INTERNATIONAL PHYTOBIOMES CONFERENCE 2024

19-21 NOVEMBER

Donald Danforth Plant
Science Center

ST. LOUIS, MO
USA

International Phytobiomes Conference 2024
Donald Danforth Plant Science Center, St. Louis, MO, USA
19-21 November 2024

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Welcome

Dear colleagues,

It is with great pleasure that we welcome you to St. Louis for the International Phytobiomes Conference 2024. We look forward to connecting with each of you and engaging in insightful conversations about Phytobiomes research.

Plants grow in association and interaction with complex communities of organisms and environmental conditions. These interactions are captured by the term “Phytobiome”, which refers to a plant (“phyto”) in a specific environment (“biome”). Phytobiomes research is a holistic, system-level approach studying the complex interactions between plants, microorganisms, soils, climate, environment, and the influences of management practices.

Understanding entire systems of Phytobiomes will be critical to ensuring sustainable global food security in the context of population growth, climate change, and the necessity to preserve biodiversity and natural resources. The goal of the International Phytobiomes Conference 2024 is to bring together a diverse group of scientists and industry representatives to collectively advance our knowledge of Phytobiomes to increase the production of safe and nutritious food, feed, and fiber.

Over the next three days, agricultural stakeholders, public and private sector agronomists, plant pathologists, geneticists, microbiologists, soil scientists, data scientists, biostatisticians, plant physiologists, nutrient management experts, regulatory experts – to name only some disciplines – will present their research, engage in discussions, and share their expertise to enhance our understanding of how Phytobiome components interact and influence each other.

The Conference program covers a wide range of topics related to Phytobiomes: agricultural production and sustainability, genetic enhancement, interactions between microbial communities and associated plants, soil health, nutrient management and uptake, the use of models and imaging to probe the Phytobiome, digital management of Phytobiomes systems, the development of databases and modeling tools for next generation agriculture, and the transformation of Phytobiome discoveries into products.

We hope that the Conference will generate stimulating discussions and initiate collaborations within and across disciplines for the advancement of Phytobiomes research.

We would like to thank the Conference partners for their financial support: the International Alliance for Phytobiomes Research, Bayer Crop Science, the Nebraska Center for Biotechnology, Syngenta Group, NewLeaf Symbiotics, the U.S. Culture Collection Network, Trace Genomics, and the Phytobiomes Alliance Controlled Environment Agriculture Working Group.

We also would like to thank the U.S. Department of Agriculture’s National Institute of Food and Agriculture (NIFA) for their financial support and the U.S. National Science Foundation (NSF) for providing travel support to twelve early career scientists to attend the Conference.

We wish you an excellent Conference, stimulating interactions with colleagues, and a great time in St. Louis.

The Conference Organizing Committee

Acknowledgments

The International Phytobiomes Conference 2024 is organized by the International Alliance for Phytobiomes Research.

This is the fifth Phytobiomes Conference. The first was held in 2015 in Washington, D.C. (USA), the second – a Keystone Symposia – was held in 2016 in Santa Fe, New Mexico (USA), the third in 2018 in Montpellier (France) and the fourth in 2022 in Denver, Colorado (USA).

Organizing Committee

- Gwyn Beattie, Iowa State University, USA
- Kirsten Benjamin, Pivot Bio, USA
- Natalie Breakfield, NewLeaf Symbiotics, USA
- Richard Broglie, Pivot Bio (Retired), co-chair of the Phytobiomes Alliance Microbiomes Working Group, USA
- Joseph Cammack, FarmBox Foods, USA
- Trevor Charles, University of Waterloo, Canada
- Kellye Eversole, Eversole Associates, USA
- Daniel Jacobson, Oak Ridge National Laboratory, USA
- Prasanna Kankanala, Trace Genomics, USA
- Jan Leach, Colorado State University, USA
- Claire Rogel-Gaillard, INRAE, France
- Matthew Ryan, CABI, United Kingdom
- Jason Wallace, University of Georgia, USA
- Matthew Wallenstein, Syngenta, USA

Local Organizing Committee

- Natalie Breakfield, NewLeaf Symbiotics, USA
- Anne Mwaniki, Bayer Crop Science, USA
- Tam McGuire, Donald Danforth Plant Science Center, USA

Conference Office – Phytobiomes Alliance

- Dusti Gallagher (Coordination)
- Isabelle Caugant (Communication)
- Lori Leach (Logistics & Finance)
- Ying Sun (Volunteer Coordination)

Support

The International Phytobiomes Conference 2024 is supported by the Agriculture and Food Research Initiative grant No. 2024-67013-43804/project accession No. 1033236 from the USDA National Institute of Food and Agriculture and by the U.S. National Science Foundation under Grant No. 2431115.

USDA National Institute of Food and Agriculture
U.S. DEPARTMENT OF AGRICULTURE

Practical Information

Venue Address

The Donald Danforth Plant Science Center
975 N Warson Rd
St. Louis, MO 63132, USA

@phytobiomes
#Phytobiomes2024

Conference Office Contacts

The registration desk will be staffed for the duration of the Conference. Please go to the desk for all your Conference related questions.

Organizers and Volunteer Assistants will be present throughout the Conference venue and can be identified by their blue name tags.

Contact email: leach@eversoleassociates.com

Photographs and Recording

The Conference organizers will take photographs and make video and audio recordings throughout the event. By attending, you grant the organizers permission to use and publish your image and/or recorded footage for print, digital communications, and marketing purposes.

Recording of the presentations is strictly prohibited, and Conference presentations will not be shared without the express permission of the respective authors.

Social Media Policy

Live-posting and sharing content from the International Phytobiomes Conference on social media is welcomed and encouraged to help spread awareness about the event. For X/Twitter, please consider using the Conference hashtag **#Phytobiomes2024** and tagging **@phytobiomes**.

Please refrain from posting pictures of presentation slides. If a speaker prefers that their research not be shared on social networks, they should announce it before and during their presentation.

Wifi

Available throughout the venue. **Network name: #1PlantScience**

Poster Sessions

Presenters should stand by their posters during the assigned poster sessions on:

- Tuesday 19 November from 5:20 to 6:20 pm (even numbers)
- Wednesday 20 November from 5:35 to 6:35 pm (odd numbers)

Best Poster – Public Award

All attendees are encouraged to vote for the “Best Poster” by casting their vote at the registration desk.

Online Platform & Networking

An online platform is available via this QR code to enhance your Conference experience. This allows mobile access to the Conference program, abstracts, sponsor booths, networking, and more.

Online Platform

Code of Conduct

The International Phytobiomes Conference is committed to providing a safe and productive meeting environment that fosters open dialogue and the exchange of scientific ideas, promotes equal opportunities and treatment for all participants, and is free of harassment and discrimination.

This Code of Conduct outlines the Conference organizer's expectations for all meeting attendees, speakers, exhibitors, staff, contractors, and guests at the Conference and social events. All participants in attendance are expected to abide by this Code of Conduct to help ensure a pleasant and safe meeting experience. All participants are expected to treat others with respect, professionalism, and consideration and to uphold standards of scientific integrity and professional ethics.

Conference participants violating these rules may be sanctioned or expelled from the Conference without a refund at the discretion of the Conference organizers.

Unacceptable Behavior

The following represent types of behaviors that will not be tolerated during the International Phytobiomes Conference and related events:

- Harassment, intimidation, or discrimination in any form.
- Engaging in biased, demeaning, intimidating, coercive, harassing, or hostile conduct or commentary, whether seriously or in jest, based on sex, gender identity or expression, sexual orientation, race, ethnicity, national origin, religion, marital status, veteran status, age, physical appearance, disability, power differential, or other identities.
- Engaging in sexual harassment. Sexual harassment refers to unwelcome sexual advances, requests for sexual favors, and other verbal or physical actions of a sexual nature such as, but not limited to: unnecessary touching; use of sexually degrading words to describe an individual; and display of sexually suggestive objects or images or other materials; and sexually explicit jokes, regardless of the means by which the material is communicated.
- Intentionally talking over or interrupting others.
- Engaging in personal attacks of any kind.
- Commenting on personal appearance.
- Retaliating against persons who file a complaint or assist in an investigation.
- Disrupting the Conference or engaging in harm or threats of harm of any kind.
- Advocating for, or encouraging, any of the above behaviors.

Reporting

If an individual experiences or witnesses harassment or misconduct, they should immediately report it to the Conference staff identified by their special badges, or contact Lori Leach at leach@eversoleassociates.com or the Conference office at contact@phytobiomesalliance.org. All reports will be treated seriously and confidentially and responded to promptly.

If an individual experiences or witnesses harassment or misconduct, it is recommended that, in addition to notifying the contacts mentioned above, they write down the details. They are not expected to discuss the incident with the offending party. Their confidentiality will be maintained to the extent that it does not compromise the rights of others.

All reports will be investigated. We will gather all relevant details and information (verbal or written) from the reporter, the target (if they are not the reporter), and witnesses. Investigations may extend beyond the end of the Conference.

Enforcement

Conference organizers may take action to redress anything designed to, or with the clear impact of, disrupting the event or making the environment hostile for any participants.

Participants asked to stop any harassing behavior are expected to comply immediately.

If a participant engages in harassing behavior, the Conference organizers retain the right to take any actions to keep the event a welcoming environment for all participants. This includes, but is not limited to, warning the offender or expulsion from the Conference with no refund, and barring the person from participating to future Phytobiomes Conferences.

We expect participants to follow these rules at all event venues and event-related social activities. We think people should follow these rules outside event activities too!

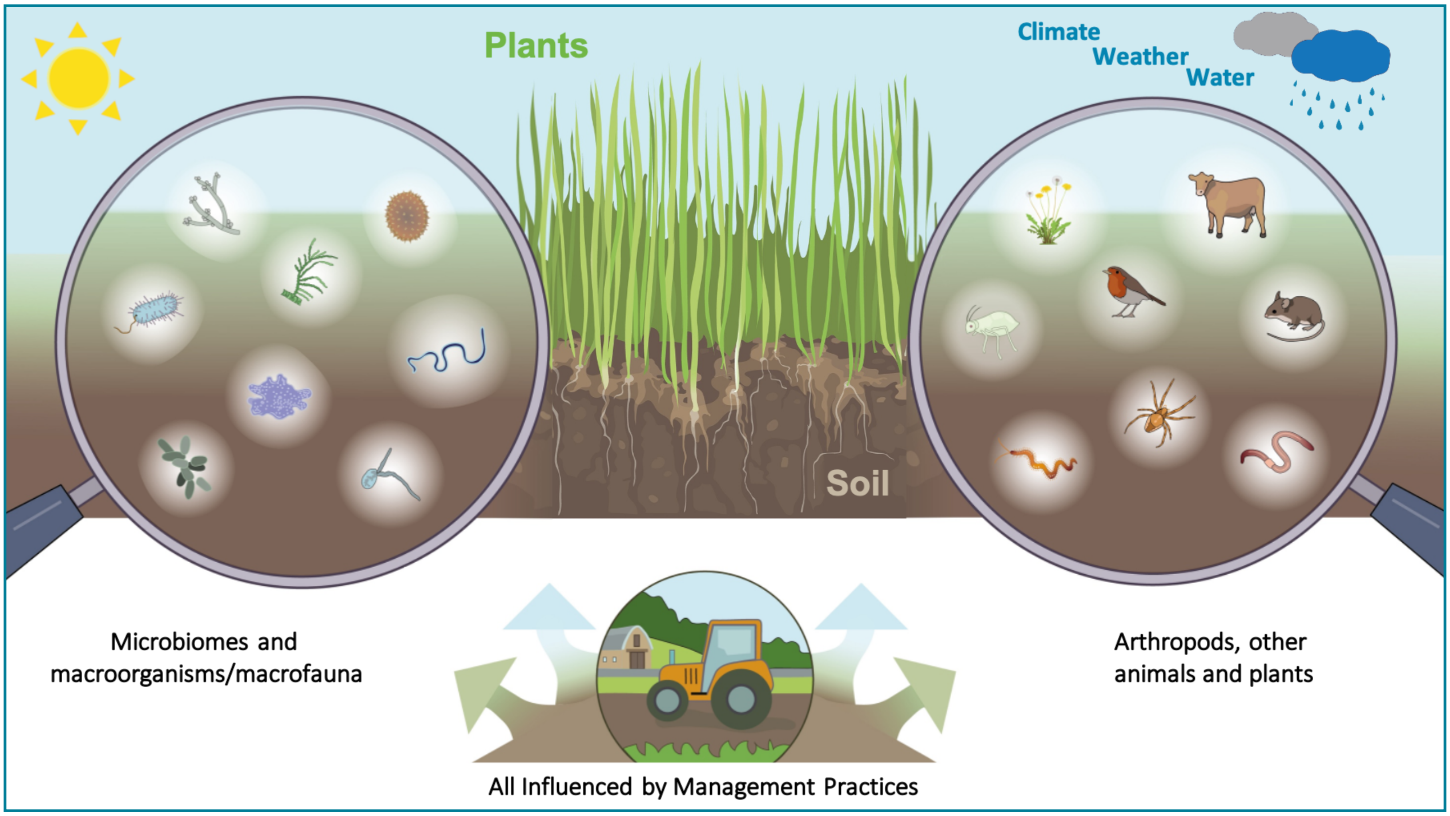
The Phytobiomes Concept

Plants grow in association and interaction with complex communities of organisms, environmental conditions, and management practices. The term "Phytobiomes" encompasses all of this complexity.

A "Phytobiome", which refers to a plant ("phyto") in a specific environment ("biome"). Phytobiomes research is a holistic, system-level approach studying the complex interactions between plants, microorganisms, soils, climate, environment, and the influences of management practices.

Phytobiomes have an important role in the sustained health and productivity of plants and plant ecosystems.

Because interactions within Phytobiomes are dynamic and complex, there is a need to build a foundation of systems-level knowledge of various Phytobiomes. This includes an understanding of how the different components interact and influence each other to empower the development of predictive and prescriptive analytics for use in next generation precision agricultural systems.



Establishing a foundation of knowledge on how Phytobiome components interact and affect each other will be critical to ensuring sustainable global food security in the next decades in the context of population growth, climate change and necessity to preserve biodiversity and natural resources.

INTERNATIONAL ALLIANCE FOR PHYTOBIOMES RESEARCH

An international, nonprofit alliance of industry, academic, and governmental partners

PHYTOBIOMES
ALLIANCE

Vision

By 2050, all farmers have the ability to use predictive and prescriptive analytics based on geophysical and biological conditions for determining the best combination of crops, management practices, and inputs for a specific site in a given year

Mission

Establish a science and technology foundation for site-specific, phytobiome-based enhancement of sustainable food, feed, and fiber production

Goals

Identify research gaps and help coordinate projects to address those gaps

Establish national, international, and multi-national public-private projects and networks

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in internationalphytobiomesalliance

Conference Sponsors

The International Phytobiomes Conference 2024 is made possible thanks to the generosity of our sponsors, including the Phytobiomes Alliance as a Platinum sponsor. We thank all of them for their dedication to advancing collaborative science.

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Invited Speakers

Samiran Banerjee

North Dakota State University, USA

Samiran Banerjee is Assistant Professor in the Department of Microbiological Sciences at North Dakota State University. Previously, he held research positions at the Commonwealth Scientific and Industrial Research Organization in Australia and Agroscope in Switzerland. Banerjee is a microbial ecologist with expertise in omics and machine learning approaches, and experience in plant-soil-microbe interactions. His research utilizes a combination of high-throughput sequencing, synthetic biology, and advanced statistical approaches to understand the rules that govern the microbiome assembly and microbe-microbe interactions. He also examines microbiome recruitment into the rhizosphere and roots, and how various abiotic and biotic factors alter the structure and functions of plant and soil microbiomes. He serves as a reviewer for several federal and international funding agencies, including the U.S. Department of Agriculture, National Science Foundation, and Genome Canada.

Rebecca Bart

Donald Danforth Plant Science Center, USA

Becky Bart is a Member, Principal Investigator and VP of Research at the Donald Danforth Plant Science Center. Her research focuses on the complicated interactions between plants, microbes and the environment and encompasses disease-causing microbes such as bacteria and viruses and the less well understood multitude of beneficial microbes that associate with plants. Becky's team applies computational, lab and field-based methods to dissect the complicated web of these interactions and to understand how they ultimately affect plant health and the sustainability of agriculture.

Becky also serves as the Director of the Subterranean Influences on Carbon and Nitrogen (SINC) Center. At the SINC Center, Becky and her colleagues are working to improve the sustainability of agriculture by developing technologies to track the flow of nitrogen and carbon across plant roots, discovering novel beneficial microbes, and understanding the genetic mechanisms that influence these interactions. Through this work they are developing technologies to decrease the use of nitrogen fertilizer without the loss of crop productivity. Becky received a BA from Reed College, her PhD from the University of California, Davis, and was a NIFA postdoctoral scholar at the University of California. In 2019, she received the Innovation Award from the St. Louis Academy of Sciences.

Gwyn Beattie

Iowa State University, USA

Gwyn Beattie is a professor at Iowa State University in the USA where she holds an endowed Chair as the Robert Earle Buchanan Distinguished Professor of Bacteriology. Her research is exploring the mechanistic drivers of plant-bacteria-environment interactions, including how the abiotic environment dictates bacterial strategies for success on plant leaves and bacterial community development on plant roots. She is also investigating insect-vectored plant pathogens, with an interest in how climate change may be contributing to the emergence of plant diseases. Gwyn Beattie is a Fellow of the American Phytopathological Society, the Co-Editor-in-Chief of the Annual Review of Phytopathology, and a founding member of the Board of Directors for the International Phytobiomes Alliance.

Terrence Bell

University of Toronto, Canada

Terrence Bell is a soil microbial ecologist and is an Assistant Professor at the University of Toronto – Scarborough. He is based in the Department of Physical and Environmental Sciences, cross-appointed in Ecology & Evolutionary Biology, and is a member of the Sustainable Food and Farming Futures Cluster. His first faculty appointment was at Penn State University from 2017-2022, after working as a postdoctoral fellow at l'Université de Montréal and Cornell University. He earned his BSc from Queen's University, his MSc from Western University, and his PhD from McGill University. He has published >60 scientific articles, has received funding from varied sources, including the USDA, DOE, NSERC, and Genome Canada, and is currently a Senior Editor for ISME Communications. His work explores the constraints on microbial niche breadth and the extent to which niche breadth can be modified by new environmental pressures. This work has implications for both the intentional manipulation of microbes and microbiomes (e.g. microbial breedings) and incidental manipulations (e.g. global change factors).

Francesca Cotrufo

Colorado State University, USA

Francesca Cotrufo is a Professor in the Department of Soil and Crop Sciences at Colorado State University (CSU). She is a soil ecologist and biogeochemist, internationally recognized for her work in the field of litter decomposition and soil organic matter dynamics, and in the use of isotopic methodologies in these studies. She strives to advance understanding of the mechanisms and drivers of formation and persistence of soil organic matter, and their response to global environmental changes and disturbances. She uses this understanding to improve modelling of soil C-climate feedback to inform climate and land use policy and management. She also pursues applied research to innovate and increase throughput of soil carbon and health testing, and to propose soil management practices that regenerate healthy soils and mitigate climate change.

As a scientist fully aware of the current and future challenges expecting humanity, Francesca Cotrufo is interested in promoting research education, and outreach activities to help mitigating the current human impacts on the Earth System and assure a better sustainable path for humanity. To this end, with other colleagues at CSU, she recently formed the Soil Carbon Solution Center.

Laramy Enders

Purdue University, USA

Laramy Enders is an Associate Professor in the Department of Entomology at Purdue University, where she leads the Plant-Insect Microbiomes lab. She has an interdisciplinary background in ecology, evolutionary biology, population genetics, plant-insect interactions, molecular defenses and stress responses, and insect microbial symbionts. Her research program employs a systems-level approach to investigate relationships between insect herbivores, host plants and their microbial partners to improve understanding of ecological factors driving microbiome assembly in agricultural environments and apply this knowledge to support crop health and pest management. Her work spans several areas including development of precision microbiome management practices in agriculture, microbe-mediated protection against insect damage across diverse crop plants, and how insect microbial symbionts influence transmission of plant pathogens that limit agricultural production.

Invited Speakers

Catherine Feuillet

Inari, USA

Catherine Feuillet received her PhD in 1993 from the Paul Sabatier University in Toulouse (France) and completed her postdoctoral studies at the University of Zurich, focusing on the isolation of disease resistance genes and the genome structure and evolution of wheat and barley. Following her passion for wheat science, in 2004 Catherine was appointed research director by the INRA (French National Agricultural Research Institute) to lead and develop wheat genomics projects. Catherine joined Bayer Crop Science in 2013 and became the head of trait research.

Since 2018, she has been the Chief Scientific Officer at Inari, the SEEDesign™ company working to solve the critical issues of food security and sustainability by designing nature-positive seed. Catherine leads a group of ~100 scientists (located in Cambridge, MA, USA and Ghent, Belgium) working to advance a technology platform that integrates A.I.-powered predictive design and advanced multiplex gene editing tools to develop seeds that meet the world's needs – all in far less time and with much greater precision and far fewer resources than current approaches.

As one of the founders of the International Wheat Genome Sequencing Consortium, Catherine was elected the French "Golden woman of the year for research" in 2008. The following year, she received the "Prix Foulon" from the French Academy of Sciences for her achievements in wheat research. Her recognitions also include the Legion of Honour (2010), Fellow of the American Association for the Advancement of Science (2011) and the "Prix J. Dufrenoy" from the French Academy of Agriculture (2012).

Catherine is dedicated to developing and guiding the next generation of scientists, having supervised the work of more than 30 master's, PhD and postdoc scientists. Her work has been published in more than 130 peer-reviewed journals and books.

