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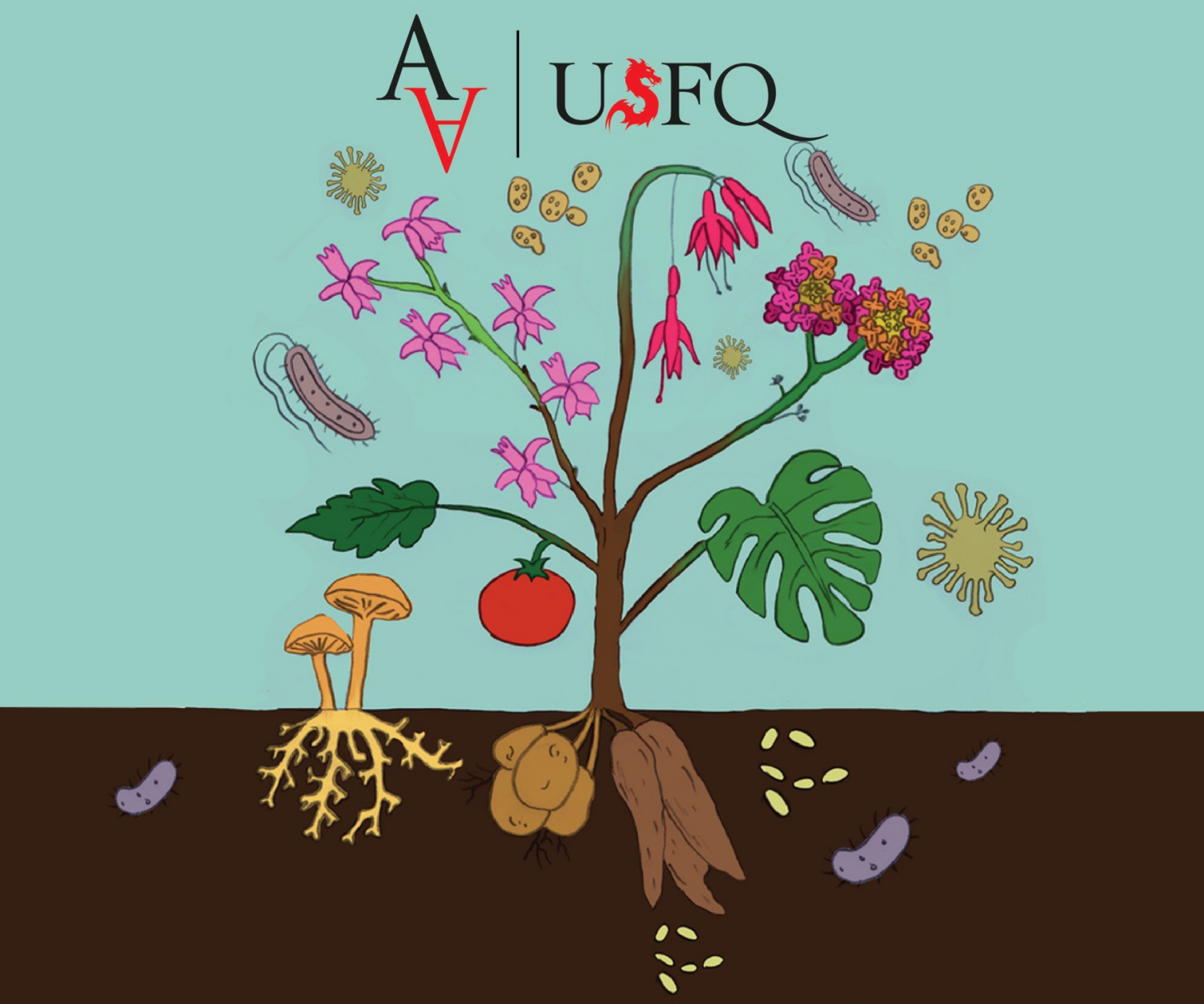

