a framework to identify potential competition, niche partitioning, and facilitative metabolic interactions among early- and late-arriving bacteria. Building on these predictions, we are experimentally validating carbon utilization profiles and constructing different synthetic communities (SynComs) to study how seed-borne bacteria influence community assembly. By manipulating the arrival order of seed bacteria and performing drop-out experiments, we aim to determine whether seed bacteria act as major drivers of wheat rhizosphere microbiome assembly through priority effects. This framework will also allow us to test how plant-beneficial inoculants establish within communities shaped by inherited bacteria, providing ecological principles to improve inoculant integration in the rhizosphere microbiome

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S2-P01	Sasiwimon Siricharoen	Arabidopsis seed microbiome and its effects on seed germination
S3-K01	Seth Bordenstein	Winds of Change: Holobiont Biology, Phylosymbiosis, and Biology's Shifting Disciplinary Matrix
S3-FT01	Marta Robledo	Seed-Bottleneck Dynamics and Transmission Pathways Shape the Diversity and Persistence of Endophytic Bacterial Lineages
S3-FT02	Cristian Andres Salinas Castillo	The impact of domestication and selection on seedborne microbiomes in tomato
S3-T01	Gillian Bergmann	Effects of plant identity and pollination strategies on seed microbiomes
S3-T02	Alex K Alexander	Metagenomic analysis reveals seed lot effects and microbial filtering during parsnip seed to seedling transition
S3-T03	Luke Moe	Maize seed endophyte microbiome assembly: from ear to field scale
S3-T04	Adrian Wolfgang	Microbiome Assembly Differs in Selected Sugar Beet Varieties Depending on Tolerance Towards Fungal Pathogens
S4-K01	Tomislav Cernava	What is shaping the seed microbiome?
S4-FT01	Birgit Wassermann	Drivers of Seed Microbiome Assembly: Roles of Breeding, Fertilization, and Storage
S4-FT02	Stéphane Compant	The Seed Microbiome: From Research to Field Applications
S4-T01	Kristina Michl	A semi-invasive method linking the seed microbiome to stress resilience in wheat
S4-T02	Joseph King	Seed-Derived Diazotrophic Redundancy Associated with Belowground Taxonomic Identity of Sugar beet
S4-T04	Allen Yi-Lun Tsai	Seed coat mucilage regulates spermosphere microbiome composition, which influences root architecture of the emerging seedling
S4-P04	Tina Unuk Nahberger	From Seed Microbiome to Seedling Success: Functional Role of Endophytic Fungi in Douglas Fir
S5-K01	Marie Simonin	Rewiring the Seed Microbiome: From Chaos to SynCom Symphony
S5-FT01	Daniel Garrido-Sanz	First come, first served? Seed-borne bacteria drive the assembly of the wheat rhizosphere microbiome
S5-FT02	Davide Gerna	Rethinking dormancy through a holobiont lens: inactivation and reactivation of seed-microbiome partnerships
S5-T02	JAY PRAKASH VERMA	Chickpea Seed Endophytes as a Source of Potent Bio-inoculants for enhancing Sustainable Agricultural productivity
S5-T03	Chiara Platania	Seed treatment with bacterial and fungal endophytes reshapes rice microbiome while suppressing bakanae disease

S5-T04	Louna Colaert-Sentenac	Seed Microbes Affect Seedling Metabolism, Microbiome Assembly, and Phenotype in Common Bean depending on Host Variety and Conditions
S6-K01	Gabriele Berg	Sowing the seed of success - translating the seed microbiome
S6-FT01	Alexandre Jousset	AI-Driven Seed Microbiome Engineering
S6-FT02	Kabiru Muhammad	PlantMetaBase: Harmonizing Public Plant Microbiome Metadata Reveals Taxonomic and Geographic Bias
S6-T01	Juan Ignacio Vílchez	Stress reshapes microbiota inheritance in tomato, consistent with metabolic filtering and enhanced heat resilience
S6-T02	Fede Berckx	Presentation of NordGen – Nordic Genetic Resource Center and Svalbard Global Seed Vault experiments
S6-T03	Shervin Hadian	Genomic and Functional Insights into an Artemisia-Derived Endophyte Enhancing Pea Growth and Disease Resistance
S6-T04	Gaurav Pal	Functional roles of seed endophytic bacteria in seedling development and biotic stress tolerance in maize
S7-K01	Manuel Delgado Baquerizo	Title TBC
S7-FT01	Hamed Azarbad	Seed microbiota mediate transgenerational drought adaptation in wheat
S7-FT02	Natalia González Benítez	Seed Microbiota as a Driver of Plant Adaptation in the Current Context of Climate Change
S7-T01	Dinesh Ramakrishnan	A global analysis reveals biased exploration in flower microbiome research
S7-T02	Valentin Gfeller	Seed multiplication imprints seed-associated fungal communities in a farming system- and year-specific manner
S7-T03	Carolyn Lowry	Seed microbiomes change in the soil over time and predict seed mortality.
S7-T04	Raquel Tera Martínez	Seed microbiota as a functional driver of biodiversity benefits in mixed-cropping systems