Richard Lankau

University of Wisconsin-Madison, USA

Richard Lankau is Professor in the Department of Plant Pathology at the University of Wisconsin-Madison. His research group seeks to understand how the structure of microbial communities in and around plant roots responds to external forces, like climate change and agricultural management, and effects plant health and ecosystem function. They are interested in understanding fundamental relationships between microbial community diversity, abundance, and community structure and plant growth and soil processes. They are also interested in practical applications to 1) predict agronomic outcomes from the state of soil ecosystems, 2) capitalize on existing variation in microbial interactions to promote restoration and agronomic goals, and 3) restore microbial diversity and function to soils through management interventions.

James Lowenberg-DeBoer

Harper Adams University, United Kingdom

James Lowenberg-DeBoer holds the Elizabeth Creak Chair in Agri-Tech Applied Economics at Harper Adams University (HAU), Newport, Shropshire, United Kingdom. He is responsible for economics in the Hands Free Farm (HFF) team at HAU. He is also past president of the International Society of Precision Agriculture (ISPA) and was co-editor of the journal Precision Agriculture from 2016 to 2022. His research focuses on the economics of agricultural technology, especially precision agriculture and crop robotics. Lowenberg-DeBoer's research and outreach is founded in hands-on experience in agriculture, including production of corn and soybeans in NW Iowa in the USA.

Alhagie K. Cham

University of Tennessee, USA

Early Career Award Winner

Alhagie K. Cham is a dedicated Plant Pathologist with extensive experience in plant-microbe interactions, bioinformatics, and sustainable agriculture. He earned his Doctorate in Plant Pathology and Biotechnology from The Autonomous University of Nuevo Leon, Mexico, with a dissertation focusing on resistance metabolite production in tomato. He also holds a Master's degree in Entomology and Biocontrol from The Autonomous University of Nayarit, Mexico, and a Bachelor's in Agronomy from the University of Ciego de Avila, Cuba. Currently, Alhagie is a Postdoctoral Research Associate at the University of Tennessee Institute of Agriculture, where his research explores genomic and metagenomic approaches to understand plant-pathogen-microbe dynamics, particularly in sweetpotato and maize. His expertise spans molecular techniques, field trials, and laboratory management. He has published numerous peer-reviewed articles and actively contributes to academic communities, including the American Phytopathological Society and the Council for Agricultural Science and Technology. With a strong foundation in both fundamental and applied agricultural sciences, Alhagie is committed to advancing sustainable crop production and improving plant health through innovative research and biotechnological approaches.

Veronica Escalante

Lawrence Berkeley National Laboratory, USA

Early Career Award Winner

Veronica Escalante is a microbe enthusiast and postdoctoral researcher at Berkeley Lab focused on plant-microbe interactions. Currently, her research employs engineered plants and microorganisms to investigate how specific plant root exudates, like aromatic acids, modulate plant-microbial interactions in the rhizosphere. She enjoys thinking about host-microbe interactions in different contexts and is always excited about exploring ways microbes can support plant health and productivity in agricultural and bioenergy systems.

Maede Faghihinia

Iowa State University, USA

Early Career Award Winner

Maede (Madi) Faghihinia is a Postdoctoral Research Associate at Iowa State University, specializing in Microbial Ecology, Metagenomics, and Plant-Microbiome Interactions. She earned her PhD in Environmental Sciences from the University of Liverpool and has conducted research at the Czech Academy of Sciences and the Chinese Academy of Sciences. Her expertise includes studying microbial interactions, with a particular focus on nitrifying bacteria and arbuscular mycorrhizal fungi, and their role in soil nutrient cycling and plant health. She employs cutting-edge techniques, such as stable-isotope probing and nanopore sequencing to investigate how microbial communities contribute to plant nutrient uptake and ecosystem health.

Adrien Fremont

Lawrence Berkeley National Laboratory, USA

Early Career Award Winner

Adrien Fremont is a Postdoctoral Researcher specializing in Rhizosphere Meta'omics at Berkeley Lab. His research focuses on unravelling the intricate biochemical cross-talk between plants and microorganisms in the rhizosphere, aiming to develop strategies for climate-resilient agriculture. Several third-party funded projects have contributed to improve our knowledge of the effects of biological control methods against diseases caused by soil-borne pathogens. This includes the impact of applied beneficial microbes on plant health under consideration of their rhizosphere competence and their effects on the rhizosphere microbiome. In addition, we aim to answer the question how long-term farming practice affect the performance of microbial inoculants and thus plant health at field scale.

Rita Grosch

Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Germany

Rita Grosch‘s main research areas are plant–pathogen interactions with a particular emphasis on soil-borne pathogens such as Rhizoctonia solani and Fusarium spp. Soil-borne pathogens are difficult to control and disease incidence and severity are affected by various (a)biotic stressors. Therefore, the research goal is to determine how (a)biotic stressors affect diseases caused by soil-borne pathogens and how severity can be reduced by management practices. The group studies the impact of the stressors and management practices on plant responses at molecular and metabolomic level. Because of the importance of soil and plant associated microorganisms for plant productivity and health, the group aim to answer the questions how environmental conditions (e.g. drought) affect plant-microbe interaction and seek to understand the underlying mechanisms of supporting measures towards plant tolerance to stressors. Several third-party funded projects have contributed to improve our knowledge of the effects of biological control methods against diseases caused by soil-borne pathogens. This includes the impact of applied beneficial microbes on plant health under consideration of their rhizosphere competence and their effects on the rhizosphere microbiome. In addition, we aim to answer the question how long-term farming practice affect the performance of microbial inoculants and thus plant health at field scale.

Laura Mathieu

Early Career Award Winner

INRAE, France

Laura Mathieu is a third-year PhD candidate at the French National Institute for Agriculture, Food and the Environment (INRAE), based at the Plant Health Institute of Montpellier (PHIM). Her research interests include ecophysiology, quantitative genetics, multi-omics, plant-microbe interactions and crop mixtures. She is particularly interested in understanding how diversity affects agro-ecosystem services. During her PhD, she studied how plant-plant interactions modulate disease susceptibility in intraspecific wheat mixtures. She has investigated the genetic basis of these interactions, examined how wheat plants respond to their neighbors, and analyzed the below-ground signals exchanged between plants within these mixtures.

Melanie Medina López

Early Career Award Winner

The Ohio State University, USA

Melanie Medina López earned her BSc in Industrial Microbiology from the University of Puerto Rico, Mayagüez, with a focus on food science and technology. Currently, she is in the final year of her PhD in Plant Pathology at The Ohio State University, where she is co-advised by Dr. Soledad Benitez Ponce and Dr. Horacio Lopez-Nicora. Her research examines spatial and temporal shifts in fungal communities associated with the soybean cyst nematode (SCN) using culture-dependent and independent techniques. She is particularly interested in the study of agricultural microbiomes to inform management practices and identify biocontrol agents that can support the management of plant pathogens.

Ally Miners

Early Career Award Winner

University of Waterloo, Canada

Ally Miners completed her BSc at the University of Waterloo (Canada), specializing in microbiology and plant biology. During this time, she began investigating relationships between plants and symbiotic bacteria under the mentorship of Trevor Charles, PhD. Currently, she is a first-year MSc student at the University of Waterloo (Canada), in the Department of Biology. Her research focuses on enriching 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase-producing bacteria in the plant microbiome to improve plant growth. She is interested in leveraging plant-beneficial bacteria to reduce synthetic fertilizer dependence and promote sustainable agriculture practices.

Angelica Miraples

Early Career Award Winner

University of Guelph, Canada

Angelica Miraples completed her BSc at the University of Toronto (Canada), St. George, with majors in cell and molecular biology, and human biology. She earned her MSc at the same institution, in the Department of Cell and Systems Biology, where she worked with *Arabidopsis* to investigate the functional redundancy of a subset of non-selective Ca^{2+}-permeable channels, known as cyclic nucleotide gated-ion channels (CNGCs), under various physiological stimuli. Currently, she is a PhD candidate at the University of Guelph (Canada), in the Department of Plant Agriculture. Her research focuses on the maize microbiome, specifically on understanding the origins of the maize pollen microbiome and the mechanisms that may permit vertical transmission from pollen to progeny.

Mallory Morgan

Early Career Award Winner

Oak Ridge National Laboratory, USA

Mallory Morgan is a Postdoctoral Research Associate in the Computational and Predictive Biology Group at Oak Ridge National Laboratory, working under Dr. Daniel Jacobson. Her research leverages genetic data from single nuclei through population scales, using computational systems biology approaches to uncover genetic mechanisms influencing plant phenotypes. Mallory's current work through the Plant Microbe Interfaces Scientific Focus Area investigates the genetic mechanisms of microbial colonization in Populus trichocarpa, which supports the prioritization of gene candidates for experimental validation. She completed her PhD at the University of Florida in the Forest Genomics Lab with Dr. Gary Peter, where her work focused on identifying candidate genes to enhance pine feedstocks for bioenergy and climate resilience. Her doctoral research was supported by an NSF Graduate Research Fellowship and a DOE SCGSR award.

Daniel Naylor

NewLeaf Symbiotics, USA

Daniel Naylor is a Senior Scientist in Plant Biology at NewLeaf Symbiotics. His research background has been in examining plant and soil microbiome responses to abiotic stresses such as drought or nitrogen deficiency, as well as leveraging beneficial microbes to improve crop performance. His projects at NewLeaf include testing a diverse array of microbes for their ability to stimulate growth, mitigate greenhouse gas emissions, or improve drought tolerance in a variety of row crops. He obtained his PhD in Plant Biology from the University of California, Berkeley, and his Bachelor in Science in Biotechnology from the University of California, Davis.

Anne Phillips

Early Career Award Winner

NewLeaf Symbiotics, USA

Anne Phillips is a Senior Staff Scientist at NewLeaf Symbiotics. She is a plant pathologist and microbiologist with a passion for sustainable agriculture solutions. Her current focus is on the field research development of biocontrol and biostimulant products on specialty crops. She received her PhD from Washington University in Saint Louis where she studied the re-emergence of cotton bacterial blight under the mentorship of Rebecca Bart, PhD at the Donald Danforth Plant Science Center.

Jose Sanchez-Gallego

University of Wisconsin-Madison, USA

Jose A. Sanchez-Gallego completed his BSc at Universidad ICESI in Cali, Colombia. While majoring in biology, he worked at the plant molecular physiology lab investigating nitrogen fixing bacteria populations associated with wild-rice species and characterizing their aluminum-stress tolerance. Currently, he is a PhD candidate at the University of Wisconsin – Madison (USA), in the Department of Plant Pathology. One of his research lines focuses on the use of the disaccharide trehalose as a potential plant biostimulant, specifically with the aim of using it to fight bacterial wilt caused by Ralstonia solanacearum on tomato.

Asha Thapa

University of Louisiana at Monroe, USA

Early Career
Award Winner

Asha Thapa is currently pursuing a Master's in Biology at the University of Louisiana at Monroe. She earned a Bachelor's in Agriculture from Tribhuvan University in Nepal. She is working on the role of Trichoderma afroharzianum T22 on the host transcriptome and helper microbes that aid pea plants in coping with iron (Fe) deficiency in soil. Her research showed that T22 colonizes pea roots in a host-specific manner, improving growth and iron accumulation in Fe-deficient peas. RNA-seq analysis identified differentially expressed genes linked to flavonoid biosynthesis, mineral transport, and redox homeostasis in T22-inoculated roots. Interestingly, T22 restored the abundance of rhizobia, along with the induction of nitrogen-fixing genes in nodules, suggesting a connection between T22 and rhizobia under Fe starvation. Furthermore, T22-mediated Fe mitigation depends on flavonoid-driven symbiosis and rhizobial restoration, likely stemming from their interactions rather than just improved Fe status in plants. Amplicon sequencing further showed the enrichment of several bacterial (Pseudomonas, Acidovorax) and fungal (Pseudallescheria) genera that may act as helper microbes to T22, collectively promoting Fe deficiency tolerance in garden pea. These findings may advance microbiome strategies to alleviate Fe deficiency in peas and other legumes.

Ilksen Topcu

Texas A&M University, USA

Early Career
Award Winner

Ilksen Topcu is a Ph.D. candidate in the Department of Plant Pathology and Microbiology at Texas A&M University. She earned her Bachelor of Science in Plant Protection and Master of Science in Entomology in Turkiye. Her Ph.D. research focuses on using metagenomic and metabarcoding approaches to examine the composition and functions of microbial communities in the rhizosphere and leaf endosphere of ancestral maize and modern inbred lines. Her research aims to understand the dynamics and co-evolutionary relationships of these microbes during the process of maize domestication and breeding. Her goals are to develop biopesticides and biofertilizers to enhance maize crop productivity by utilizing microbial inocula from wild maize plants and transferring these beneficial microorganisms to modern maize varieties, thereby improving pest defenses and reducing the reliance on harmful pesticides.

Chuntao Yin

North Central Agricultural Research Laboratory, USDA-ARS, USA

Chuntao Yin is a research microbiologist at the USDA-ARS North Central Agricultural Research Laboratory in Brookings, South Dakota. Her research team seeks to develop and promote soil, crop, and pest management practices that are ecologically sustainable while maintaining producer profitability. Her research focuses on understanding the interactions between agricultural management practices and soil microbial communities. She unitizes lab, field-based, and computational methods to identify key management factors driving soil microbiomes that support the productivity, efficiency, and resilience of cropping systems. She is also interested in understanding the complicated interactions between plants, phytopathogens, soil microbes, and the environment, as well as developing suppressive soils to improve plant health and resilience.

The Early Career Awards are awarded to talented early career scientists working on Phytobiomes research. The goal of this recognition is to encourage students and early career scientists to participate in the International Phytobiomes Conference 2024.

Congratulations to the Award Winners

- Alhagie K Cham – University of Tennessee, USA
- Elsie Enow – Polish Academy of Sciences Institute of Plant Genetics, Poland
- Veronica Escalante – Lawrence Berkeley National Laboratory, USA
- Maede Faghihinia – Iowa State University, USA
- Adrien Fremont – Lawrence Berkeley National Laboratory, USA
- Laura Mathieu – INRAE, France
- Melanie Medina López – Ohio State University, USA
- Ally Miners – University of Waterloo, Canada
- Angelica Miraples – University of Guelph, Canada
- Anne Phillips – NewLeaf Symbiotics, USA
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Phytobiomes Journal

As the official journal for the Phytobiomes Conference 2024, *Phytobiomes Journal* is offering a special 20% publication discount for conference participants who submit a manuscript between August 2024 and February 2025. All submissions will undergo peer review before acceptance.

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Tuesday 19 November | 8:00am – 8:00pm

Day 1: The Value of a Systems Approach for Agriculture

8:00 am	Registration and packet pick-up	*Donald Danforth Plant Science Center Foyer*
8:50 am	Welcome – **Dusti Gallagher, International Phytobiomes Alliance** Introductions & Conference Overview – **Kellye Eversole, International Phytobiomes Alliance**	*AT&T Auditorium*
9:10 am	Kickoff Plenary – **Gwyn Beattie, Iowa State University, USA** *Exploring the roles of climate and plant-insect-bacteria interactions in emerging plant diseases*	
10:00 am	**Coffee Break & Networking**	*McDonnell Gallery*
Morning Chair: Gwyn Beattie, Iowa State University, USA		
10:30 am	**A Conversation about Production Agriculture & Sustainability** *Moderator: Dusti Gallagher, International Phytobiomes Alliance* • **Emerick Larkin, Plenty, USA** • **Lisa Weaver, United Soybean Board, USA** • **Alex Wiedeman, 80 Acres, USA** • **Jessica Christiansen, Bayer Crop Science, USA**	
11:35 am	Plenary Lecture – **Catherine Feuillet, Inari, USA** *Solving our food system challenges through integrated innovation*	
12:20 pm	Talk – **Rita Grosch, Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Germany** *Impact of farming practices on microbial community in the rhizosphere of winter wheat under consideration of plant fitness*	
12:40 pm	Poster Flash Talks • **Marissa Roghair Stroud, Iowa State University, USA** *The MAize Rhizosphere Synthetic Community (MARSc): A consortium to reveal principles underlying bacteria-bacteria interactions in the rhizosphere* • **Joshua Zuber, Bayer Crop Science, USA** *Difficulties in effective microbial-based product testing on Apis mellifera (L.) in the laboratory*	
12:50 pm	**Networking Lunch & Poster Viewing**	*McDonnell Atrium & Gallery*
Afternoon Chair: Matthew Ryan, CABI, United Kingdom		
2:00 pm	Plenary Lecture – **Francesca Cotrufo, Colorado State University, USA** *Regenerating soil organic matter for the benefit of climate and food production: A systemic multifaceted approach*	
2:45 pm	Talk – **Richard Lankau, University of Wisconsin-Madison, USA** *Capitalizing on microbial communities to meet restoration and agricultural goals in changing climates*	

3:15 pm Poster Flash Talks

- **Sarah Richards, Pennsylvania State University, USA**
  Directed evolution of beneficial microbial inoculants to improve in-soil survival
- **Janice Parks, Washington State University, USA**
  Nitrogen fertilizer application impacts the composition and predicted function of the microbial community in a pea (Pisum sativum) and canola (Brassica napus) intercropping system (peaola)
- **Spencer Arnesen, Donald Danforth Plant Science Center, USA**
  Identifying diazotrophs from root rhizosphere using variable nifH primers
- **Ashley Paulsen, Iowa State University, USA**
  Interrogating individual and collective contributions of members of a synthetic community to maize growth promotion under low nitrogen fertilization

3:35 pm **Coffee Break & Networking** *McDonnell Gallery*

4:00 pm **Phytobiomes Alliance Regulatory Working Group Discussion:** *How are research and product development decisions influenced by the regulatory framework?*

- **Keith Matthews, Matthews Law, USA**
  Regulatory overview
- **Bernadette Juarez, USDA-APHIS, USA**
  A regulator's perspective
- **Lisa Ortego, Bayer Crop Science, USA**
  Identifying and addressing the testing and risk assessment challenges of biological-based crop protection products: Progress of the Organization for Economic Co-operation and Development (OECD) expert group on biopesticides

Panel Discussion: *Experiences with regulations*
Moderator: Keith Matthews, Matthews Law, USA

- **Trevor Charles, Earth Microbial, USA**
- **Shade Sabitu, Pivot Bio, USA**
- **Bernadette Juarez, USDA-APHIS, USA**
- **Lisa Ortego, Bayer Crop Science, USA**

5:05 pm Poster Flash Talks

- **Elizabeth Njuguna, University of California Berkeley, USA**
  International capacity building for CRISPR genome editing technology
- **J. Miguel Bonnin, CABI, United Kingdom**
  Underpinning Phytobiomes research: The first insights from a European soil microbiome cryopreservation experiment

5:15 pm Wrap-up & Closing Remarks

5:20 - 6:20 pm **Poster Session (Even Numbers)** *McDonnell Atrium*

6:00 - 8:00 pm **Welcome Reception**

Partially sponsored by NewLeaf symbiotics *McDonnell Atrium*

Wednesday 20 November | 7:55am – 9:00pm

Day 2: Harnessing Interactions and Influences within the Phytobiomes

7:55 am
Welcome, Announcements & Overview of Day 2 *AT&T Auditorium*
Dusti Gallagher, International Phytobiomes Alliance

Morning Chair: Richard Broglie, International Phytobiomes Alliance

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8:00 am
Plenary Lecture – **Terrence Bell, University of Toronto, Canada**
The influence of near-term conditioning on microbial survival and function in Phytobiomes

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8:45 am
Talk – **Laramy Enders, Purdue University, USA**
Engineering beneficial agricultural microbiomes to improve protection against insect pests

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9:15 am
Talk – **Veronica Escalante, Lawrence Berkeley National Laboratory, USA**
Unraveling the role of aromatic acids in plant-microbe interactions
Early Career Award Winner

9:35 am
Talk – **Anne Phillips, NewLeaf Symbiotics, USA**
Developing a microbial product for tomato with Pink Pigmented Facultative Methylotrophs (PPFMs): A field technical development journey
Early Career Award Winner

9:55 am
Poster Flash Talks

- **Xiaoping Li, Virginia Tech, USA**
  Rhizosphere microbial composition and mycorrhizal fungi associated with Boxwood Blight resistance?
- **Noh-Hyun Lee, Seoul National University, South Korea**
  Development of a hybrid prediction model for Fusarium head blight in wheat considering both meteorological factors and surrounding microbial community
- **Kara Reardon, University of Toronto, Canada**
  Contrasting the performance of soil microbiomes conditioned to individual and combined local environmental changes
  Early Career Award Winner

10:10 am **Coffee Break & Networking** *McDonnell Gallery*

10:45 am
Talk – **Angelica Miraples, University of Guelph, Canada**
Investigating the microbiome of early maize pollen progenitor cells and its subsequent transmission to mature maize pollen
Early Career Award Winner

11:15 am
Phytobiomes Alliance Microbiomes Working Group Discussion

- **Devin Coleman-Derr, University of California, Berkeley, USA**
  SRC1, a synthetic rhizosphere community of sorghum, modifies immunity and cell wall composition
- **Kirsten Benjamin, Pivot Bio, USA**
  Development of gene-edited microbial diazotrophs for partial replacement of nitrogen fertilizer on cereal crops
- **Daniel Jacobson, Oak Ridge National Laboratory, USA**
  Mechanisms, networks, and AI (Oh my!): Unraveling host-microbiome systems biology

Panel Discussion
Moderator: Richard Broglie, co-chair of the Phytobiomes Alliance Microbiomes Working Group

12:20 pm	Talk – **Asha Thapa, University of Louisiana at Monroe, USA** *Trichoderma afroharzianum T22 induces rhizobia and flavonoid through systemic signaling to combat Fe deficiency in garden pea*	
12:40 pm	**Group Photo, Networking Lunch & Poster Viewing**	*McDonnell Atrium & Gallery*
Afternoon Chair:	Trevor Charles, University of Waterloo, Canada	
1:45 pm	Plenary Lecture – **James Lowenberg-DeBoer, Harper Adams University, United Kingdom** *Envisioning digital management of phytobiome systems*	
2:30 pm	Talk – **Rebecca Bart, Donald Danforth Plant Science Center, USA** *Novel microbes and newly assembled syncoms to promote sustainable agriculture*	Early Career Award Winner
3:00 pm	Talk – **Melanie Medina, Ohio State University, USA** *Within field spatial variability of soil fungal communities and soybean cyst nematode interactions*	Early Career Award Winner
3:20 pm	Talk – **Maede Faghihinia, Iowa State University, USA** *Central role of Thaumarcheota in microbial network cohesion and robustness in agricultural cropping systems*	
3:40 pm	**Coffee Break & Networking**	*McDo Gallery* Early Career Award Winner
4:10 pm	Talk – **Ilksen Topçu, Texas A&M University, USA** *Domestication of Zea mays results in divergent impacts on leaf endosphere microbiota*	
4:30 pm	Poster Flash Talks • **Leah Zorrilla, Bayer Crop Science, USA** *Human health risk assessments for biopesticides – Can we evolve to next generation risk assessments?* • **Adriana Giongo, Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Germany** *Microbial inoculants increase tolerance to drought stress conditions* • **Shweta Priya, Lawrence Berkeley National Laboratory, USA** *Dissecting the role of plant cell wall composition in modulating plant-microbe interactions*	
4:45 pm	Talk – **Daniel Naylor, NewLeaf Symbiotics, USA** *Methanotrophs for methane mitigation and growth promotion in rice*	
5:05 pm	Talk – **Chuntao Yin, USDA-ARS, USA** *Cover crop effects on soybean health and associated rhizosphere microbiome*	
5:25 pm	Wrap-up & Announcements	
5:35 - 6:35 pm	**Poster Session (Odd Numbers)**	*McDonnell Atrium*
7:15 - 9:00 pm	**Gala dinner** Partially sponsored by BAYER Bayer	*Missouri History Museum*

Thursday 21 November | 8:00am – 4:10pm

Day 3: Building Collaborations to Drive Innovative Systems-based Research

8:00 am	Welcome & Overview of Day 3 **Dusti Gallagher, International Phytobiomes Alliance**	*AT&T Auditorium*
8:05 am	**Early Career Recognitions**	
Morning Chair: Natalie Breakfield, NewLeaf Symbiotics, USA		
8:45 am	Plenary Lecture – **Samiran Banerjee, North Dakota State University, USA** *The role of microbiomes in One Health*	
9:30 am	Talk – **Laura Mathieu, INRAE, France** *Plant-plant interactions modulate wheat severity to Septoria Tritici Blotch in some specific mixtures through intergenomic epistatic interactions and transcriptomic-metabolomic changes*	**Early Career Award Winner**
9:50 am	Talk – **Alhagie K. Cham, University of Tennessee, USA** *Metagenomic profiles reveal that a mild constitutive defense response in maize maintains microbial diversity, limits pathogens and promotes beneficial microbes*	**Early Career Award Winner**
10:10 am	**Coffee Break & Networking**	*McDonnell Gallery*
10:40 am	**Industry Roundtable Discussion:** *Current state of industry & needs; Public-private collaborations* *Moderator: Charles Cowden, Valent BioSciences, USA* • **Anthony Neumann, NewLeaf Symbiotics, USA** • **Myles Herbert, Trace Genomics, USA** • **Matthew Wallenstein, Syngenta, USA** • **Kirsten Benjamin, Pivot Bio, USA**	
11:50 am	Talk – **Adrien Fremont, Lawrence Berkeley National Laboratory, USA** *The chemical toolkit of cover crops: Engineering belowground chemical and microbial diversity*	**Early Career Award Winner**
12:10 pm	Talk – **Ally Miners, University of Waterloo, Canada** *Sustainable biofertilizer development with ACC enrichment communities to maximize plant growth*	**Early Career Award Winner**
12:30 pm	Best Poster Awards – Sponsored by UNITED STATES CULTURE COLLECTION NETWORK	
12:40 pm	**Networking Lunch & Poster Viewing**	*McDonnell Atrium & Gallery*

Afternoon Chair: Dusti Gallagher, International Phytobiomes Alliance	
2:10 pm	Talk – **Mallory Morgan, Oak Ridge National Laboratory, USA** *MENTOR identifies functional relationships among P. trichocarpa genes associated with fungal colonization*
2:30 pm	Talk – **Jose Sanchez-Gallego, University of Wisconsin-Madison, USA** *Trehalose, an environmentally friendly low-cost biostimulant to increase plant stress tolerance*
2:50 pm	**Industry Career Discussion:** *Moderator: Kellye Eversole, International Phytobiomes Alliance* • **Prasanna Kankanala, Trace Genomics, USA** • **Jordon Wade, Syngenta, USA** • **Kirsten Benjamin, Pivot Bio, USA** • **Christina Lawrence, Bayer Crop Science, USA**
4:00 pm	Conference Wrap up & Closing Remarks
4:10 pm	End of Conference

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Giongo, Adriana	122	*Microbial inoculants increase tolerance to drought stress conditions*
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Lee, Noh-Hyun	127	*Development of a hybrid prediction model for Fusarium head blight in wheat considering both meteorological factors and surrounding microbial community*
Li, Xiaoping	128	*Rhizosphere Microbial Composition and Mycorrhizal Fungi Associated with Boxwood Blight Resistance?*
Machado, Tulio	129	*Factors influencing the use of PNA clamps for surveys of endophyte communities*
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Zorrilla, Leah	163	*Human Health Risk Assessments for Biopesticides – Can we evolve to Next Generation Risk Assessments?*
Zuber, Joshua	164	*Difficulties in effective microbial-based product testing on Apis mellifera (L.) in the laboratory*

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Exploring the roles of climate and plant-insect-bacteria interactions in emerging plant diseases

Gwyn Beattie

Iowa State University, Ames, IA, USA

Abstract

Emerging and re-emerging plant diseases threaten the health and productivity of agroecosystems and native landscapes. Many factors are driving this increase, including climate change, pressures from population growth, and globalization of trade and travel. These can cause shifts in the geographic range of insects, plants, and their associated microbes and in the environmental conditions in which these organisms live. Such shifts can lead to opportunities for novel contact among plants, insects and bacteria and thus to spillover events in which a new pathogen can grow and spread plant-to-plant. Insect-vectored plant pathogens may have a particularly high probability of promoting spillover events because the insects enable transmission of microbes among plants. This talk will address questions of how insect-vectored bacterial pathogens evolve within the context of emerging diseases, and how this evolution may be impacted by the many biotic and abiotic components of phytobiomes. I highlight our work on a disease caused by a phloem pathogen, Serratia ureilytica, for which the pathogen's uncommon interactions with its plant host may be linked to its interaction with an unusual breadth of insect vectors and to interactions with microbes within those vectors. Lastly, I will use efforts to address threats posed by emerging diseases to illustrate strategies by which the phytobiome research community could accelerate the process of harnessing the potential of phytobiomes to provide societal benefits.

D1P1

Solving Our Food System Challenges Through Integrated Innovation

Catherine Feuillet

INARI Agriculture, Cambridge, MA, USA

Abstract

Inari Agriculture is designing seeds to meet the challenges of feeding a growing global population while minimizing environmental impact of agricultural production. Addressing such a complex challenge under the pressure of climate change requires radical innovation driven by bold product concepts, non-linear systems approaches, and trans- and multidisciplinary research. The Inari SEEDesignTM technology platform integrates Predictive Design and advanced Multiplex Gene Editing tools to develop higher-yielding varieties of soybean, corn and wheat that require fewer natural resources and inputs in a shorter time and at lower costs than current approaches. In Predictive Design, we harness the power of data, artificial intelligence, and in-cell/in-planta assays to gain an understanding of the genes and pathways that underpin crop traits crucial for performance under varying environmental conditions. Once the target sequences and the types of edits have been identified, we generate combinations of new allelic diversity at the target sites using our Multiplex Gene Editing toolbox to deliver multiple changes into elite parental lines. Examples of the tools and technologies we are using to tackle this complex challenge will be presented.

D1P2

Regenerating soil organic matter for the benefit of climate and food production: A systemic multifaceted approach

Maria Francesca Cotrufo

Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO, USA

Abstract

Soil organic matter (SOM) provides critical agroecosystem services. Its stewardship, including its preservation and further accrual, is key to increasing resilience of food production to a changing climate, and to avoid an irreversible climate crisis. Recently our understanding of the processes and drivers of SOM formation and persistence has advanced within a coherent framework. Applying this framework can support the design of integrated measurement-modeling platforms to inform best agriculture management practices for the stewardship of SOM. I will present our latest framework to conceptualize SOM structure, formation, and persistence, and a coherent measurement-modeling approach we implemented and use. I will illustrate how SOM may affect soil properties which in turn determine the soil's capacity for functioning and ability to provide desired outcomes including supporting plant productivity, and climate adaptation and mitigation. Finally, I will provide examples of applications of our approach to quantify and forecast SOM changes under regenerative agriculture.

D1T1

Impact of farming practices on microbial community in the rhizosphere of winter wheat under consideration of plant fitness

Rita Grosch[1], Adriana Giongo[1], Jan-Helge Behr[1], Babin Doreen[2], Loreen Sommermann[3], Kornelia Smalla[2], Uwe Ludewig[4], Neumann Günter[4], Joerg Geistlinger[3]

[1]Leibniz Institute of Vegetable and Ornamental Crops (IGZ) e.V., Großbeeren, Germany. [2]Julius Kühn Institute (JKI), Braunschweig, Germany. [3]Anhalt University of Applied Sciences of Agriculture, Bernburg, Germany. [4]University of Hohenheim, Stuttgart, Germany

Abstract

Farming practices with high input of agrochemicals have resulted in negative impacts on soil ecosystems. Sustainable management of soil microbiota might bear a high potential as soil microbes play an important role for soil functions and plant productivity. But little is known how farming practices influences plant-microbe interactions in the rhizosphere and thus plant health. A field experiment compares the effects of two long-term soil management practices [conventional mouldboard plough (MP) vs. cultivator tillage (CT)], each including two nitrogen (N) fertilization intensities [intensive N-fertilization including pesticides (Int) vs. reduced extensive N-fertilization without fungicides (Ext)], on winter wheat-microbe interactions. In addition, the impact of different preceding crops (maize or rapeseed) of winter wheat was analyzed. We installed root observation windows in the differently managed winter wheat plots at early plant developmental stage. Soil and rhizosphere samples were taken for microbial community and root exudation profile analyses. Soil management and preceding crop altered significantly microbial community composition in the rhizosphere. In contrast to the fungal community, the bacterial community in the rhizosphere was affected to a lesser extent by N-fertilization intensity. Secondary metabolite profiles in the rhizosphere soil solution of wheat plants grown in MP vs. CT soils showed different patterns, particularly with respect to benzoxanoids as a group of plant metabolites with high biological activity. Tillage practice significantly affects the stress tolerance of the plants independent of the N-intensity and the preceding crop. The results show that suitable farming practice can contribute to enhance the resilience of plant production systems.

D1T2

Capitalizing on microbial communities to meet restoration and agricultural goals in changing climates

Richard Lankau

University of Wisconsin-Madison, Madison, WI, USA

Abstract

Microbial communities in soils and rhizospheres are exceedingly complex, which makes manipulating or engineering natural communities toward desired states very difficult. Nevertheless, microbial communities vary in their structure and functional capabilities across space, due to environmental gradients, land use history, and land management practices. I will discuss two projects in which we are seeking to capitalize on naturally occurring microbiome variation to achieve restoration and agronomic goals. First, in forested systems we have found that tree seedlings inoculated with soil microbial communities sourced from drier, hotter, or colder environments displayed greater survival under drought, heat, or cold stress in field experiments. We are now testing whether the unintentional pre-inoculation with microbial associates, especially mycorrhizal fungi, that occurs in seedling nurseries may be used as a tool to enhance tree seedling success in reforestation projects facing increasing climate stressors. Secondly, in potato cropping systems, we have developed a large database of pre-planting soil chemical, physical, and biological properties from hundreds of fields in Wisconsin and Minnesota, and are using it to test whether soil-borne disease severity and yield potential can be predicted from the state of soils prior to planting. By developing robust predictive models, we hope to transform our descriptive understanding of soil microbiomes into decision support for growers.

D1T3

Identifying and Addressing the Testing and Risk Assessment Challenges of Biological-Based Crop Protection Products: Progress of the Organization for Economic Co-operation and Development (OECD) Expert Group on Biopesticides

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Abstract

The interest and use of biological materials in crop production is increasing globally at a rapid pace. Although these technologies are viewed as safer alternatives to conventional chemicals, assessments are needed to confirm safety. The OECD Expert Group Biopesticides (EGBP) works to harmonize methods and approaches used to assess biopesticides. The EGBP hosts an annual seminar to discuss a topic in biopesticide testing and assessment. In 2022, the EGBP held a conference to focus specifically on these issues. Based on these outcomes, the EGBP has developed a workplan to improve biopesticide testing and assessment with the following focus areas.

- Develop guidance document on best practices for ecological testing
- Revise bee testing guidance and organize ring-testing to optimize pathogenicity evaluation
- Adapt US EPA mammalian toxicity/pathogenicity guidelines to an OECD guideline
- Explore new approach methodologies (NAMs) for sensitization and adverse outcome pathway screening tools and their applicability to biologicals
- Develop guidance document to determine when an in vivo test is needed
- Revise aquatic invertebrate guidance to address technical issues related to particulate test substances, attenuated controls, dose confirmation
- Develop a list of secondary metabolites of concern
- Develop a list of non-target insect species amenable to laboratory testing

The work of the EGBP involves a multi-stakeholder approach including participants from government, academia, business, and non-governmental organizations providing a comprehensive set of experiences to tackle the issues. The focus of the presentation will be the rationale for the key focus areas, the approaches taken to advance the science and the progress to date.

D2P1

The influence of near-term conditioning on microbial survival and function in phytobiomes

Terrence Bell[1], Laura Kaminsky[2], William King[3], Caylon Yates[4]

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Abstract

Microorganisms guide many soil and plant processes, but are much harder to manage than other components of human-controlled systems, such as plant composition, nutrient concentrations, and water availability. Many factors contribute to this challenge (e.g. rapid microbial turnover; difficulty excluding microbial “pests” or “weeds”), but our group is especially interested in the compatibility between microbes and new environments and the extent to which this can change due to short-term environmental pressures. First, this is relevant for the production and application of microbial probiotics for soils, as consistent in-field survival and performance has long been a major challenge. Second, this can inform us on how land use choices might shape global microbial spread and impacts. In this talk, I will discuss some of our work on how different types of environmental conditioning shape the downstream survival and function of 1) individual bacterial strains and 2) whole microbiomes. Ultimately, our goal is to better inform microbial management in agriculture, both at the industrial level and in the design and oversight of agroecosystems.

D2P2

Envisioning Digital Management of Phytobiome Systems

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Abstract

Some aspects of digital agriculture technology are being rapidly adopted and more is in pipeline. While this technology is largely developed to serve high input commercial agriculture based on large scale monocropping, it could also be used for more sustainable management of phytobiome systems. In particular, digital technology could be used to reduce the need for human labour and management in sustainable management of agricultural systems. For example, sensors, robotics and artificial intelligence (AI) decision support systems could facilitate mixed species cropping systems that increase yields (at least of some crops), enhance field biodiversity, reduce use of pesticides and augment soil health. Other examples include early prediction and detection of plant diseases and pest facilitating biological management, robotics to allow cost-effective frequent application of biologicals with little residual activity and AI synthesis of research and farmer experience to more quickly adapt cropping systems to climate variability and other changes. The first step in making the vision of digital management of phytobiome systems a reality is developing technology that improves the lives of farmers and their families. Other steps include developing technology input supply chains to provide benefits for every link in that chain, considering post-harvest impacts of sustainable management of phytobiome systems and creating entrepreneurial opportunities in phytobiome management technology. Sustainable digital management of phytobiome systems would require creativity, responsible innovation and entrepreneurship.

D2T1

Engineering Beneficial Agricultural Microbiomes to Improve Protection Against Insect Pests

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Abstract

Microbial communities are essential for plant health and protection. Recently, it has been suggested that the natural mechanisms plants employ to manage relationships with microbes can be used to selectively engineer whole microbial communities with beneficial or protective properties. This approach, known as host-guided selection, is underdeveloped for crop plants in agricultural settings. Our goal was to naturally engineer tomato root-associated microbiomes that increase resistance to common insect pests. First, we tested several approaches for engineering insect-suppressive rhizosphere soil microbiomes that reduce damage from aphid feeding (*Macrosiphum euphorbiae*) or caterpillar defoliation (*Manduca sexta*, *Spodoptera exigua*) using an iterative soil microbial inoculation process. Second, using metabarcoding approaches we characterized the bacterial and fungal communities of selected soils associated with differences in aphid performance on tomato. Overall, host-guided soil microbiome selection for higher or lower insect performance was successful for aphids but not caterpillars, although effects were transient over time. There were minor shifts in relative abundance of fungal and bacteria taxa observed in insect-suppressive communities, but substantial changes in community composition occurred over time. Network analysis indicated aphid feeding was disruptive to rhizosphere microbiome assembly, resulting in lower community complexity, connectivity and keystone taxa compared to un-infested controls. Overall, our results suggest several factors are critical for successful host-guided engineering of beneficial microbiomes, particularly microbial community stability and microbe-microbe interactions, external environmental influences, and the extent to which the crop trait of interest is microbially mediated.

D2T2

Unraveling the Role of Aromatic Acids in Plant-Microbe Interactions

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Abstract

Plant-microbial interactions are essential for shaping plant health, growth, and resilience. Among the compounds exuded by plants, aromatic acids have gained attention for their role in shaping the microbial composition in the rhizosphere. In this study, we use engineered plants and microorganisms to investigate how aromatic acids, such as protocatechuate (PCA), modulate these interactions. Leveraging *Burkholderia* OAS925, a bacterium capable of uptaking aromatic acids and colonizing plants, we utilized a randomly barcoded transposon sequencing library to explore key genes involved in aromatic acid metabolism. This approach identified a *Burkholderia* mutant deficient in protocatechuate 3,4-dioxygenase (-PCA) that was unable to metabolize aromatic acids, including PCA. In small mesocosms planted with *Brachypodium distachyon*, both the wild-type (WT) and -PCA mutant strains colonized the rhizosphere similarly; however, the -PCA mutant displayed delayed colonization of the endosphere. These findings suggest that aromatic acid metabolism, particularly PCA utilization, may be essential for efficient endosphere colonization. Ongoing work involves testing an engineered Sorghum bicolor line that overproduces PCA to assess how elevated PCA levels impact the colonization dynamics of the *Burkholderia* WT and -PCA strains. To further explore the effects of manipulating aromatic acid production in plant and bacterial metabolism, we are employing the EcoPOD – a laboratory ecosystem that mimics field conditions by integrating sensors for temperature, moisture, CO2, as well as programmable lights, irrigation, and wind speed. By bridging the gap between controlled lab studies and real-world ecosystems, this study will offer valuable insight into improving plant health and productivity in agricultural and bioenergy systems.

D2T3

Developing a Microbial Product for Tomato with Pink Pigmented Facultative Methylotrophs (PPFMs): A Field Technical Development Journey

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Abstract

Once a PPFM isolate or combination of isolates has been identified as a lead for a particular product concept, the process of field technical development begins. Crop response is used to evaluate the commercial viability of the active ingredients, formulation, application method and timing. When applied as a drench to seedlings 7 – 10 days prior to transplant, a combination of *Methylobacterium radiotolerans* and *Methylobacterium komagatae* demonstrated a statistically significant yield response in 3 seasons of small plot testing of +1.5 tons/A (+10%, 5 locations). On-farm assessment of the product over 2 seasons with large acreage side by sides in processing tomato demonstrated a yield response of +2.46 tons/A (+5.6%, 15 locations). In addition to tracking harvest weights at the cannery by treatment, treatments were georeferenced in the field to enable additional insights via satellite imagery. Through NewLeaf Precision, a proprietary spatial data analysis platform, Sentinel-2 satellite imagery was used to visualize and assess season long crop stress response via numerous vegetation indices. For each treatment, pixel values were extracted and aggregated on all dates between planting and harvest without cloud cover. The area under the curve method was used to summarize crop response by treatment over 21 locations. When compared to the untreated control, vegetation indices of *M. radiotolerans* and *M. komagatae* treated areas were greater than 0.9-3.8% relative to the untreated control and demonstrated similar trends to yield response.

D2T4

Investigating the Microbiome of Early Maize Pollen Progenitor Cells and its Subsequent Transmission to Mature Maize Pollen

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Abstract

Pollen is an essential vector for plant sexual reproduction and microbiome transmission, contributing to host plant fitness, but also bee and hive fitness, and human allergenicity. Pollen exposure to the atmosphere is believed to be a key mechanism for microbial inoculation onto the pollen surface, suggesting that most of the microbial load resides here. An endogenous (internal) pollen microbiome has also been alluded to but has not been explored to the best of our knowledge. An internal pollen microbiome would suggest that pollen inoculation may occur from the host plant itself (vertical transmission). The proposed research tested the hypothesis that the maize pollen microbiome first forms during the early stages of pollen progenitor cell (microspore) development. To test this, field grown LH82 inbred maize was collected at two timepoints, dissected to isolate microspores and ultracentrifuged to extract microspores from three stages of development. The taxonomic profiles of the staged microspore microbiomes were compared to that of mature LH82 pollen using full-length 16S rRNA based PacBio sequencing and bioinformatic analysis, replicated across two field seasons. A diversity of bacterial taxa was observed in microspores which increased from early to late timepoints and microspore developmental stages. The microspore microbiome overlapped with mature pollen, suggesting that bacteria are delivered internally to pollen by the microspores. This research advances our fundamental understanding of the origins of the pollen microbiome in maize, with implications for other plants.

D2T5

Trichoderma afroharzianum T22 induces rhizobia and flavonoid through systemic signaling to combat Fe deficiency in garden pea

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Abstract

The role of beneficial fungi in mitigating iron (Fe) deficiency in garden pea is understudied. In this study, *Trichoderma afroharzianum* T22 colonized the roots of different cultivars exposed to Fe-deficiency in a host-specific manner. In Fe-deficient Sugar Snap, T22 improved growth parameters consistent with increased tissue Fe and rhizosphere siderophore. RNA-seq analysis showed 575 and 818 differentially expressed genes upregulated and downregulated in the roots inoculated with T22 under Fe deficiency. The upregulated genes were mostly involved in flavonoid biosynthetic pathway along with genes related to mineral transport and redox homeostasis. The split-root assay demonstrated systemic signaling between T22 and the host promoting symbiotic associations. Interestingly, T22 restored the abundance of rhizobia, particularly *Rhizobium leguminosarum* and *Rhizobium indicum*, along with the induction of *NifA*, *NifD*, and *NifH* in nodules, suggesting a connection between T22 and rhizobia under Fe-starvation. A flavonoid precursor restored plant health even without T22 inoculum, confirming the role of microbial symbiosis in mitigating Fe deficiency. Further, the elevated rhizosphere siderophore, root flavonoid, expression of *PsCoA* (4-coumarate-CoA ligase) and the abundance of *R. leguminosarum* diminished when T22 was substituted with exogenous Fe. This suggests that exogenous Fe eliminates the need for microbiome-driven Fe mobilization, while T22-mediated Fe mitigation depends on flavonoid-driven symbiosis and *R. leguminosarum* abundance. Thus, the effect of T22 on rhizobia likely stems from their interactions, not just improved Fe status. This provides the first mechanistic insights into T22 interactions with host and rhizobia, advancing microbiome strategies to alleviate Fe deficiency in peas and legumes.

D2T6

Novel microbes and newly assembled syncoms to promote sustainable agriculture

Rebecca Bart

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Abstract

Estimates suggest that by 2050 agricultural outputs must double to feed a growing world population and avoid food scarcity. At the same time, we must prepare crops to withstand climate change and develop more sustainable agricultural systems to reduce further harm to the Earth. Within this grand challenge, microbes are a promising source of solutions. Over one hundred products are available to farmers as commercial seed and/or soil amendments to increase plant health and decrease the use of exogenous chemical fertilizers. Unfortunately, existing products show highly variable performance and in general, mechanistic explanations for potential benefit are lacking. Even in the most promising cases, potentially beneficial microbes fail to colonize and persist within the context of complex agricultural soils. Enter – plant and microbial scientists! Our work aims to combine multiple experimental scales to identify novel, beneficial microbes, reveal their modes of actions and develop methods of increasing colonization and persistence of microbial consortia in complex systems. This talk will cover recent technological advances to address these challenges and perspective on future emphases.

D2T7

Within field spatial variability of soil fungal communities and soybean cyst nematode interactions

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Abstract

Our previous research has identified fungal community shifts associated with soybean cyst nematode (SCN) abundance at state level in Ohio soybean fields. SCN significantly limits soybean yield, and its interaction with fungi may decrease or exacerbate its impact. This study aimed to evaluate the field-level distribution of fungi, as influenced by SCN abundance. During 2022 and 2023, four soybean fields were partitioned into 66 grids of approximately 0.4 ha. In each grid, bulk and rhizosphere soil samples were collected at the beginning and end of the growing season. ITS sequencing was used to identify the fungal communities in the samples while bulk soil was used to determine SCN abundance (eggs/100cm3 soil). Grids were categorized by their rate of change in SCN abundance during the growing season. Preliminary results from twelve of the grids sampled show that this rate of change influenced fungal community composition in bulk soil (P=0.038), but not in rhizosphere soils. We also found that 7 fungal core genera identified in our state-level study were also core taxa in this experiment. Some of the core taxa identified have shown potential SCN antagonism in previous studies and are likely more abundant at high SCN infestation (> 600 SCN eggs/100cm3 soil). Therefore, we selected grids with high SCN abundance for high throughput fungal isolation. Of the 235 morphotypes isolated 30% exhibited extracellular protease and chitinase activity which are associated with nematode antagonism. The antagonistic activity of these isolates against SCN is being tested, and we hypothesize that some will exhibit antagonism.

D2T8

Central role of Thaumarcheota in microbial network cohesion and robustness in agricultural cropping systems

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Abstract

There is great interest in understanding the yield benefits of diversified cropping systems that may result from the potential microbial associations contributing to enhancing nutrient availability or limiting nutrient loss. Here we examined bacterial co-occurrence relationships to assess how the maize rhizosphere influences those associations in diversified and conventional cropping systems (four vs two crops in rotation) at a developmental stage at which the peak rate of nitrogen uptake occurs. We employed both a classical correlation- and a conditional dependence-based technique since each revealed contrasting and complementary insights. Based on global topological properties the diversified systems are more interconnected, particularly the bulk soil, while the rhizosphere had greater modularity and positive links. Moreover, network robustness was greater in the diversified than conventional systems, consistent with the greater cohesiveness of the diversified systems, particularly in the rhizosphere. To identify crucial interactions, we extracted shared edges in the conventional and diversified systems in both bulk soil and rhizosphere. This revealed that many *Thaumarcheota* OTUs had positive links to families such as *Acidobacteriota DA023* and *Actinomycota Gaiellaceae*, and negative links to *Pseudomonadota Comamonadaceae*. In the original networks, we observed that *Thaumarcheota* nodes were generally over-represented in node-degree and eigenvector centrality ranks suggesting these ammonia-oxidizers are important taxons in the networks, except in the conventional rhizosphere. These findings indicate *Thaumarcheota* play a central role in structuring robust and cohesive microbial networks, and the lack of their contribution in conventional rhizospheres could contribute to their poorer ability to enhance nutrient availability or limit nutrient loss.

D2T9

Domestication of Zea mays Results in Divergent Impacts on Leaf Endosphere Microbiota

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Abstract

Modern crop cultivars are the products of anthropogenic selection through domestication and breeding. The selection has focused on enhancing crop yield with unfortunate trade-offs introduced on plant defenses. Plant microbiomes are essential for plant health and stress resilience. Despite their importance in crop fitness, our knowledge of how domestication has influenced crop microbiomes is scarce. In natural environments, wild crop ancestors, such as Balsas teosinte (*Zea mays parviglumis*), the progenitor of maize, partially rely on their microbiomes to tolerate various environmental stresses. We investigated whether the known reduction in plant defenses observed in elite maize cultivars, compared to their wild and early cultivated ancestors, is linked to alterations in their microbial communities. Our study focused on the leaf endosphere microbiotas of teosinte (*Zea* spp.) and various maize accessions, spanning the evolutionary transition from perennial (*Zea diploperennis*) to annual wild (Balsas teosinte, *Zea mays parviglumis*) and domesticated (maize landraces and elite inbreds) life histories. We demonstrate that the leaf endosphere microbiota of tesointes exhibits greater microbial diversity and richness compared to landraces and inbred cultivars. Notably, the leaf endosphere microbiota of tesointes harbored more biomarker microbiota than the landraces and inbred cultivars, with domestication significantly influencing leaf-associated microbial communities. Furthermore, domestication coincided with patterns indicative of microbial imbalance in the leaf endosphere microbial community, aligning with the Anna Karenina principle. This study provides the first evidence of dysbiosis associated with crop domestication. Finally, we present preliminary findings on utilizing Balsas teosinte leaf endosphere microbes for developing biopesticides.

D2T10

Methanotrophs for methane mitigation and growth promotion in rice

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Abstract

Our objective was to investigate the potential of methanotrophic bacteria for methane mitigation and growth promotion in rice. Rice is a staple crop, feeding much of the world's population. However, rice cultivation is also a notable source of methane, a potent greenhouse gas with greater than 28x the heat trapping potential of carbon dioxide. **Methanotrophs**, microorganisms that are capable of oxidizing methane, offer a possible solution to mitigating the environmental impact of rice cultivation. Additionally, certain methanotrophs show promise as biostimulants due to their ability to fix nitrogen and colonize the rhizosphere of emergent plants.

To obtain methanotrophs for testing, we isolated a phylogenetically diverse collection of methanotrophs from wetland environments across the United States. A defined eight-member methanotroph consortium was constructed and evaluated in rice grown under simulated paddy conditions in our greenhouse. Methane emissions and rice growth metrics were monitored over the course of the experiments. Molecular detection of specific methanotrophs in the consortium via qPCR was also performed.

We observed significant reductions in methane emissions (>10%) in rice under the methanotroph treatment, at six and seven weeks after transplant of seedlings to pots. Yield metrics at harvest were also significantly higher for methanotroph-treated rice plants. qPCR results suggested that certain methanotrophs are better colonizers of rice roots and may be more strongly associated with reductions of methane emissions. This work establishes proof of concept to support the further development of a methanotroph inoculant product for rice.

D2T11

Cover crop effects on soybean health and associated rhizosphere microbiome

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Abstract

Cover crops benefit soil health by improving soil aggregation and organic matter, decreasing disease and weed pressure, and changing soil microbial diversity and structure. However, cover crop effects in different cropping systems are inconsistent and mixed. In this study, we evaluated the soil legacy effects of five years of cover crop implementation in a two-year corn and soybean rotation under no-till on soybean rhizosphere microbiome and soybean responses to *Fusarium graminearum* and soybean cyst nematode (SCN) infection. We found that cover crops significantly reduced soybean root rot disease, caused by *F. graminearum*, compared to no cover crop treatments. But cover crops did not affect soybean responses to SCN infection. Microbial analysis showed that cover crop treatments did not change the microbial richness of soybean rhizosphere. Both pathogen infections and cover crops significantly altered the structures of rhizosphere bacterial and fungal communities, with *F. graminearum* infection appearing to be a major microbial driver compared to cover crop and SCN infection. Furthermore, both pathogen infection and cover crops changed the abundance of some bacterial and fungal taxa. Notably, *F. graminearum* infection recruited beneficial bacteria for soybean combating pathogen attack.

D3P1

The Role of Microbiomes in One Health

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Abstract

Microbial communities inhabiting plants, animals, and humans act as a second genome, an extended genotype, or an eco-holobiont, influencing the fitness and performance of nearly all organisms on Earth. The One Health concept emphasizes how human health is intricately connected to the health of animals, plants, and the environment. Recent studies have shown that the microbial communities of different organisms are interconnected, forming a circular loop. However, compared to the health of plants, animals, and humans, the importance of the soil microbiome and soil health has remained understudied. Soils serve as the foundation of One Health, acting as a source and reservoir of pathogens, beneficial organisms, and overall microbial diversity in ecosystems. Numerous functions of the soil microbiome directly or indirectly contribute to the health of plants, animals, and humans, highlighting that soil, plant, and human microbiomes may be more interconnected than previously thought. Indeed, various microbial groups inhabit the soil and play a role in animal and human health. Such findings underscore the necessity of understanding soil microbial contributions to One Health and emphasize the need for systematic monitoring tools to evaluate trends, threats, and long-term developments of the soil microbiome.

D3T1

Plant-plant interactions modulate wheat severity to Septoria Tritici Blotch in some specific mixtures through intergenomic epistatic interactions and transcriptomic-metabolomic changes

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Abstract

Cultivar mixtures are increasingly recognized for their potential to enhance yield stability and reduce disease severity in crops, making them a growing practice[1] and an increasingly studied research topic[2]. While reduced plant susceptibility to pathogens in mixtures has traditionally been attributed to epidemiological processes[2], a novel mechanism involving plant-plant interactions has recently been identified as a modulator of disease severity[3]. A genome-wide association study (GWAS) revealed plant-plant interactions at the allelic level that impact disease severity to a similar extent as an epidemic[4]. Our aim was to uncover the physiological and genetic determinants driving these interactions, with a focus on how wheat susceptibility to *Zymoseptoria tritici* is modulated in binary mixtures. By employing a novel high-throughput image analysis[5], we first confirmed the hypothesis that wheat varietal mixtures modulate Septoria severity through specific plant-plant interactions, affecting the mean and variance of symptoms[6]. Secondly, we developed a novel GWAS approach to simultaneously analyze the two plants composing the mixture, thereby enabling the detection of allelic interactions between different loci. This first co-GWAS between two plants allowed the identification of specific loci driving these interactions, unveiling 54 intergenomic epistatic interactions with significant effects on Septoria severity and biomass. Thirdly, we demonstrated that in a binary mixture model, the modulation of severity to Septoria is associated with transcriptomic and metabolomic changes due to root signals from a specific neighboring genotype. These approaches provide deeper insights into the complex architecture underlying plant-plant interactions in wheat mixtures and shed light on ways to improve mixture design.

D3T2

Metagenomic profiles reveal that a mild constitutive defense response in maize maintains microbial diversity, limits pathogens and promotes beneficial microbes

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Abstract

In maize, the *Rp1-D21* auto-active nucleotide binding leucine-rich-repeat (NB-LRR or NLR) protein triggers a hypersensitive response (HR) without pathogen recognition, with its intensity influenced by the plant's genetic background. This study investigates how the *Rp1-D21*-induced HR affects rhizosphere metagenome composition and previously observed enhanced disease resistance. We sampled the rhizospheres from ten pairs of near isogenic lines of hybrids differing for the presence of the *Rp1-D21* gene, with varying HR levels (mild, moderate, or severe). Using a cost-effective quantitative reduced representation sequencing (OmeSeq-qRRS) method and an exact-matching algorithm-based pipeline (Qmatey) for strain-level metagenomic profiling, *Rp1-D21*-induced HR had a greater impact on the metagenome than the plant's genetic background. Species richness and Shannon diversity indices were not significantly different between wild-type and mild HR plants, but significantly decreased in moderate and severe HR plants. Mild HR plants exhibited the highest abundances and diversity of disease-suppressing microbes, including *Acropilus*, *Sphingomonas*, *Epicoccum*, and *Talaromyces* species, but the lowest diversity and abundance of pathogens. The wild-type plants had the highest diversity and abundance of pathogens, while moderate and severe HR plants had more opportunistic necrotrophic and saprophytic pathogens. To optimize plant health, these findings support the importance of balancing microbiome diversity and maintaining high diversity of beneficial microbes. While *Rp1-D21* upregulates pathogenesis-related genes and defense responses, our study suggests that through HR-induced systemic acquired resistance, mild HR plants can directly limit pathogens and promote the growth of beneficial microbes that might in turn trigger the induced systemic resistance for broad-spectrum disease resistance.

D3T3

The Chemical Toolkit of Cover Crops: Engineering Belowground Chemical and Microbial Diversity

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Abstract

Cover crops are essential for sustainable agriculture, enhancing soil health, carbon capture, biodiversity, and nutrient cycling. However, the biochemical processes driving these ecosystem services remain unclear. This study investigates the root exudation profiles of eight common cover crop species in sterile hydroponic conditions and agricultural soil mesocosms, aiming to link exudate composition to microbial community dynamics. Using untargeted liquid chromatography-mass spectrometry, we characterized the composition of root exudates from eight widely used cover crops that span a diversity of plant families: C3 grasses (rye, wheat), C4 grasses (sorghum, millet), brassicas (mustard, canola), and legumes (pea, clover). Our results revealed significant differences in exudation profiles among species, with notable similarities within functional groups. Brassicas exhibited the highest coumarin exudation, including compounds such as scopoletin and fraxetin that are involved in iron acquisition, while legumes exuded high concentrations of isoflavonoids such as genistein and daidzein, which can interact with nitrogen-fixing bacteria. Other exuded compounds included phytohormones such as auxins, jasmonate and cytokinins, which are involved in stress signaling and allelopathic interactions. These findings indicate that exudation chemistry is linked to plant functional traits, influencing interactions with soil microbiomes and neighboring plants. Utilizing amplicon sequencing of synthetic and native soil communities exposed to root exudates, this study next aims to pinpoint the predominant exudate classes influencing microbial community composition and function in the rhizosphere of different cover crop monocultures and mixes. Understanding how cover crop exudates affect microbial communities, nutrient dynamics, and carbon sequestration will help develop more resilient and sustainable agricultural systems.

D3T4

Sustainable Biofertilizer Development with ACC Enrichment Communities to Maximize Plant Growth

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Abstract

Bacteria that produce the enzyme ACC deaminase boost plant growth by preventing the conversion of 1-aminocyclopropane-1-carboxylate (ACC) to ethylene in plants. Under several abiotic and biotic stressors, plant ethylene biosynthesis triggers growth-inhibitory mechanisms, known as the ethylene stress response. Some biofertilizers exploit ACC bacteria to enhance plant growth under drought, flooding, salinity, heavy metals, and phytopathogens. However, biofertilizers often vary in effectiveness due to poor colonization of the rhizosphere or endosphere. In this study, an alternate approach is taken in biofertilizer development where communities of beneficial ACC bacteria are enriched from the plant microbiome and applied to plants to improve growth. The aim of this approach is to cultivate ACC bacteria that are already adapted to thrive in the plant microbiome to improve biofertilizer efficacy. Soybean root nodules and rhizospheric soil were used to seed ACC enrichment cultures and output cultures were evaluated for their potential to be used as a biofertilizer. Various root exudate sugars either abundant in soybean or tomato or neither microenvironment were used to evaluate the effect of varying carbon source on proportion of ACC bacteria in enriched communities. Abundance of ACC bacteria relative to the total bacterial population of each enrichment was quantified using *acdS/tuf* comparative qPCR. Lastly, bacterial community diversity was evaluated using 16S rRNA sequencing to investigate the effect of varying carbon source on dominant bacterial families.

D3T5

MENTOR identifies functional relationships among P. trichocarpa genes associated with fungal colonization

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Abstract

Investigating genetic mechanisms influencing plant-microbial interactions is fundamental for improving plant disease resistance and productivity. Our goals were to use large-scale computational and multiplex-network biology approaches to identify genes and mechanisms involved in fungal colonization. RNA-sequencing data in xylem across a diverse population of Populus trichocarpa were collected under field conditions. Reads were mapped to the host genome and non-mapping reads identified fungal taxa using a parallelized k-mer-based approach (ParaKraken). Ascomycetes genera Stagonosporopsis and Ilyonectria were identified and selected for further analysis due to their classification as tree-root fungi in Populus spp. We used the resulting fungal presence/absence patterns as phenotypes in a genome wide association study (GWAS) to identify significant associations between poplar SNPs and selected taxa. We combined genes mapping to significant SNPs for each fungal taxa as the input used in Multiplex Embeddings for Network Team-Based Omics Research (MENTOR) software. MENTOR leverages multiplex networks containing millions of lines of evidence of the mechanistic and regulatory interactions among genes/proteins to identify complex sets of mechanisms involved in controlling the colonization of selected taxa. We identified genes across both fungal taxa with functions that include receptors, signal cascades, pathogen defense, growth and immunity tradeoffs, and transcriptional regulation. We used the DOE Systems Biology Knowledgebase (KBase) Lines of Evidence (LOE) application to expand upon the GWAS findings and explore gene/protein dynamics within multiplex networks across mechanistically related gene sets. Finally, we integrated these results as a conceptual mechanistic model detailing host responses to Stagonosporopsis and Ilyonectria colonization.

D3T6

Trehalose, an environmentally friendly low-cost biostimulant to increase plant stress tolerance

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Abstract

Trehalose is an environmentally benign non-reducing disaccharide that is present in all kingdoms of life. Previous studies suggested that trehalose has potential as a biostimulant to increase plant drought tolerance and bacterial wilt resistance. Farmers suffer large losses to bacterial wilt, a widespread plant disease caused by soilborne Ralstonia species. There is no good control for bacterial wilt, which affects many economically important crops, including tomato. We sought to determine optimal strategies to use this biostimulant for tomato plant protection. Imbibing seeds with a 12% (w/v) trehalose solution before planting slightly increased drought tolerance but did not increase bacterial wilt resistance. However, exogenous application of 30mM trehalose solutions substantially reduced wilt disease severity on tomato plants inoculated with high doses of Ralstonia pseudosolanacearum strain GMI1000. Trehalose activated multiple tomato defense pathways, leading to systemic induced resistance and increased drought tolerance. Trehalose was protective when applied either by soaking bare root seedlings at time of transplant or as a soil drench to older plants. Three or more trehalose soil drenches made tomato plants almost completely resistant to Ralstonia but also decreased their biomass and leaf chlorophyll content. Reducing the number of soil drenches to two resulted in good protection from bacterial wilt without phytotoxicity. Soaking bare root seedlings in trehalose also increased bacterial wilt resistance without significantly reducing plant health. Together, these experiments identified an environmentally sustainable solution for a destructive plant disease.

P101

Effects of anaerobic soil disinfestation combined with grafting on microbial communities in tomato production in North Carolina

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Abstract

Anaerobic soil disinfestation (ASD) is a method that utilizes easily degradable carbon sources and anaerobic soil conditions to suppress soilborne pathogens. This study explores the synergistic effects of combining ASD with grafting on fungal and bacterial communities in tomato production. Field experiments were conducted over two consecutive years (2022 and 2023) at the Mountain Horticultural Research Station, Mills River, North Carolina. The soil treatment (ST) was the primary factor, and grafting (GrT) was the secondary factor. The ST treatments included: 1) untreated control (UTC); 2) standard fumigation (using Pic-Clor 60 at 0.168 Mg ha-1); 3) ASD applied with brewer's spent grain (14 Mg ha-1); and 4) ASD applied with heat-treated sweet potato waste (10 Mg ha-1). The GrT treatments involved tomatoes grafted onto "Beaufort" rootstock or non-grafted tomatoes. In 2022, Permanova analysis showed that the rhizosphere's bacterial and fungal community composition was significantly influenced by ASD treatments, grafting, and their interaction ($P < 0.05$). In 2023, only the ASD treatments had a significant effect ($P < 0.05$). However, grafted plants demonstrated a trend toward higher diversity. These results highlight the potential of combining ASD with grafting to improve microbial diversity and effectively reduce soilborne pathogens. This combined approach provides a sustainable and effective strategy to enhance the health and productivity of tomato plants.

P102

Investigating the interplay between soil history and plant type diversity on plant growth

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Abstract

Historical soil conditions are dictated by the changing environment and consequentially, can shape the current phenotypes of plants. One key feature of soil is its microbial composition, shaped jointly by plants and other environmental pressures. Insomuch as soil microbes can influence plant productivity, which has clear impacts for agriculture, but also natural plant communities. For instance, if a plant selects over time for microbes that favour or disfavour its growth, its relative success in a community should be impacted. A previous study of native grassland plants from near Toronto, ON, showed that each plant type recruited a specific microbial assemblage. Other studies have also demonstrated that environmental regimes influence downstream plant success and microbiome formation. In this study, we seek to understand the relative impact of microbial conditioning under different environmental regimes and plant types to determine which matters most in shaping plant growth and competition. We hypothesized that microbial conditioning under an environmental stressor (Salt vs. No Salt) would have a larger impact on plant growth than conditioning under different plant species. We are selecting microbial assemblages over four passaging generations, with or without the addition of NaCl, and in the presence of various native Ontario grassland plants. After passaging, selected microbiomes will be transplanted across different environmental regimes used in conditioning to assess plant responses, in terms of both growth and plant-plant interactions. The data generated by this study will highlight the importance of short-term microbiome conditioning on plant success in natural ecosystems.

P103

Leveraging BioMADE to Enable Domestic Bio-based Product Development

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Abstract

BioMADE is a Department of Defense-catalyzed Manufacturing Innovation Institute whose mission is to enable domestic bioindustrial manufacturing at all scales, develop technologies to enhance U.S. bioindustrial competitiveness, de-risk investment in relevant infrastructure, and expand the biomanufacturing workforce to realize the economic promise of industrial biotechnology. BioMADE's vision is to build a sustainable, domestic end-to-end bioindustrial manufacturing ecosystem. Currently, there are nearly 300 BioMADE member organizations across 37 states. Members have opportunities to apply for project funding, as well as to build direct connection to R&D partners, workforce development professionals, and the U.S. Government.

Bio-based products are increasingly critical in sustainable food production and security. Biomanufacturing and formulation scale-up of such products, including microbial biologicals for crop efficiency and protection, have long been challenges that delay product launch and limit product application. Bio-based product development is a complex process that requires multiple stages and various operations to consistently demonstrate the active ingredient's mode of action and efficacy on target application. Companies developing bio-based products often face prohibitively expensive cost of goods and lack ready access to biomanufacturing facilities to scale-up, adversely impacting product commercialization. BioMADE project calls, designed to develop underlying technologies, can help bio-based products for crops scale faster and more economically. Organizations can leverage BioMADE to connect, collaborate and innovate to reduce barriers to commercialization. This talk will highlight several BioMADE projects that effectively scale the production of bio-based products, as well as how your organization can benefit by joining BioMADE.

P104

Identifying diazotrophs from root rhizosphere using variable nifH primers

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Abstract

Heavy chemical fertilizer use has led to unintended negative impacts on plant and ecosystem health including the eutrophication of water sources and negative shifts in soil microbiomes and soil nutrient profiles. Plant growth-promoting rhizobacteria (PGPR) associate with plants at the root rhizosphere and impact plant health. Importantly, some PGPR fix atmospheric nitrogen, supplying plants with critical plant-accessible nitrogen. Free-living nitrogen-fixing bacteria (diazotrophs) have the potential to fix a significant portion of the nitrogen needs in non-leguminous plants. Therefore, the identification and isolation of free-living diazotrophs associated with common crops, such as maize, represents a promising avenue for decreasing synthetic fertilizer use. The *nifH* gene, encoding the dinitrogenase reductase component of the nitrogenase enzymatic complex, is often used to identify diazotrophs. Here we evaluate *nifH* gene abundance across a field planted to a variety of maize genotypes and investigate the diversity of diazotrophs found in association with maize rhizosphere using several variable *nifH*-targeting PCR primers. We find that *nifH* abundance is concentrated in regions of the field and may be associated with higher root biomass in a specific maize genotype. Assessment of *nifH* gene presence in rhizosphere bacterial strains cultured on nitrogen-free media, utilizing four distinct PCR primer pairs, indicates that *nifH* in potential diazotrophs is detected by different PCR primers in a genera-specific manner. These results highlight the variability in *nifH*-positive bacteria associated with the maize rhizosphere and emphasize the necessity of employing multiple nifH-targeting PCR primer pairs to comprehensively detect the range of *nifH* variability in rhizosphere samples.

P106

The U.S. Culture Collection Network – A Central Resource for Microbe Culture Collections and Their Users

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Abstract

Created in 2012, the NSF-founded USCCN brings together scientists working with collections of living microbes.

During its first phase (2012-2020) the network launched initial engagements with the global culture collection community through meetings, webinars, and site visits and produced publications and position papers to support the safe and responsible utilization of microbial resources.

Now in its second phase (2022-2027), USCCN is actively working on expanding its scope and reach by building relationships with current and new sources of culture and living collections and by engaging scientists across multiple disciplines to work toward addressing challenges and needs shared by all microbial collection managers and users.

In particular, USCCN is currently developing a registry of U.S. microbe collections – an easily accessible and searchable online database of plant associated microbial culture collections of all sizes, from small university-based research collections to large federally funded collections worldwide. The goal of this registry is to facilitate a greater access to collections of all types.

P107

Modeling the microbiome of the grape rot fruit fly, Spotted Wing Drosophila

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Abstract

The Spotted Wing Drosophila (SWD) (*Drosophila suzukii* Matsumura) is an invasive fruit fly that has become a significant threat to commercially valuable berry crops, particularly grapes. This pest is unique because it lays eggs inside fresh grapes rather than decaying grapes, severely damaging the fruit and causing substantial yield losses. The presence of SWD in Missouri vineyards has escalated management efforts and resulted in millions of dollars in economic losses.

Advancements in microbiome research have shed light on the critical role of the fly's microbiome in its health, development, aging, pesticide biotransformation, and disease resistance. However, the SWD also plays a part in spreading microbial communities that contribute to grape rot, a serious issue for vineyards. The emergence of cross-resistance to various insecticide classes among fruit flies in Missouri underscores the urgency for new, sustainable pest control methods.

Our research involved surveying SWD-infested vineyards and analyzing their associated microbiota through a microbiome-based approach. Our goal was to identify specific microbial communities that either support or hinder the growth of bacteria responsible for grape rot. This vital information paves the way for developing cutting-edge, sustainable technologies to reduce the SWD population and prevent the spread of grape rot. Such innovations are expected to significantly improve pest management strategies, ensuring grape crops' protection and productivity.

P108

Underpinning Phytobiomes Research: The first insights from a European soil microbiome cryopreservation experiment

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Abstract

Soil microbiomes are complex communities of microorganisms that, together with their "theatre of activity", provide crucial ecosystem services which is essential to the well-being of plants, animals and the environment and to the functioning 'Phytobiome'. To enable science to fully harness the functions of microbiomes to address global challenges, methods/technologies are needed to capture, create or perturb microbiomes to allow their long-term stable maintenance. MICROBE is an EU project dedicated to tackling these challenges.

In a comprehensive study between three different European research organizations, two well-defined and previously characterized soil samples were used to assess a range of different cryo preservation protocols (i.e., different storage temperatures, with / without cryoprotectants, with / without controlled cooling rate freezing). The samples were analyzed at different time points to assess the viability and composition and functional potential of the soil microbiome using both cultivation-based and cultivation-independent methods.

Preliminary results indicated that tested preservation methods could maintain the overall culturability of bacteria and fungi, as relatively constant colony-forming units were detected under tested experimental conditions across different treatments and time points. The assessment of the effects on the functional and community composition is yielding results that give us confidence that our preservation approaches are appropriate. The best practices identified in this study will be translated with the Phytobiomes research community for further validation. Furthermore, insights into the effect of the different preservation methods on different microbiome members will be used to design the most promising strategies for other matrices such as seeds and marine systems.

P109

Resolving the host genetic control of the barley rhizosphere microbiota

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Abstract

A prerequisite to exploit soil microbes for sustainable crop production is the identification of plant genes shaping microbiota composition in the rhizosphere, the interface between roots and soil. Using the staple crop barley as an experimental model, we pioneered the use of microbiota composition as an “external” quantitative phenotype in genetic investigations. This allowed us to identify a root immune receptor belonging to the Nucleotide-Binding-Leucine-Rich-Repeat (*NLR*) family among candidates shaping microbial composition in the rhizosphere. This receptor maps in an area of structural variation of the barley genome, possibly representing a footprint of human selection on plant’s capacity of shaping soil microbes. To further validate these observations, we recently subjected the candidate *NLR* to a gene editing approach and generate a novel allelic variant harbouring a deletion at the 5’ termini leading to a premature stop codon. Gene-edited lines could be reproduced, suggesting that the induced mutation is not associated with deleterious pleiotropic effects. This allowed us to grow homozygous edited lines in soil and test their microbiota composition. Strikingly, edited alleles led to a reconfiguration of the rhizosphere microbiota manifested by a shift in the Actinobacteria/Proteobacteria ratio compared with control plants. This breakthrough supports the notion of *NLR*s as host genetic determinants of the microbiota thriving at the root-soil interface and opens attractive avenues for follow-up investigations, in basic science and translational applications alike.

P110

Microbial Interactions in the SCN Suppressive Soil Microbiome

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Abstract

Our research investigates microbiomes of soils suppressive to soybean cyst nematode (SCN; *Heterodera glycines*), a destructive pathogen of soybean. We hypothesized that antagonistic interactions among microbes in suppressive soils may induce production of nematicidal secondary metabolites and other enzymes involved in parasitism or toxicity to plant parasitic nematodes. To better understand the role(s) of fungi and bacteria in nematode suppression, we sampled bulk soil, rhizosphere soil, soybean roots, and SCN cysts from a long-term crop rotation experiment. We compared crop rotations conducive to SCN (annual rotation (Sa) with corn), a three-year soybean rotation (S3), and long-term monocultures of both a susceptible soybean variety (Ss) that has developed suppressive properties over the past 40 years and a resistant (PI8878) soybean variety (Sr). Culture-based, as well as culture-independent approaches using metabarcode sequencing of the 16S and ITS regions identified key microbial taxa in these communities enriched in suppressive soils. Co-occurrence networks constructed for SCN cyst communities did not support the hypothesis that suppressive soils communities harbor more antagonistic interactions but identified distinct modules and key hub taxa for each treatment. Additionally, shotgun metagenomes were sequenced from SCN cyst microbial communities to identify differences in functional gene content. Two classes of secondary metabolite biosynthetic gene clusters, PKS-NRPS hybrid and ribosomally synthesized and post-translationally modified peptides (RiPPs), as well as fungal chitinases, in the suppressive soil treatment. Analyses of these microbial interactions in suppressive soils provides a framework for selection of syncoms for *in-planta* experiments towards development of biocontrol solutions for SCN.

P111

Exploring the Hydroponic Microbiome

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Abstract

An essential difference between crop cultivation in hydroponic systems and field agriculture is the absence of the soil microbiome and its benefits. Understanding the baseline or core microbiome, as well as the prevalent populations in hydroponic systems, is crucial for ensuring food security through optimized controlled environment agriculture, especially as field agriculture becomes increasingly unreliable due to climate change. In this study, we address questions regarding the types of microorganisms prevalent in hydroponic systems, their associations with specific crops, and the relative abundance of pathogens. Our first objective was to use 16S rRNA gene, 18S rRNA gene, and fungal intergenic transcribed spacer (ITS) sequencing to identify the bacterial, oomycete and fungal compositions in hydroponic farms growing lettuce, tomatoes, kale, cucumbers, berries, and microgreens. We focused on the established microbiomes in the leachate, nutrient solution, and rhizosphere at harvest. To further understand the specific microbiomes of vegetables and fruits, our second objective was to identify taxonomic groups associated with the aforementioned crops in the leachate and rhizosphere. Finally, our third objective was to identify key species and prevalent pathogens across the hydroponic systems. The data from this study has facilitated the development of an in-house database and a pathogen surveillance program through Healthy Hydroponics InnoTech. This program aids growers in monitoring the hydroponic microbiome and detecting pathogens early, thus helping to reduce crop loss and food waste by mitigating pathogen pressures before they escalate.

P112

Evidence-Based Standards to Keep Offshore Ornamental Production Pathogen-Free: the case of Select Agent Ralstonia solanacerum R3bv2

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Abstract

The bacterium *Ralstonia solanacearum* Race 3 biovar 2 (R3bv2) is a Select Agent pathogen because it could threaten the valuable U.S. potato industry. R3bv2 can also infect geraniums which are also a high-value crop. Geranium cuttings infected with R3bv2 have been accidentally imported to the U.S. five times since 1980, triggering costly eradications. USDA APHIS PPQ regulates offshore geranium production practices to prevent further introductions. Geraniums are grown in volcanic scoria rock. Currently, growers must steam scoria at 80°C for 120 min before re-use. Re-using scoria saves labor and carbon, but the required heat treatment is both costly and environmentally destructive. Is it necessary? We empirically determined the precise time and temperature conditions required to inactivate RsR3bv2 in volcanic scoria, with the long-term goal of conserving resources while maintaining rigorous biosecurity. Roots of *R. solanacearum*-infected geraniums grown in scoria under typical production conditions were exposed to a range of time/temperature conditions. Surviving pathogen populations were quantified using a sensitive combination of serial dilution plating and enrichment culture. These experiments showed that plant pathogenic *Ralstonia* are eradicated from infected geranium roots in volcanic scoria by cooler and shorter heat treatments than currently required. Indeed, no viable R3bv2 cells remained after just 15 minutes at 60°C. Thus, we can protect U.S. agriculture while saving money and reducing carbon emissions.

P113

Community Immunity: Exploring the relationship between plant immunity and the microbiome

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Abstract

One of the largest threats to agriculture is bacterial pathogens. To address this issue, researchers have pushed to enhance our understanding of plant-pathogen interactions, primarily through the use of single inoculation or mono-association studies. While these studies are important in understanding the mechanisms of pathogenesis and host resistance, they do not account for the role the plant microbiome plays in influencing host immunity. By complementing insights gained from mono-association studies with microbial ecology, we aim to achieve an understanding of plant immunology that is more reflective of the interactions occurring in nature. We hypothesize that the microbiome protects plants through priority effects and the regulation of plant defense phytohormones. To test this, we utilize synthetic communities (SynComs), which are microbial communities composed of well-characterized bacterial isolates, and the opportunistic pathogen *Paenibacillus sp.* MF181. In mono-association studies, MF181 kills plants. However, when included in a 35-member SynCom, the plants remain healthy. Interestingly, preliminary studies using smaller SynComs derived from the 35-member community show variability in plant health outcomes when MF181 was included. The variability in protection from MF181 suggests that the microbiome plays an important role in plant defense. By exploring health outcomes, we can clarify how the microbiome influences plant health and apply this information to agricultural questions. This research could aid in the development of microbially based biocontrol agents and help protect agriculture against bacterial pathogens.

P114

Predicting Microbiome and Species Networks in Hydroponic Systems Using Machine Learning

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Abstract

Hydroponic systems provide a sustainable method of crop production, with dynamic microbial communities playing a crucial role in plant health and productivity. Maintaining a balanced biodiversity of beneficial microbes in the water can effectively reduce pathogen levels through competitive interactions. To optimize the system's microbiome, enhance plant growth, and boost resilience, it is essential to understand the interplay between environmental conditions and microbiome composition. This study presents a Machine Learning model developed to predict the presence and abundance of both pathogenic and beneficial microbes, as well as species networks in hydroponic water and plant roots. Using environmental variables such as pH, electrical conductivity, oxidation-reduction potential, and water temperature, we trained a Random Forest model to identify microbial patterns that correlate with these factors. The model leverages microbiome data obtained through sequencing, targeting bacterial and fungal communities. Our approach integrates polynomial and interaction terms between environmental features, enhancing the model's ability to capture complex relationships. Through hyperparameter tuning and cross-validation, the model achieved over 65% accuracy in predicting key microbial metrics, such as diversity indices and the relative abundance of significant taxa. These predictions enable proactive management of microbial communities, optimizing the hydroponic environment for enhanced plant resilience and yield. The results demonstrate the potential of using advanced machine learning techniques for real-time microbiome monitoring and control in vertical farming systems. Future work will focus on incorporating time-series analysis to capture temporal shifts in microbial communities in hydroponic farms over 12 months, further improving predictive capabilities and hydroponic management strategies.

P115

Mutualism Maintenance: Plant antimicrobial peptides challenge bacterial symbionts after incorporation into plant tissue

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Abstract

Legumes (*Fabaceae*) develop symbiotic relationship with nitrogen fixing bacteria, rhizobia, to meet their nutritional needs. Legumes recruit rhizobia from soil, house them in root organs called nodules, and provide carbon receiving biologically available nitrogen in return. The transition from free living rhizobia to host controlled bacteroid is poorly understood. One mechanism of host manipulation is a family of small antimicrobial peptides called Nodule-specific Cysteine-Rich (NCR). They are exclusively expressed in the nodule and the shared 4 or 6 cysteine motif. The genes and subsequent peptides vary in number, sequence, and function across the legumes. They are secreted to the symbiosome-bacteroid complex, causing endoreduplication of the bacterial genome, arrest of cell division, increased membrane permeability, branching and swelling. The objectives of this research are to 1. Identify and describe the NCR gene family structure in *Trifolium*, highlighting species-specific changes. 2. Quantify the degree of swelling and branching that indicates the transition from free living rhizobia to host dependent bacteroids inside plant nodules. To address these research objectives, we use PacBio CLR whole genome sequencing of eight *Trifolium* species to identify NCR genes. Preliminarily results show gene family expansion in *Trifolium* (>1,000) compared to the model legume *Medicago truncatula* (~600). To quantify changes in bacteroid morphology we use fluorescent labelled rhizobia symbionts and confocal microscopy. Understanding host manipulation of bacterial symbionts after incorporation into plant tissues, gives researchers targets for engineering more efficient nitrogen fixing plant/bacteria relationships that can be used in crop plants as alternative to synthetic nitrogen fertilizer application.

P116

Heat Stress and Soil Microbial Disturbance Influence Soybean Root Metabolite, Microbiome Profiles, and Nodulation

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Abstract

Heat stress is a major limiting factor for soybean productivity worldwide. Recent research highlights the crucial role of plant microbiomes in helping plants adapt to heat stress. To investigate the role of native soil microbes in enhancing heat tolerance in soybean genotypes, we examined the rhizosphere's bacterial and fungal communities through 16S and ITS sequencing and analyzed key root metabolites and anatomical traits influenced by both the soil microbiome and heat stress in soybean. Soybean plants were grown under controlled conditions with either natural soil containing native microbiomes or soil with a disturbed microbiome, resulting from a 3-hour autoclaving treatment, under both optimal and elevated temperature conditions. Alpha and beta diversity analyses revealed significant differences between treatments, showing distinct groupings of bacterial, fungal, and metabolite profiles in response to high temperature and microbial disturbances. Nodule-forming bacteria, such as *Rhizobium* and *Janthinobacterium*, were significantly impacted by heat stress, with below-ground phenotypes particularly sensitive, showing a marked reduction in nodule numbers and nodulation efficiency under high temperatures and microbial perturbation. Through non-targeted root metabolomics profiling, we identified 372 significantly differentially accumulated metabolites. Integrative analysis of multi-omics datasets revealed a strong correlation between metagenomics, untargeted metabolomics, and N-fixation-related traits, indicating coordinated modulation of root physiological traits. Our study contributes to a holistic understanding of heat and microbial interactions, supporting the breeding of soybean cultivars with broader adaptation to future variable climatic conditions.

P117

Role of cyclic lipopeptides -producing Pseudomonas species in the biological control of Verticillium Wilt in sweet pepper (Capsicum annuum L.)

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Abstract

Verticillium wilt, caused by the soil-borne pathogen *Verticillium dahliae*, significantly affects sweet pepper (*Capsicum annuum* L.) production worldwide, leading to substantial crop losses. The pathogen is difficult to control due to the production of a melanised long-lasting resting structures called microsclerotia, which it uses for long-term survival in the soil. Conventional control measures, such as chemical treatments and crop rotation, have proven inadequate and raise concerns regarding environmental sustainability. Recent studies have identified Pseudomonas species, particularly those that produce cyclic lipopeptides (CLPs), as promising biocontrol agents against *V. dahliae*. In this study, we evaluated the efficacy of seven CLP-producing *Pseudomonas.* spp and two mutant strains in controlling *V. dahliae* both *in vitro* and *in vivo*. Our findings revealed that all tested strains provided a significant level of biocontrol, enhancing sweet pepper plant growth parameters such as plant height and root weight. *In vitro* assays demonstrated that both the strains and their cell-free supernatants effectively reduced fungal mycelial growth and microsclerotia viability. Additionally, treatments with higher concentrations of specific CLPs reduced fungal biomass. Moreover, quantitative real-time PCR confirmed a lower level of *V. dahliae* in *Pseudomonas*-treated plants compared to untreated ones, highlighting the potential of these biocontrol agents. This study lays a foundation for using CLP-producing *Pseudomonas* species to control not only *V. dahliae* but also other soil-borne pathogens like *Fusarium* spp. in sustainable agriculture.

P118

Microbes 4 Climate: Microbial services addressing climate change risks for biodiversity, agricultural and forestry ecosystems

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Abstract

Funded by the European Union's Horizon Europe Research and Innovation Programme, the five-year Microbes-4-Climate (M4C) project aims to deepen the understanding of the complex relationships between microorganisms, plants, and soil and how these interactions are impacted by changing climates. The Phytobiomes Alliance is one of 31 partners from 13 countries engaged in the project.

The four main objectives of the project are: 1) **Develop** and refine frameworks and tools to facilitate access to data and services essential for research; 2) **Enhance** the integration of services offered by multiple research infrastructures and provide comprehensive training and technical assistance; 3) **Simplify** access to a tailored suite of services aimed at supporting research to minimize climate change impacts; 4) **Promote** active engagement from user communities and ensure long-term sustainability of services developed in the project.

Microbial interactions will be studied to advance our understanding of the complex challenges posed by climate change and its impact on terrestrial biodiversity and ecosystems, including resilient plants and crops and other agricultural and forestry systems.

P119

The Role of host species difference in phylloplane pH regulation is shaping bacterial communities

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Abstract

In this study, we investigated how the ability of plant leaves to regulate pH levels may influence microbial community functions on leaf surfaces and within the leaf. We used a metatranscriptomic approach to examine phylloplane and whole leaf bacteriomes on five plant species that differ in pH regulation, including two *Nepenthes* species representing the acidic extremes, relatively neutral *Beta vulgaris*, and two hyperalkaline *Gossypium* species. To examine microbial responses on the phylloplane, we inoculated young leaves with a common microbial community to observe potential host filtering effects and subsequently exposed leaves to either pH 6.5 or pH 2 to investigate bacterial responses to external pH perturbation, also in light of leaf pH regulation. Leaves were sonicated to collect phylloplane microbes for total RNA sequencing. To examine microbial responses to pH regulation in the whole leaf environment, including potential endophytes, we examined microbial data from leaf transcriptome data from a separate experiment, where the same five host plant species were exposed to a pH treatment spray (pH 6.5, 4, or 2) for five minutes. We assembled meta-transcriptomes with SAMSA2. We found that host species significantly shaped community composition of microbial genes, which diverged from the source inoculum in our first experiment; however, this was not significantly impacted by pH treatment. Indicator genes analysis also revealed specific functional gene groups significantly associated with each plant species, underlining the importance of the active recruitment by plant hosts in shaping their leaf microbiota.

P120

Microbial community assembly on cider apple fruit is influenced by geography and cultivar

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Abstract

Changing consumer preferences and climate conditions are prompting fruit growers in Michigan to plant more cider apple acreage. Cider apple cultivars differ in biochemical composition of fruit, and are grouped based on sugar and acid content. These fruit and juice characteristics are intentionally combined by cider makers to produce high quality products, but can be influenced by tree management and growing conditions. Fungi, in particular the yeasts, colonize apples during the growing season. The presence of these yeast can provide an opportunity to cider makers for value-added products such as natural- or wild-fermented hard ciders. To parse the influence of cultivar, location, and management on the microbial community we classified the fungi colonizing fruit across the growing season at three different locations in Michigan.

P121

Characterization and genomic insights for the emerging rice pathogen, *Pantoea ananatis*

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Abstract

New and emerging pathogens continuously threaten the security of vital crops worldwide. *Pantoea ananatis*, a bacterial pathogen of rice, was first reported in the United States in 2021 in a research plot in Arkansas. The pathogen caused leaf blight lesions, panicle sterility, and yield reductions in susceptible rice varieties. To assess the potential threat that this pathogen poses to United States agriculture, we tested its impact on commonly grown rice varieties in the United States under greenhouse conditions and analyzed genomes of *P. ananatis* obtained from Arkansas. Analysis of over 150 publicly available *P. ananatis* genomes from around the world alongside those from Arkansas revealed two distinct clusters based on average nucleotide identity, confirming a separation of *P. ananatis* isolated from rice hosts from isolates found on other host species. Using comparative genomics, we have identified rice-unique regions and are now developing a set of primers that will specifically amplify *P. ananatis* isolated from rice. These primers will be used as diagnostic tools and will provide key insights into genomic variation between isolates across hosts. The knowledge gained from this research addresses an urgent need for effective monitoring of this disease to protect rice production.

P122

Microbial inoculants increase tolerance to drought stress conditions

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Abstract

Microbial inoculants influence the rhizosphere microbiome. However, their effect on plant performance across different farming practices and growing seasons remains unclear. To explore this, maize plants, both untreated and inoculated with a microbial consortium (BMc), were grown under different farming practices in two growing seasons (2020 and 2021). The goals were to assess (i) the rhizosphere competence of the inoculants, (ii) the impact of the BMc on plant performance, (iii) the effect of BMc on bacterial rhizosphere communities, and (iv) the functional microbial genes in the rhizosphere of untreated and BMc-inoculated plants. In 2020, plants experienced severe drought periods. Sufficient rhizosphere competence of individual strains in the BMc was observed in both years, regardless of farming practice. Improved plant health, induced by the BMc, was noted based on the expression levels of stress response and iron uptake genes, independent of the farming practice in both years. Additionally, the BMc altered the rhizosphere bacterial community each year, though the taxonomy of responding bacteria varied between the seasons. Functional microbial genes were enriched in BMc-treated plants compared to untreated controls in both years. ASVs positively associated with iron uptake were identified, with a significant increase in these ASVs due to BMc inoculation in 2020, but not in 2021. However, in 2021, these iron-associated ASVs (classified as Comamonadaceae) were generally more abundant in both treatments compared to 2020. Microbial inoculants can boost plant performance under abiotic stress like drought, but more field trials are needed to confirm their effectiveness across different environments.

P123

Management of nutrient solution influences bacterial community composition in hydroponic systems

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Abstract

Hydroponics is a method of growing plants without soil, where nutrients in solution are controlled for optimal plant growth. Unlike soil-based systems, the drivers of microbial community variation in hydroponics remain understudied. We hypothesize that nutrient solution parameters including pH and nutrient concentration measured as electrical conductivity (EC) shape bacterial communities in hydroponics. To test this, we established replicated experiments on research Deep water culture (DWC) and Nutrient film technique (NFT) systems with different levels of pH (low=5.0 and control=5.8) and EC (low=1.2 and control=1.8 mS/cm); followed by 16S rRNA amplicon sequencing from lettuce roots, growing media and nutrient solutions. Beta diversity analysis, based on Bray-Curtis distances, showed that bacterial community composition differed between pH levels in roots and nutrient solutions from DWC and NFT systems, but not between EC levels in any sample and system type. Bacteria richness was higher in low pH and low EC in growing media from NFT systems, suggesting a buffering effect on the substrate, which in NFT systems is not fully submerged in the nutrient solution. Furthermore, 15% more unique bacteria were identified in growing media in NFT systems with low EC conditions compared to the control. Understanding the factors influencing microbial community variation in hydroponic systems can guide for optimal cultural practices, enabling the effective application of biocontrol agents and plant growth promoters or guiding in the use of native microbial communities in hydroponic production.

P124

Assessing the tree bark microbiome of bald cypress (Taxodium distichum) in the Yazoo-Mississippi Delta as a function of hydrologic and water quality dynamics.

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Abstract

Bald cypress (Taxodium distichum) is a deciduous conifer tree, endemic to the southeastern United States, which provides surface areas for hosting wetland microbial communities. However, as bald cypress occurs near agricultural lands, these trees- and hosted communities- experience variable hydrology via natural and anthropogenic causes (precipitation, irrigation, drainage, etc.). Consequently, nutrient and agrochemical runoff may influence microbial communities and derived ecosystem services. Thus, we sought to document how the microbiome of bald cypress bark responds to altered hydrology and water quality in the Yazoo-Mississippi Delta (YMD).

We collected bald cypress bark samples (n=282) over a six-month timespan (9/2023 –5/2024) from 18 trees located in three wetlands (six trees per site), reflecting a continuum of land use. From each tree, bark was sampled at: a) ~80 cm. above the water line; b) ~20 cm. above the water line (i.e., a "splash zone" for waves); and c) ~20 cm. below the water line. Preliminary results indicate a vertical gradient in the tree bark microbiome. The highest amounts of DNA recovered were from below the water line, with decreasing amounts moving upward. After Illumina 16S amplicon sequencing, community composition will be correlated with hydrology and water quality metrics (e.g. DO, nitrogen content, phosphorus content, and turbidity), to determine primary abiotic drivers of the bald cypress bark microbiome within the YMD. Results are also expected to enhance nutrient cycling models and may provide insight into potential biodegradative properties.

P125

How do initial carbon substrates used in microbial capture from soils constrain the short-term evolutionary trajectories of cultivable microbiomes?

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Abstract

Diverse biological communities can respond to environmental changes through both species sorting and evolution of individual lineages. A broader range of adaptive traits can provide stability in community function, allowing diverse communities to recover faster from bottleneck effects than those with little diversity. However, prior environmental shifts may alter the capacity for community function following subsequent shifts. In this study, we investigated the constraint of community bottlenecking due to initial in-culture capture conditions (i.e. available carbon source) on the evolutionary trajectories of soil-derived microbial communities. We hypothesized that the specific carbon substrate used at capture would negatively impact the community's ability to make use of other carbon substrates, even following a period of experimental evolution. To test this, microbial communities were captured from different soil types through culturing with minimal media supplied with one of five carbon substrates: glucose, citric acid, glycine, sodium succinate, or a mixed source. After one week of growth in the capture media, subsets of each captured community were grown for an additional thirty days in each of the five substrates. This approach allows us to investigate the differences in community structure after growth in both pre-conditioned and novel environments. Automated growth assays along with 16S community profiling will be used to quantify these changes. By performing these assays, we hope to assess the extent that initial capture conditions constrain the directed evolution of microbes.

P126

The roles of plant-derived coumarins and *Bosea* sp. CL19 in improving plant biomass under acid pH stress

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Abstract

Plants rely on their microbiomes for mitigating stresses ranging from pathogens to pH change. Identifying beneficial plant-microbe interactions is essential for the design of plant-growth promoting communities and their subsequent application. Plants play an active role in selecting their microbiomes. One method by which plants tailor their microbiome composition is through the production of small, fluorescent, phenolic compounds in the coumarin family. Coumarins are selectively antimicrobial, and many pathogens experience inhibited growth in their presence, while many beneficial microbes are resistant to high coumarin concentrations and can even induce their production in plants. Here, we report findings of a potentially coumarin-mediated plant-microbe interaction between *Arabidopsis thaliana* and the beneficial bacterial isolate Bosea sp. CL19. To investigate this interaction, we grew wildtype *Arabidopsis thaliana* plants and mutant plants deficient in coumarin production in association with CL19 on unbuffered Murashige and Skoog media, as well as buffered media at acidic, optimal, and alkaline pH. In unbuffered and buffered conditions at optimal and acidic pH, Arabidopsis plants inoculated with CL19 exhibit higher biomass than axenic controls as well as increased root fluorescence, indicating an increase in coumarin production. Mutant plants deficient in coumarin production do not exhibit this phenotype. Interestingly, this phenotype is not observed in wildtype plants at alkaline pH. We also report *in vitro* growth responses of CL19 to two major plant-derived coumarins, scopoletin and fraxetin. This plant-growth promoting interaction presents a promising avenue for the investigation of mechanisms by which microbes can protect plants from pH stress.

P127

Development of a hybrid prediction model for Fusarium head blight in wheat considering both meteorological factors and surrounding microbial community

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Abstract

Fusarium head blight (FHB) is one of the most devastating wheat diseases, posing an emerging threat to wheat production in Korea. Although a few studies indicated the influence of surrounding microorganisms on the FHB development, no one have tried to look at the combined effects of meteorological factors and the composition of microbial community on FHB. In this study, we developed a hybrid prediction model that accounts for both factors affecting FHB incidence. From two-year-field data, we found 11 microorganisms showed positive correlation with FHB incidences, while five microorganisms with negative correlation. The effect of meteorological factors on the corresponding FHB incidences was simulated using a process-based model, the GIBSIM. Lastly, a multiple linear regression hybrid model was developed by considering the GIBSIM results and the relative abundance of selected microorganisms, which are highly correlated with FHB incidence. Compared to the GIBSIM performance ($R^2 = 0.49$), the hybrid model performed better at explaining FHB incidence ($R^2 = 0.72$). These findings indicate that surrounding microorganisms partially but significantly contribute the FHB incidence in addition to the meteorological factors.

P128

Rhizosphere Microbial Composition and Mycorrhizal Fungi Associated with Boxwood Blight Resistance?

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Abstract

The rhizosphere microbiome is known to play an important role in supporting plant growth and health. The objective of this study was to determine how rhizosphere microbial composition may be associated with plant disease resistance levels under field conditions, using boxwood (a broadleaf evergreen shrub) as a model crop. We collected rhizosphere soils from four cultivars representing three boxwood blight resistance levels (tolerant, intermediate, and susceptible) at Oregon and Virginia nurseries in May, August, and November. We then applied amplicon sequencing to characterize the bacterial and fungal communities. Bacillus and Clonostachys were the most abundant bacterial and fungal genera across all cultivars, locations, and sampling times. The structure of the fungal community was influenced by the level of blight resistance in May and August, and that of the bacterial community was only affected in August at both locations. Importantly, co-occurrence network analysis of mycorrhizal fungi and bacteria indicated that the tolerant cultivar had more positive interkingdom associations than the susceptible cultivar. In particular, a cluster of mycorrhizal fungi was present and connected to the bacterium Blastococcus in the tolerant cultivar network, with Amanita identified as a hub taxon. Collectively, these findings demonstrated the impacts of plant traits on the assembly of rhizosphere microbiomes and highlighted the potential of microbial interactions for mediating plant disease resistance. Our study provides important information that will be useful in boxwood breeding programs to enhance plant resilience to disease and environmental stress.

P129

Factors influencing the use of PNA clamps for surveys of endophyte communities

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Abstract

Bacterial 16S rRNA gene amplicon surveys of plant tissues are hampered by the co-amplification of plant chloroplast and mitochondrial rRNA genes. The resulting loss in sequencing depth (‘sampling effort’) obscures the assessment of microbial diversity, especially for low abundance endophytes. Peptide nucleic acid (PNA) clamps are synthetic oligonucleotides that bind to plant 16S rRNA gene DNA, preventing its PCR amplification. Our objectives were to test (i) the efficacy of PNAs (designed for maize) on other plant species, (ii) the influence of PNA concentration on blocking efficiency, (iii) the tangible improvements to cost and quality of microbiome analyses. To quantify PNA efficiency, qPCR assays were conducted without and with PNA at 6 concentrations (0.25 – 5 µM). Blocking efficiency positively correlated to PNA concentration, but the effect plateaued at 1.5 µM, delaying amplification by 13 PCR cycles. Illumina sequencing revealed an increase in bacterial sequences from 3% (-PNA) to 98% (+PNA). Due to the 32-fold increase in sampling effort, our characterization of endophyte communities improved. An additional 364 Amplicon Sequence Variants (ASVs) in PNA-treated PCR reactions versus 75 ASVs without. Shannon diversity rose from 2.98 to 4.65 with PNA, illustrating major distortions that can be remedied with PNA (or deeper sequencing). Cost analysis revealed that the per sample savings ($5.73) in sequencing outweighed the per sample cost of PNA clamps ($0.53 1.5 µM). Our experiment demonstrates the use of PNA clamps to achieve a greater sampling effort, serving as a cost-effective way to enhance 16S rRNA gene amplicon surveys of plant tissues.

P130

Long-term use of radish and rye cover crops shifts the soil microbiome and increases plant growth-promotion potential

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Abstract

Cover cropping improves soil health and protects soil from erosion; however, its long-term effects on soil microbial communities and microbial plant growth-promotion (PGP) potential are not well understood. We hypothesized that long-term fall cover cropping would shift soil prokaryotic communities and increase microbial PGP potential compared to uncovered soils, and that changes would persist into the summer. Soil samples were taken from a 14-year agricultural field trial with five different fall cover crop treatments (no cover crops, oat, rye, radish, and radish/rye combination). Bulk soil samples (0-15cm) were taken in November 2021 (when different cover crop treatments were present), and bulk soil and root-associated soil samples were taken in July 2022 (when corn crop was present on all plots). Total microbial DNA was extracted from all samples. To compare prokaryotic communities, 16S rRNA amplicons were sequenced from extracted DNA. To compare PGP potentials, genes encoding enzymes facilitating select microbial plant-beneficial processes (phosphorus mobilization, nitrogen cycling, sulfur cycling, and plant stress tolerance) were quantified from extracted DNA using quantitative polymerase chain reaction. Significant increases in PGP genes encoding phosphorus mobilization, nitrification, and plant stress tolerance processes were seen in fall soils from radish and rye-containing treatments compared to uncovered soils, though these differences were not seen in summer soils. Preliminary sequencing results showed that long-term cover cropping with radish and rye significantly shifted soil prokaryotic communities in both fall and summer soils compared to uncovered soils, indicating that prokaryotic community changes may persist months after cover crop termination.

P131

Metagenomic approaches comparing soil microbiome profiles from agricultural systems to native environments

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Abstract

Bayer Crop Science is evaluating the effects of different sustainable intensification practices, no-till and cover crops, on cultivated lands (CL) in a multi-year testing system. In this assessment, adoption of sustainable practices on CL over years showed higher and more stable yields, increases in biomass production, and improvements in soil health indicators. The objective of this project was to characterize soil microbiome communities in CL associated with different levels of sustainable intensification practices compared to native soils (NS) in South America. Four locations across two years were selected for metagenomics and soil nutrient analysis. We identified that microbiome profiles from CL in Argentina had a similar relative abundance of microorganisms as compared with NS (grasslands), although significant differences were still found between individual treatments. Argentina CL have been under long-term sustainable practice use (8 years), signifying CL have stabilized. On the other hand, microbiome profiles from CL in Brazil displayed remarkable differences in relative abundance compared with NS (forest) and CL. These variable results in Brazil under the different practices were run over a short period (3 years) and were preceded by many years of soil health erosion. The results suggest that this location is still under a stabilization process. Finally, consolidation of this work will allow us to track potential changes in the identity and composition of microbial communities to support our customers in the adoption of sustainable practices as well as establish a baseline understanding to evaluate potential sustainability benefits associated with the use of Bayer products.

P132

Advocating STEM Equity in Sub-Saharan Africa Through High School Partnerships

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Abstract

Zaidi STEM is dedicated to promoting STEM equity in Sub-Saharan Africa through strategic partnerships with local secondary and high schools. Our goal is to help our partners gain access to resources needed for collaborative learning, and to help empower the next generation of innovators.

In Sub-Saharan Africa, the issue of the "leaky STEM pipeline," is a critical problem facing a generation of STEM students, particularly girls and the marginalized groups. This problem contributes a great deal to these students disengaging from STEM fields due to insufficient support and lack of resources. To combat this, Zaidi STEM employs several strategies, including mentoring, supplemental academic tutoring, and project-based learning (PBL).

Our PBL programs help engage students in hands-on, real-world projects that ignite interest and highlight the relevance of STEM in their communities. Coupled with mentoring programs, our PBL programs provide essential guidance and encouragement, helping to bridge the gaps in knowledge and build confidence. This comprehensive approach not only meets their immediate educational needs but also ensures that more students remain committed to STEM pathways.

By fostering connections between students and educators across regions, Zaidi STEM is able to cultivate a vibrant community of learners and future leaders. Ultimately, our efforts contribute to a more inclusive and innovative STEM landscape in Sub-Saharan Africa, which helps to empower diverse talents to shape the future.

P133

Plant species and pH interactions shape rhizosphere bacterial diversity in peat-based systems

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Abstract

Soil pH shapes rhizosphere microbial structure and diversity, influencing nutrient cycling, plant growth, and ecosystem health, but how pH affects the microbiome in greenhouse-grown ornamental plants in soilless substrates is less understood. This study examined the impact of substrate pH (4.5, 5.5, 6.2, and 7) and plant species (geranium, marigold, petunia, and tomato) on bacterial communities in peat-based substrates. Our results showed that petunia at pH 5.5 had the highest microbial richness and diversity, significantly greater than tomato, marigold, and geranium at the same pH ($p = 0.0159$). Beta diversity showed pH as the dominant factor, explaining 56.23% of variation in Bray-Curtis and 51.17% in weighted UniFrac ($p < 0.001$). The interaction with plant species explained 83.18% of variation in weighted UniFrac, indicating that species modulate pH effects on microbial communities. *Proteobacteria*, *Actinobacteriota*, and *Bacteroidota* were identified as the top 3 most abundant phylum across treatments, with Proteobacteria consistently showing the highest relative abundance. At pH 4.5, genera such as *Bordetella*, *Curtobacterium*, *Gryllotalpicola*, and *Roseiarcus* were among the top 5% significant genera. *Conyzicola* was more prominent at higher pH levels (6.2–7) in geranium. *Klebsiella* was more prominent in marigold and tomato at pH 5.5–6.2, while *Tahibacter* thrived in petunia, marigold, and tomato at pH 6.2–7. This study demonstrates that substrate pH and plant species interactions shape bacterial communities in greenhouse-grown ornamental plants, with broader implications for optimizing pH management to enhance nutrient cycling and improve sustainability in soilless horticultural systems.

P134

Evaluating the potential of using plant growth promoting microorganisms (PGPMs) as biofertilizers to improve wheat yields for agricultural sustainability

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Abstract

The food and agriculture organization reported a gradual increase of human world population. The population is anticipated to increase to 9.8 billion by 2050. As a result, the demand for major grain crops such as wheat is also increasing. This enforces agronomists to produce more wheat to contribute to food systems for wheat crop production in the prompt to meet the global demand. Chemical fertilizers are used to promote plant growth. However, these pose a threat to the environment and human health. Therefore, we aim to evaluate the potential of using plant growth promoting microorganisms as biofertilizers to enhance plant growth and maximize yields for agricultural sustainability. We aim to employ eco-friendly strategies that will yield advanced and improved crops in alignment with the EU green Deal. Microorganisms were isolated from the rhizosphere of wheat. Isolates were tested for plant growth promoting abilities *in vitro* including phosphate solubilization, indole-3-acetic acid, ammonia, and siderophore production. Those that exhibited positive results for two or more of the tests were selected and identified based on 16S rRNA. All the isolates exhibited the ability to produce ammonia, 70% exhibited siderophore production ability, 55% produced indole-3-acetic acid and 30% solubilized phosphate. Based on 16S rRNA gene amplification, isolates belong to *Bacillus*, *Pseudomonas*, and *Serratia* genera, whilst fungal isolates belong to *Trichoderma*, *Penicillium and Aspergillus* genera. These are promising as plant-growth modulators and are effective to be integrated as active ingredients in biofertilizers to promote plant growth, maximize yields, improve plant health to maintain agricultural sustainability.

P135

International Capacity Building for CRISPR Genome Editing Technology

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Abstract

CRISPR technology spurred a technological leap in crop genetic improvement due to its unprecedented ease of use, applicability in different plants and reduced breeding time scales. Increasingly, CRISPR genome editing is being recognized as an important tool in climate change adaptation for enhanced food security, environmental stewardship and biodiversity protection. In tandem, there is a rapid global adoption of the technology and different jurisdictions are reviewing their stringent biosafety regulations or developing genome editing guidelines.

Efforts by the Innovative Genomics Institute (IGI) to enhance equitable access and distribution of CRISPR technology among various stakeholders in low and middle income countries (LMICs) are discussed. i) To support regulators implementing genome editing guidelines, in LMICs, to reduce existing knowledge gap and enhance informed evaluation of genome editing submissions, we convened a regulatory capacity building workshop for genome edited agriculture bringing 20 participants from 18 countries to Berkeley. ii) On invitation by the Indian Department of Biotechnology, IGI conducted an advanced hand-on CRISPR genome editing in plants workshop for 32 postgraduate researchers at the National Institute of Plant Genomic Research, New Delhi, as the country seeks to build capacity of CRISPR experts using the technology for crop genetic improvement. iii) As a recent part of the African Plant Breeding Academy, IGI members conduct a series CRISPR courses for molecular plant breeders from various African countries at the World Agroforestry Center, Nairobi, to empower the breeders to use CRISPR technology in developing crop varieties that address their specific local challenges.

P136

The seed, the spermosphere, and the seedling: microbiome assembly in seedling establishment

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Abstract

Many plant microbiome studies focus on germinated plants but overlook the assembly process from seed sowing to seedling establishment. For instance, diverse fungal and oomycete pathogens can kill seeds before they germinate. Here we present current knowledge on the microbiome of developing seedlings, emphasizing the spermosphere microbiome and the diversity of fungal and oomycete pathogens in field crops. We detail methods to sample the short-lived spermosphere, revealing crop-specific microbiome assembly within 18 hours of sowing and identifying key organisms enriched in this environment. Additionally, a multi-state effort monitored soil-borne pathogens affecting cotton seedlings across the U.S. Cotton Belt, correlating occurrence data with seed treatment efficacy and environmental conditions, uncovering fundamental biogeographic patterns. Expanding this research, we examined microbiome functional and taxonomic diversity, weather data, and soil data, using random forest models to predict cotton seedling emergence. Future work will involve multi-institutional collaborations to explore the functional convergence of the microbiome in the spermosphere and the specific roles of pathogen secondary metabolites. Overall, this research enhances management strategies for seedling diseases, identifies key microbes for robust seedling growth and protection, and underscores the significance of early plant microbiome assembly in influencing plant health.

P137

Qmatey: an automated pipeline for fast exact matching-based alignment and strain-level taxonomic binning and profiling of metagenomes

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Abstract

Metagenomics is a powerful tool for understanding organismal interactions; however, classification, profiling and detection of interactions at the strain level remain challenging. We present an automated pipeline, quantitative metagenomic alignment and taxonomic exact matching (Qmatey), that performs a fast exact matching-based alignment and integration of taxonomic binning and profiling. It interrogates large databases without using metagenome-assembled genomes, curated pan-genes or k-mer spectra that limit resolution. Qmatey minimizes misclassification and maintains strain level resolution by using only diagnostic reads as shown in the analysis of amplicon, quantitative reduced representation and shotgun sequencing datasets. Using Qmatey to analyze shotgun data from a synthetic community with 35% of the 26 strains at low abundance (0.01–0.06%), we revealed a remarkable 85–96% strain recall and 92–100% species recall while maintaining 100% precision. Benchmarking revealed that the highly ranked Kraken2 and KrakenUniq tools identified 2–4 more taxa (92–100% recall) than Qmatey but produced 315–1752 false positive taxa and high penalty on precision (1–8%). The speed, accuracy and precision of the Qmatey pipeline positions it as a valuable tool for broad-spectrum profiling and for uncovering biologically relevant plant-microbe-microbe interactions. Qmatey-generated metagenomic profiles of maize and sweetpotato were utilized for metagenome-enhanced genome-wide association analysis and genomic prediction. The findings indicate that microbes co-evolved with the host play a significant role in shaping the host's phenotypic expression. This suggests that leveraging plants' ability to harness beneficial microbes can be a valuable strategy for crop improvement.

P139

Impact of functional interactions between microbes on microbiota assembly on corn roots

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Abstract

Plant associated microbial communities play fundamental roles in plant health, growth, and productivity. Synthetic microbial communities (SynComs) are powerful tools for dissecting microbial interactions and their effects on community function and host health. We work with a previously developed maize SynCom consisting of seven bacterial strains for which it has been shown that *Enterobacter ludwigii* (ELU) and Pseudomonas putida (PPU) are potential keystone species critical for maintaining community structure. However the mechanism by which ELU impacts community assembly remains unexplored. We hypothesize that the functions that make ELU a keystone species can be identified by analyzing gene expression in SynComs, with or without the keystone species. We conducted inoculation experiments using modified SynComs (lacking ELU or PPU) on maize seeds (Mo17 X B73 genotype), with untreated seeds (UTC) and full SynCom (FS) as controls. Single inoculations of ELU and PPU were also tested. We quantified microbial abundances, assessed seedling growth and performed metaproteomics on roots to characterize microbial gene expression. ELU removal caused significant shifts in community structure, with rapid dominance of *Curtobacterium pusillum*, while PPU removal had less impact. We identified 272 differentially abundant ELU proteins and 301 differentially abundant PPU proteins in FS vs single inoculation groups, spanning various functional categories, including protein synthesis, lipoproteins, chemotaxis and signal transduction, glycerol metabolism, capsule synthesis. These findings indicate that ELU is crucial in shaping both the structure and function of the Maize SynCom.

P140

Nitrogen fertilizer application impacts the composition and predicted function of the microbial community in a pea (*Pisum sativum*) and canola (*Brassica napus*) intercropping system (peaola)

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Abstract

Strategies to reduce the use of synthetic nitrogen fertilizers have been in high demand due to concerns relating to agricultural sustainability. A promising solution is legume non-legume intercropping. In the pea-canola (peaola) intercropping system, minimal synthetic nitrogen fertilizer is needed to maintain yields. In fact, yields decrease with its application. We hypothesized that the microbial community, specifically nitrogen fixing and plant growth promoting bacteria, could be responsible for yield decline as nitrogen application would disincentivize relationships with these bacteria. Our study sought to understand how three different levels (0, 33, and 67 kg N ha^{-1}) of nitrogen application impacted the composition and predicted function of the peaola microbial community. Our results showed that crop type contributed to 15% of the variance in the data while fertilizer treatment contributed to 2%. Bacteria were no longer differentially abundant between the pea and canola rhizosphere microbial communities with nitrogen fertilizer application (a decrease of eight taxa). Genes predicted to be involved in nitrogen cycling processes were no longer differentially abundant between the pea and canola rhizosphere bacterial communities at 67 kg N ha^{-1}, a decrease by eight at 0 kg N ha^{-1}. Concentrations of ammonium, nitrate, and nitrite were not significantly impacted by fertilizer application suggesting that the microbial community of peaola at 0 kg N ha^{-1} is providing nitrogen to the crop under these conditions. These results suggest that nitrogen fertilizer application alters plant microbial recruitment in peaola potentially resulting from altered plant-plant interactions as a result of crop nutritional needs.

P141

Tracking ACC-deaminase containing microbe abundance in the root and rhizosphere throughout Arabidopsis developmental stages

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Abstract

Plants recruit soil microbes through the root secretion of specific metabolites to shape their microbiome assembly. While recent studies suggest bacterial microbiome is robust once a plant enters vegetative phase, they only examine the microbial community structure rather than how specific activities may change over development. Microbes provide several important functions for their plant host such as nutrient acquisition, phytohormone modulation, and pathogen suppression. A specific example is ACC deaminase which is a microbial enzyme that reduces plant ethylene levels to alter the timing of developmental stages and rendering plants more resilient to stress. Therefore, microbes with ACC deaminase activity are often categorized as plant growth promoting. This study combines culture-dependent and independent approaches to determine if the abundance of microbes containing a specific enzyme, ACC deaminase, changes over a plant's life cycle. We expect that distinct ACC deaminase containing microbes will appear at different developmental stages, altering the overall abundance. These results will be used as a foundation for future studies to examine the impact of ACC deaminase in the face of drought stress and across a variety of plant hosts.

P142

The Phytobiome of Potato in Washington State: The Legacy of Cropping Systems, Soil and the Environment

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Abstract

Potato growers in the Pacific Northwest region of the USA have reported higher yields in fields recently converted to agricultural use (non-agricultural) compared to fields with a long history of potato cultivation (agricultural). The goal of this study is to understand the soil and microbial factors contributing to these variations by exploring soil microbial diversity, physiochemical properties, and potato phytobiome dynamics. In 2021 and 2022, soil samples were collected from 76 sites across Washington and Oregon, including agricultural, non-agricultural, and native fields (not in agricultural production), for soil characterization. Potatoes were grown in common garden microplots in Pullman, WA for 3 years. Bacterial, fungal, protist, and nematode communities were analyzed from different compartments (bulk soil, rhizosphere, endosphere, and tuber samples) using amplicon sequencing. Microbial communities differed distinctly between the Columbia Basin and Skagit Valley, with soil properties such as pH, carbon, and sand content, along with location and field history, being key drivers. Potato phytobiome studies revealed compartment-specific microbial dynamics and identified core and differentially abundant bacterial and fungal ASVs associated with potato production. The findings from this study will provide valuable insights into the soil communities and soil factors associated with potato fields, helping to better understand and develop soil health management strategies specific to the Pacific Northwest region for potato production.

P143

Interrogating individual and collective contributions of members of a synthetic community to maize growth promotion under low nitrogen fertilization

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Abstract

Unraveling microbe-microbe interactions in the rhizosphere is challenging given the complexity of these communities. To facilitate revealing rules governing these interactions we developed the MAize Rhizosphere Synthetic community (MARSc) comprised of 31 bacterial strains from 20 families. MARSc members were isolated from maize roots grown in Iowa soils with low inorganic nitrogen (N) inputs and includes the model rhizosphere colonist *Pseudomonas putida* KT2440. Inclusion in MARSc is based on representation in the maize root rhizosphere and endosphere communities in the field and on *in vitro* interactions with KT2440. Compared to untreated controls, MARSc-treated plants exhibit greater biomass 28 days after planting in low-N soil and roots were finer and more ramified. Plants inoculated with *Pseudoduganella* members of MARSc also show increased root branching and lateral root formation. Mining genomes of MARSc members with PLaBAse's plant growth promotion predictive tool revealed a breadth of plant growth promoting traits, including those involved in phytohormone production, biofertilization, and plant immune-response stimulation. Interestingly, enrichment in biofilm genes did not correspond with their biofilm phenotype, suggesting novel mechanisms are yet to be identified. To explore the ability of MARSc members to colonize maize roots and how MARSc treatments influence rhizosphere microbiome assembly we generated near-full length 16S rRNA amplicon profiles based on a hierarchical taxonomy classification pipeline comprised of Emu and Sintax. By combining functional assays, microbiome profiling, and genome mining we are building a framework for understanding how MARSc members individually or collectively contribute to the biofertilizer capabilities of this synthetic community.

P144

Disentangling the effects of drought severity, drought length and plant age on root microbiome assembly

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Abstract

Under climate change, environmental stressors like drought challenge crop productivity and yield stability. In response, plants can alter root exudation to recruit beneficial microbes to ameliorate the negative impacts of drought stress. The goal of this study was to disentangle drought length, drought severity and plant age to understand their effects on sorghum aboveground biomass, root exudates and root microbiome assembly. We found that plant age, length of drought, and their interaction had significant effects on sorghum biomass. Moreover, the slope of the interaction between plant age and length of drought was negative, meaning that as plants get older the effect of drought is more negative. To characterize the root microbiome, we amplified the 16S rRNA, 18S rRNA, and ITS regions using Illumina MiSeq PE300. We found that plant age, drought severity and length of drought significantly decreased bacterial Shannon diversity index. We also found that the composition of bacterial communities varied significantly depending on drought length, drought severity and plant age. Interestingly, bacterial communities became less dispersed when longer periods of drought were applied. This suggests that longer droughts may act as a deterministic force in selecting drought-tolerant bacteria. Future work will analyze the ITS, 18S rRNA dataset and root exudates to fully comprehend the climate-dependance of root microbiome communities. Results from this study will allow us to harness beneficial interactions to develop novel bioinoculants to mitigate the negative impacts of climate change on crop yield.

P145

Dissecting the role of plant cell wall composition in modulating plant-microbe interactions

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Abstract

The plant cell wall plays an important role in the interaction with microbiomes in the roots and rhizosphere. Lignin is a key component of the plant cell wall and has been extensively studied in stems primarily due to its relevance in biomass conversion for biofuels. However, the impact of root lignin composition on microbiome dynamics has received less attention. Changes in root lignin could affect the surrounding microbiome, as variations in lignin monomers or phenolics may alter the cell wall's structure and permeability as well as root surface area, potentially influencing microbial colonization. In this study, we hypothesize that the root cell wall composition significantly shapes the microbiome structure and composition in the vicinity of roots. We inoculated lignin mutant lines of *Brachypodium distachyon* with 17-member bacterial synthetic community (SYNCOM) and analyzed differences in the community composition after three weeks of inoculation compared to wild-type (wt) plants. The sample type (roots, rhizosphere, or soil) was found to be a major factor affecting microbial community composition. Additionally, plant genotype substantially influenced the microbiome profile, with COMT5139 (a mutant in caffeic acid O-methyltransferase) showing the most distinct rhizosphere community composition compared to wt. Further analysis revealed that COMT5139 also exhibited the most significant difference in root lignin composition among the mutants compared to wt *B. distachyon*. To determine whether changes in root exudate composition might also account for differences in microbial community composition, we are conducting metabolomic studies of root exudates to identify compounds that could influence the microbiome.

P146

Harnessing Agricultural and Livestock Waste Turning to Compost: Farming Practices for a Sustainable Future

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Abstract

The agro-wastes and their processing have emerged as a significant global problem since, the majority are burned or buried in soil, causing air and water pollution. Similarly, raw manure contains pathogens, weed seeds, odors, etc., which can negatively impact the environment. Effective waste management practices are crucial in achieving sustainable agriculture and food security goals. The agro-waste and livestock manure waste can be co-composted and converted into an efficient organic fertilizer. However, nitrogen loss during the composting process, including lime increases the pH, which speeds up the decomposition process and mitigates the ammonia and gaseous emission. This study investigates the influence of hydrated lime (with and without addition) on the physico- chemical changes, microbial dynamics, gaseous emission, and nitrogen retention during 49 day compost period. The results showed that, the total ammonia emissions were significantly lower in lime-amended compost mixtures than in Control treatment mixtures ($p < 0.05$). These lime treatment mixtures had significantly increased nitrate-nitrogen concentrations and decreased pH values and ammonium nitrogen concentrations ($p < 0.05$). Furthermore, CO_2 emissions in the compost treated with lime were higher in the early phases but significantly dropped as the compost matured, indicating a faster stabilization process. These results imply that lime amendment can augment the compost quality by accelerating the nitrogen conservation process.

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P147

Contrasting the performance of soil microbiomes conditioned to individual and combined local environmental changes

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Abstract

Human-influenced environmental changes (e.g. deforestation and intense fertilization) and global climate shifts (e.g. warming, CO2, and drought), can negatively impact soil microbiomes. Such changes may alter how soil microbiomes influence plant health, productivity, and tolerance to changing climate conditions. My research will leverage iterative microbiome selection to create microbiome divergence under local environmental changes (i.e. addition of salt, nitrogen, or a carbon source). We will quantify the impact of soil microbiomes on plant growth, following conditioning under 1) a single environmental change, 2) paired environmental changes within the same physical space, or 3) coalesced microbiomes, from those subjected to single environmental changes. Iterative microbiome selection, through microbiome bottlenecking and regrowth, has been shown to quickly improve crucial microbiome-influenced soil functions (e.g. nutrient cycling), demonstrating potential for probiotics in agroecosystems. I expect coalesced soil microbiomes to better promote plant growth across a wider range of environmental conditions. Soil microbiomes were bottlenecked and passaged 4 times under conditioning to nitrogen (chemical fertilizer), malic acid (crop root exudate), and salt (environmental stressor) both a) individually and b) in paired combinations. Compositional differences across soil microbiomes are being analyzed using 16S rRNA gene and fungal ITS sequencing. Hordeum vulgare were sown in soils inoculated with differentially conditioned microbiomes (single change, paired change, or coalesced), crossed with each different environmental condition (N=160). We will determine if recent environmental history of soil microbiomes influences their performance in contemporary conditions. We expect these findings to support direct and/or indirect microbial agricultural management for replacing intensive practices.

P148

Directed Evolution of Beneficial Microbial Inoculants to Improve in-soil Survival

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Abstract

The use of beneficial microbial inoculants provides an avenue to improve the sustainability and productivity of agriculture by enhancing microbial ecosystem services. However, most inoculants cannot survive and persist in a wide range of soil environments. The research objective of this project is therefore to use a directed evolution approach to enhance bacterial persistence in soil conditions. In this ongoing experiment, we cultured a commercial phosphate solubilizing bacterial inoculant *Priestia megaterium* (*Pmeg*) for approximately 500 generations in six M9 medias ranging from single carbon substrates (low resource diversity) to 24 carbon substrates (high resource diversity). We used growth curves to compare the fitness of the adapted vs. ancestral strains, finding a significant fitness increase all adapted *Pmeg* strains. Additionally, adaptation in M9 glucose media enhanced fitness when grown in M9 malic acid, but reduced fitness in other single carbon M9 media, indicating redundant metabolic pathways for malic and glucose. After approximately 700 generations, we will use strain-specific qPCR primers to track in-soil survival of ancestral and adapted *Pmeg* when introduced into soils spiked with resource amendments used during the culture period. We expect that *Pmeg* adapted under high resource diversity will have increased survival and persistence in a soil recipient compared to *Pmeg* adapted to a single resource, since its ability to use more resources effectively may confer a competitive advantage. Insights gleaned from this project will directly inform the conditioning of beneficial microbial products, while advancing our fundamental understanding of microbial adaptation and evolution in complex environments.

P149

The MAize Rhizosphere Synthetic Community (MARSc): a consortium to reveal principles underlying bacteria-bacteria interactions in the rhizosphere

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Abstract

The rhizosphere microbiome is essential to plant growth and health, but relatively little is known about the mechanisms by which these microbiomes form or the interactions that occur within. Our goals are to identify the genes required by the model rhizosphere colonist *Pseudomonas putida* for the assembly of a multi-species rhizosphere community and how those gene networks are modulated by community composition. Our approach was to create the MAize Rhizosphere Synthetic community (MARSc), modeled after the bacterial community residing on the roots of maize grown in Iowa soils, which includes *P. putida* as a tool for querying bacteria-bacteria interactions influencing its rhizosphere competence and fitness. MARSc increased maize growth in low-nitrogen soils, indicating these organisms and their interactions can function as a biofertilizer. We identified species within this community capable of stimulating or inhibiting the surface growth of other community members, finding that nutrient (resource) abundance strongly influences these interactions, with *P. putida* being highly inhibitory. Using a CRISPR interference system designed for *P. putida*, we show that a dominant factor contributing to these interactions was competition for iron, as repression of pyoverdine production relieved inhibitory interactions. Maize root exudates and specific components such as benzoxazinoids modulate biofilm formation by various species, while bacterial derived diffusible metabolites alter both growth and biofilm formation on a strain-by-strain basis. These results showcase the utility of synthetic communities for identifying principles underlying bacteria-bacteria interactions and how plant and microbial metabolites may influence microbiome assembly.

P150

The UK Crop Microbiome Cryobank – Biobanking the Phytobiome to ask biological questions

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Abstract

Microbiome Biobanks are required to underpin Phytobiomes research. Integral to this, is the need to preserve soil, plant microbiota and associated metadata. This is required to protect intellectual property, comply with legislation, validate the stringency of research and provide resources for reference and commercial use. The UK Crop Microbiome Cryobank is a newly constructed resource of 36,000 microbial isolates, and 4,800 soil rhizoplane samples representing crops including wheat, oil seed rape (canola), barley, fava bean, oats, and sugar beet.

A priority for the project was to biobank and characterize samples from a greenhouse experiment, growing plants in 3 different soil types from 9 locations in the UK. This approach allows us to ask 'biological questions' of our data resources, such as do some crops host a larger bacterial diversity than others? Do crops consistently recruit a preferred consortium of microbes from different soils and what are the trends within recruitment patterns? Would this knowledge affect crop rotation choice? Can we use the data to construct SynComs using an evidenced based approach? In this presentation we will share exciting new data that shows how different crops preferentially recruit different microbes and how the location source of the soil is a major driver. Further, we will consider evidence showing that plants select microbes on the basis of phenotype rather than the taxonomic status. Details of our cryopreserved samples and their associated datasets is available through AgMicroBiomeBase (https://agmicrobiomebase.org/) with data linked to EBI's MGnify pipeline, which provides a facility for functional analysis.

P151

Determining the role of microbial IAA metabolism in the *Arabidopsis thaliana* phosphorus starvation response

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Abstract

The plant microbiome provides advantages to plants undergoing biotic and abiotic stress. A common cause of abiotic stress in plants is the deficiency of macronutrients, such as phosphorus (P). Although P is ubiquitous in soil, plants cannot readily access it. Thus, plants have evolved mechanisms to overcome P deficiency and increase P uptake via the phosphorus starvation response (PSR) and microbial recruitment, respectively. The PSR in *Arabidopsis thaliana* (Arabidopsis) involves changes in root architecture that are driven by auxin fluxes, particularly indole-3-acetic acid (IAA). Importantly, microbes recruited by the plant can produce and degrade IAA. In this study, a diverse bacterial synthetic community (SynCom) meant to replicate taxa observed in soil and types of IAA metabolism observed was created. Arabidopsis seedlings were inoculated with this SynCom and grown under conditions to induce PSR. Microbial community structure, IAA levels, P levels, root biomass, and changes in root architecture were measured to determine the impact of SynCom IAA metabolism in the PSR. Results indicate that plants inoculated with SynCom and grown under medium and high P concentrations had inhibition of primary root growth and more biomass than other treatments. Together this data highlights how plant microbiomes differentially impact root architecture and biomass to impact overall plant health during P nutrient stress.

P152

Differences among fungal microbiomes associated with tar spot of corn in Ecuador, Guatemala, and the United States

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Abstract

Tar spot of corn, caused by the obligate fungal pathogen *Phyllachora maydis*, was associated with *Monographella maydis* (syn. *Microdochium maydis*) and *Coniothyrium phyllachorae* in Mexico. While *M. maydis* was once believed to cause fisheye lesions and *C. phyllachorae* was described as a mycoparasite of *P. maydis*, their presence and roles in tar spot remain uncertain. We hypothesize that their presence, as part of the tar spot microbiome, is influenced by geographical location and that they are not always associated with tar spot of corn.

To test this, we collected tar spot-infected leaves from Guatemala, Ecuador, and the United States. Our findings show that the distribution and abundance of these fungi exhibit a geographical pattern and are not consistently associated with tar spot lesions in all locations. We confirmed the presence of *Microdochium* in Ecuador and Guatemala but not in the United States. Additionally, we identified the likely mycoparasite *Paraphaeosphaeria* as highly prevalent across samples from all three countries. Microbiome diversity analysis grouped tar spot samples into four distinct clusters: two dominated by *P. maydis*, one primarily associated with *Microdochium*, and a fourth characterized by a combination of *P. maydis* and *Paraphaeosphaeria*.

The presence and abundance of *M. maydis* and *C. phyllachorae* depend on location. The role of *Microdochium* remains ambiguous; its absence from fisheye lesions in U.S. samples confirms that it is not required for fisheye formation. Furthermore, *Coniothyrium* was detected at low abundance in all samples but was absent in the United States.

P153

Impact of geographic variation on the influx of soil microbes with different metabolic abilities in a major urban centre

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Abstract

Soil microbiome composition plays a crucial role in shaping soil function, greenhouse gas flux, and plant-microbe interactions, leading to differences in plant traits and growth. In urban and peri-urban agricultural systems, microbial influx is a key component of potential microbial function. Previous works suggests that urban farming occurring in transplanted soils lacking a history within farmed soil may deplete dispersal-limited microbes. We expect that potential microbial immigration is related to the surrounding environment and further accentuated across vertical gradients, as rooftop farms may receive different microbial immigrants than those at ground level. Microbial traits that are included or excluded from the "dispersing pool" should elucidate important microbial functions in these environments.

We propose a novel approach to characterize the microbial colonizer pools immigrating into the soil by using sterile "traps" – 24-well no-bottom plates with nylon sheets on either side to filter the influx of bacteria and fungi. Traps were deployed at various urban locations in Toronto, Canada, to assess differences of microbial colonizing pools across urban sites. Each well of the traps is filled with sterile soil that has been inoculated with a selection of carbon substrates or with tree litter, to assess the metabolic heterogeneity of dispersing microbial pools. We hypothesize that the diversity and composition of microbes in the presence of certain carbon source pools will be more sensitive to location than in the presence of others. This research will inform sustainable urban agricultural practices through strategic management of urban microbial pools, ultimately fostering sustainable urban agriculture development.

P154

Artificial selection of *Stutzerimonas stutzeri* towards enhanced nitrogen fixation in the presence of ammonia and oxygen

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Abstract

Stutzerimonas stutzeri is a Gram-negative bacterium with diverse capabilities including nitrogen fixation, fitting under the classification of plant growth-promoting bacterium. A construct was developed using pTH1227 and the *nif* promoter preceding *nifH* in *S. stutzeri*, creating a *nif* promoter::GusA fusion that worked as a marker gene for *nif* genes expression. Liquid cultures of *S. stutzeri* were exposed to UV energy targeting 99 % killing. Survivors carrying mutations were screened for *nif* expression in oxygenic conditions, and in the presence of ammonia and complex media. Seven mutants were isolated, fully sequenced, and their capacity of nitrogen fixation in the presence of oxygen and ammonia was assessed at *the in vitro* level by acetylene reduction assay, β-Glucuronidase assay, and at *the in vivo* level by inoculating them in tomatoes in controlled environments. Chlorophyll levels and biomass were measured, and acetylene reduction assay was performed on plant tissue to compare the impact of mutants vs wild type vs non-inoculation over plant growth and product yield.

P155

Domestication and Breeding of Zea mays Shaped Fungal Microbiome Recruitment

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Abstract

Microbial recruitment from the soil into the plant microbiome is primarily driven by the plant host, which plays a key role in adapting to environmental stressors. In natural ecosystems, wild ancestors like Balsas teosinte (Zea mays parviglumis), the progenitor of maize, work in synergy with their microbiota to endure biotic and abiotic pressures, a trait reduced in domesticated maize cultivars. This study examined how domestication and breeding influence fungal recruitment in different plant compartments of teosinte compared to domesticated Mexican and US maize varieties, including landraces and elite inbreds. We focused on three compartments: bulk soil, rhizosphere, and the leaf endosphere, to assess their recruitment potential. Our results showed that Mexican maize rhizospheres had the highest Shannon diversity, indicating broader recruitment that maintained richness and evenness. Teosinte, in contrast, exhibited lower diversity in the leaf endosphere, likely reflecting stronger selective pressures or more specialized microbial recruitment. Beta diversity analysis using PCoA revealed distinct clustering by plant group and compartment, with teosinte clearly separated from maize. Venn diagrams revealed 126 shared OTUs between bulk soil and rhizosphere, 1 OTU between bulk soil and leaf endosphere, 7 OTUs between rhizosphere and leaf endosphere, and 112 OTUs shared across all compartments. Furthermore, teosinte and Mexican maize harbored more biomarker microbiota compared to US maize. These findings suggest that domestication and breeding have shaped fungal microbiome recruitment, with potential implications for plant health and productivity.

P156

Antimicrobial Activity of *Vachellia* Species on Multidrug Resistant Bacteria and Mechanism of Action

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Abstract

The health implications of Multidrug-Resistant (MDR) bacteria cannot be overemphasized as they tend to withstand the inhibitory or bactericidal effects of most commercial antibiotics. The use of medicinal plant extracts in treating diseases caused by MDR is a promising approach to protecting human health against these bacteria. *Vachellia spp*., a medicinal plant, has been adopted to treat some diseases caused by MDR. However, different species of this plant are yet to be fully utilized in the treatment of diseases associated with MDR. This current review aimed at collating information on the antimicrobial potencies of the different *Vachellia species* as well as their mechanisms of action against MDR. Based on collated information, *V. nilotica*, *V. karroo*, *V. kosiensis*, *V. xanthophloea*, *V. tortilis*, *and V. sieberiana* exhibited promising bioactivities against pathogens. Against MDR bacteria, the extracts from *V. karroo* and *V. erioloba* have shown to be potent in fighting against MDR bacteria. Their mechanisms of action against MDR bacteria include cellular membrane damage which disrupts the defence mechanisms of the bacteria. Although extracts from *Vachellia species are* promising in the fight against MDR bacteria and the associated diseases, a gap still exists in elucidating the specific parts of the plants from which extracts could exhibit high antimicrobial potencies as well as the other species that could inhibit the proliferation of MDR bacteria. Studies are recommended to unveil the impacts of the different parts/species of the plant on MDR.

Keywords: *Vachellia species*, medicinal plant extracts, Multidrug-Resistant (MDR), pathogens, antimicrobial

P157

Harnessing chickpea (Cicer arietinum L.) microbiome to develop potential microbial consortium for enhancing its sustainable productivity

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Abstract

Chickpea is a crucial legume in the human diet for protein source and co-inoculation with plant-growth-promoting bacteria on its production are not much explored. This study aimed to explore culturable bacteria and develop a potential microbial consortium for enhancing productivity. Two bacterial strains, *E. hormaechei* and *B. naejangsanensis* were isolated and molecularly characterized. These strains selected on the basis of plant growth-promoting activities such as production of IAA, ammonia, siderophore, and nutrient solubilisation). The consortium significantly enhanced plant growth promoting activities. Chickpea plants treated with the bacterial consortium exhibited significant improvements in plant growth attributes, grain yields, and nutritional content in both green plants and seeds, including higher levels of protein, carbohydrates, calcium, potassium, zinc, manganese, and iron compared to control. Soil treated with the consortium also showed increased nutrient content (N, P, K), soil enzyme activities and soil microbial diversity. Microbiome analysis revealed that the consortium enhanced soil diversity and function, with positive correlations to plant growth and soil physicochemical properties. The relative abundance of the dominant bacterial phylum “Proteobacteria” was observed in all treatments. Consortium-treated seeds showing greater diversity in bacterial phyla including Verrucomicrobia, Firmicutes, Bacteroidetes, Acidobacteria, Actinobacteria, Chloroflexi, and Proteobacteria compared to individual treatments. In the soil microbiome, consortium and single inoculants increased the diversity of bacterial phyla such as Cyanobacteria, Verrucomicrobia, Firmicutes, Bacteroidetes, Acidobacteria, Chloroflexi and Proteobacteria than control. The microbial consortium gave significant improvements in plant growth attributes, productivity, nutritional content, soil health, and microbial colonization in both soil and seed.

P158

Assessing Physiological and Microbial Changes Throughout Castanea Grafting

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Abstract

Castanea spp. are a valuable resource, yet underutilized in the United States, as they are versatile for both consumable and non-consumable products. Tree crops like chestnuts are generally grown in orchards via clonal techniques such as grafting. Chestnut grafting, however, results in astonishingly high graft failure rates. The reasons behind chestnut graft failure are currently unknown, but there are two likely hypotheses that may explain chestnut graft failure: improper graft healing specific to *Castanea* physiology, and/or endophytic microbes behaving as opportunistic pathogens. From a greenhouse experiment of 120 trees, we developed a tissue softening protocol amenable for viewing woody chestnut tissues with Scanning Electron Microscopy (SEM). We have used this protocol to visualize cross- and longitudinal sections of chestnut wood, clearly observing the in-tact ring porous structure of chestnut stem's vascular anatomy. Fungal acervuli were also consistently observed on failed grafts, both macroscopically and with our SEM technique, leading us to pursue classifying these grafts' mycobiomes. Fungi isolated from unsuccessful grafted tissue (n=36) and healthy tissue (n=41) were putatively identified using the Internal Transcribed Spacer (ITS) sequence and grouped into trophic categories based on literature review. Of these species, 31 are plant pathogens, or opportunistic pathogens. We also completed a DNA metabarcoding approach to examine fungal endophytes minimizing culture bias and providing deep quantitative data (total PF reads=273,818,134). We will repeat our greenhouse experiment this summer since investigating these potential causes of graft failure is crucial for the long-term goal of developing a more sustainable production system for chestnuts.

P159

The Influence of Roots and Rhizosphere on Phosphorus Cycling in Corn-Soy Rotations Managed with Low Phosphorus Inputs

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Abstract

In fields where phosphorus (P) fertilization is reduced as part of soil health management, corn and soy have shown the ability to maintain or recover grain yield over time. To date, these cases are more the exception than the rule, but they reveal the ability of cropping systems to make better use of the natural capacities of soils to provision plant P. On farms across Indiana, we tested the influence of reduced P fertilization (and other soil health management practices) on microbiome composition and total and extractable P from soil in proximity to roots, spanning diverse soil types in 27 corn and soybean fields across 14 farms. We hypothesized that low P soils (based on agronomic recommendations) would stimulate rhizosphere P-mining activity. We tested the rhizosphere influence using size-exclusionary mesh bags that allowed root access (1,000 µm), restricted root access (45 µm), or limited mycorrhizal access (1 µm), with bags placed either in-row or between rows. Our treatments distinguish between P cycling activity with and without stimulation by plant roots and identify which microbial populations flourish where P fertilization was restricted. We will present preliminary results on the influence of bagging on soil water content and P availability, since microbiome data is currently being generated. Our study aims to find patterns in soil microbiota that serve as predictors of the natural capacity for biological P fertilization. Harnessing this knowledge will lead to more efficient fertilizer use and substantiate (or refute) claims of reduced fertilization needs when practicing soil health management.

P160

The effects of introduced biocontrol microbes on root and flower surface microbiomes of strawberry grown in coir substrate under protection

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Abstract

Biocontrol of plant diseases is promoted as a key component of integrated pest and disease management for sustainable agriculture. Augmented introduction of biocontrol microbes is expected to affect resident phytobiome, which could lead to unintended consequences. We conducted research studies to assess the effects of three microbes (*Gliocladium catenulatum*, *Trichoderma asperellum* and *Bacillus subtilis*) on communities of living microbes on strawberry grown in table-top coir bags under protection. *G. catenulatum* and *T. asperellum* were applied to strawberry roots via drenching soon after planting. *G. catenulatum* and *B. subtilis* were sprayed onto open flowers. To specifically profile communities of living microbes, we used to a PMA-based method to treat samples before DNA extraction. Amplicon-sequencing was used to profile flower epiphytes whereas shot-gun sequencing was used for root epiphytes. Applying the three biocontrol microbes was successful, leading to significant increases in the relative abundance of the target microbes on both flowers and roots. The two introduced fungal taxa (*G. catenulatum* and *T. asperellum*) appeared to affect mainly fungal microbiome components whereas the introduced bacterial taxa (*B. subtilis*) mainly affected bacterial microbiome component. The effects of introduced biocontrol microbes on resident microbiome was more profound and long-lasting on roots than on flowers. Although biocontrol organisms led to significant changes in the overall microbial composition, their effects on individual microbial taxa groups were limited. The present research suggests that biocontrol of root pathogens may hold a greater promise than flower/fruit diseases.

P161

Perennial Cropping Systems: Enhancing Soil Health and Carbon Sequestration through Microbial Diversity and Pyrolized Amendments

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Abstract

Perennial sorghum cropping systems are emerging as an effective strategy for carbon sequestration due to their distinct root systems, especially with rhizomes that as perennial underground structures can store significantly more soil organic carbon than fibrous-rooted annual crops. This study is examining microbiome-enhanced carbon sequestration in both perennial and annual sorghum, focusing on analyzing key factors that influence microbial diversity and function. The current research applies advanced techniques in metagenomics and soil biogeochemistry, including next-generation sequencing and computational data analytics. Temporal and spatial variations of soil health indicators are also being investigated, particularly the impacts of different pyrolized soil amendments on carbon content.

These include the effects of Biochar and TBA (Torrefied Biomass Amendment) on microbial structure and composition in combination with different plant genotypes. Distinct microbial profiles have been observed with each amendment across both soil depth profiles and annual versus perennial crops, fostering unique microbial communities associated with annual and perennial plants. Our findings highlight the critical role of soil depth, amendment type, and rhizomatous roots in shaping microbial communities, offering insights into sustainable soil management practices for enhanced crop performance.

P162

Plant-Archaea Interactions: Metabolites, Genes and Nitrogen cycle

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Abstract

Although plant interactions with fungi and bacteria remain the primary focus of plant microbiome research, the discovery of archaea in soils has raised fundamental questions about the unique role this vast prokaryotic domain plays in soil nutrient cycling. Ammonia-oxidizing archaea (AOA) are abundant in soil and present in the rhizosphere of various plants, where they play a crucial role in nitrogen (N) transformations, including nitrification and the production of the greenhouse gas N_2O. However, the mechanisms behind these interactions, as well as their consequences for plant growth, nutrient cycling, and N loss from soils, remain unknown.

To address this knowledge gap, we conducted a study using sterile laboratory ecosystems to examine the interactions between *Nitrososphaera viennensis*, one of the most abundant soil AOA, and the bioenergy crop switchgrass. By integrating soil biochemistry, gas measurements, metabolomics, and transcriptomics, we investigate how these interactions affect the N cycle.

Our results showed that AOA nitrification was influenced by plant exudates. The presence of AOA also altered plant exudation, leading to increased production of specific metabolites in the rhizosphere, including polyketides, fatty acids, and alkaloids. Notably, metabolites overproduced by plants during periods of complete AOA inhibition—such as flavonoids, alkaloids, and phenolic acids—showed potential as biological nitrification inhibitors, which are associated with reduced N loss through nitrification and lower N_2O emissions. Additionally, we explored archaeal gene expression in response to different plant exudates, offering deeper insights into the complex interactions and N flow between plants and archaea in the rhizosphere.

P163

Human Health Risk Assessments for Biopesticides – Can we evolve to Next Generation Risk Assessments?

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Abstract

Requirements to register microbial pesticides in the United States were first established in 1983, revised in 1996, and since then, have become the basis for the hazard identification and risk assessment of microbial pesticides globally. The OPPTS 885 guideline studies evaluate whether a microbe can cause infection, disease or toxicity through various routes of administration. In addition, standard acute “6-pack” studies that are required for registration of conventional pesticides, are also required for biopesticide formulations as well. These studies aid in categorizing hazard potential for label safety details and assure safe use of the product. For the past several decades there have been efforts to reduce, replace, and refine the use of animal testing. As such, many regulatory authorities have set targets to reduce animal testing and rely on more relevant models for assessing human safety. These goals are supported by rapid increases in new approach methodologies (NAMs), which may better predict human health hazard for use in next generation risk assessments (NGRA). Several NAMs paradigms have been validated and accepted by regulatory authorities in many regions of the world. However, validation of these alternative methods has primarily focused on their use in chemical substances or cosmetics, and microbial pesticides have thus far not been included in these validation efforts. This presentation will discuss some of the challenges for testing microorganisms, and what the pesticide industry is doing to support reducing animal testing where feasible, and toward a NAMs-based, NGRA approach to human health risk assessment for biopesticides.

P164

Difficulties in effective microbial-based product testing on *Apis mellifera* (L.) in the laboratory

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Abstract

The production of microbial-based plant protection products has resulted in the necessity for novel risk assessment protocols to observe potential effects. Microbial pesticides are required to be evaluated for pathogenicity, which requires an extended observation from the standard honey bee 10-day test (OECD 245). The current EPA guideline for assessing pathogenicity of a microbial pesticide (OCSPP 885.4380) requires a 30-day observation to properly evaluate safety, but this test duration is typically difficult to achieve with adult honey bees in bioassay cages due to control performance. Furthermore, homogeneity in test diets is difficult due to the physical properties of a microbial test substance. Larval testing also presents challenges due to the innate anti-microbial activity of royal jelly that is used to create the diet, which can inhibit the active microbe in a diet assay and may result in a false negative. Here we present some of our recent experiences in developing novel experimental approaches for honey bees to overcome the challenges of microbial product testing. We have evaluated factors that may increase adult honey bee longevity in the laboratory. Additionally, assessment based on genomic evaluation comparing microbial genetic sequences to known honey bee pathogens may be a method to overcome the technical barriers for evaluating the safety of a microbial product to honey bee larvae. It is also critical that we develop approaches for microbial products that can separate mortality from pathogenicity and infectivity. Our goal is to contribute to internationally-standardized testing approaches to strengthen the effective evaluation for microbial-based products.

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