4th Plant Microbiome Symposium

Octubre 2023 Número 50

Archivos Académicos USFQ
Número 50

4th Plant Microbiome Symposium

Editores:
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Expositores:
Jos Raaijmakers, Omri Finkel, Corné Pieterse, Britt Koskella, Joana Falcao Salles, Philip Poole, Mark Liles, Tsai Siu Mui, Gilles van Wezel, Chunxu Song, Mario Serrano, Rodrigo Mendes, Viviane Cordovez da Cunha, George Kowalchuk, Jessica Duchicela, Stephen Sherwood, David Johnston-Monje, Gontran Arnault, Milton Gordillo, Guillaume Chesneau, Stalin Sarango Flores, Susan Mosquito, Dario X. Ramirez-Villacis, Lucas William Mendes, Jelle Spooren, Zayda Morales Moreira, Jonathan Fortt, Muhammad Syamsu Rizaludin, Eva Cea Torrescassana, Jie Hu, Caroline Sayuri Nishisaka, Sandra Cortés-Patiño, Juan José Sánchez Gil, Farah Boubsi, Luzia Stalder, Johan Leveau, Peter Erdmann Dougherty, Linda Gouka, Hanna Susi, Antonio León-Reyes, Mason Kamalani Chock, Adrien Anckaert, Simon Roy Law, Sietske van Bentum, Estefania Pena-Zuniga, Melissa Uribe Acosta, François Nimbeshaho, Julian A. Liber, Vanessa Otero Jiménez, Payton Yau, Rachel Tavares, Yang Song, Barbara Pivato, Jessie Zimmerman, Anderson Santos de Freitas, Cristian Andres Salinas-Castillo, Deborah Cornadó Carbó, Gabriel Silvestre Rocha, Haikun Ma, Carin Ragland, Juan Quijia Pillajo, Miguel Pazmiño-Vela, Rodrigo Alegría Terrazas, Rosa Soria, Thierry A. Pellegrinetti, Venancio Arahana, Xavier Chiriboga, Brandon Ford, Allison East, Nicolás Rodríguez-Romero, Alejandra Sanchez, Pieter van 't Hof, Stalin Sarango flores, Leticia Pereira, Guillaume Chesneau, Linda Gouka, Daniel Uribe Velez, Alberto Pascale, Abdul Aziz Eida, Aracely Zambrano-Romero, Guilherme Lucio Martins, Gustavo Adolfo de Freitas Fregonezi, Renato Ducati Delarco, Ivan Astudillo, Luzia Stalder, Sandra Cortés-Patiño, Sara Ramírez Restrepo.

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4th Plant Microbiome Symposium

Welcome

After successful editions in Sao Paulo, Amsterdam, and Dundee, and due to the great importance of the theme, Universidad San Francisco de Quito (USFQ) is proud to host the 4th Plant Microbiome Symposium in Quito, Ecuador, from August 1st to August 4th, 2023.

The 4th edition of the Plant Microbiome Symposium is this year's premier opportunity to connect with plant-microbiome colleagues from all over the world, where you can take advantage of outstanding plenary speakers, multiple networking events, poster fairs and receptions, in the conference and exhibition halls at the USFQ campus in Cumbaya in the valley situated East of Quito.

We welcome our Keynote speakers Jos Raaijmakers, Omri Finkel, Corné Pieterse, Britt Koskella, Joana Falcao Salles, Phil Poole, Mark Liles, Tsai Siu Mui, Gilles van Wezel, and our Invited speakers Chunxu Song, Mario Serrano, Rodrigo Mendes, Viviane Cordovez da Cunha, George Kowalchuk, Jessica Duchicela, Stephen Sherwood, and David Johnston-Monje, for kindly participating in this conference. We also welcome and thank everyone who submitted abstracts, and will be sharing their findings through short oral talks or poster presentations.

Thank you for joining us at what truly will be an exciting and memorable Plant Microbiome Symposium!

Feel very welcome at USFQ, and welcome to visit Ecuador!

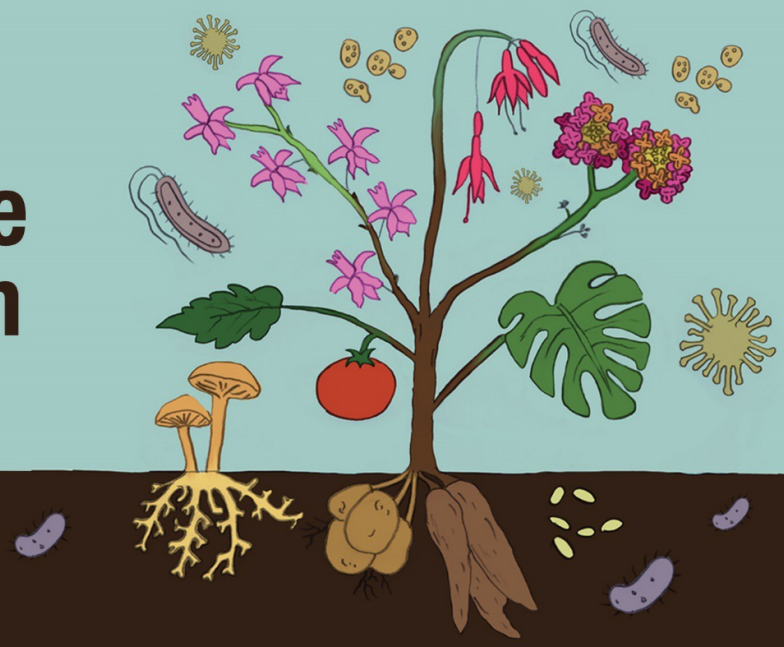
On behalf of the local organizing committee,

Pieter van 't Hof *PhD* and Antonio Leon-Reyes *PhD*

4th PMS official website: https://plantmicrobiome2023.usfq.edu.ec/

4th Plant Microbiome Symposium

Conference Venue



4th Plant Microbiome Symposium

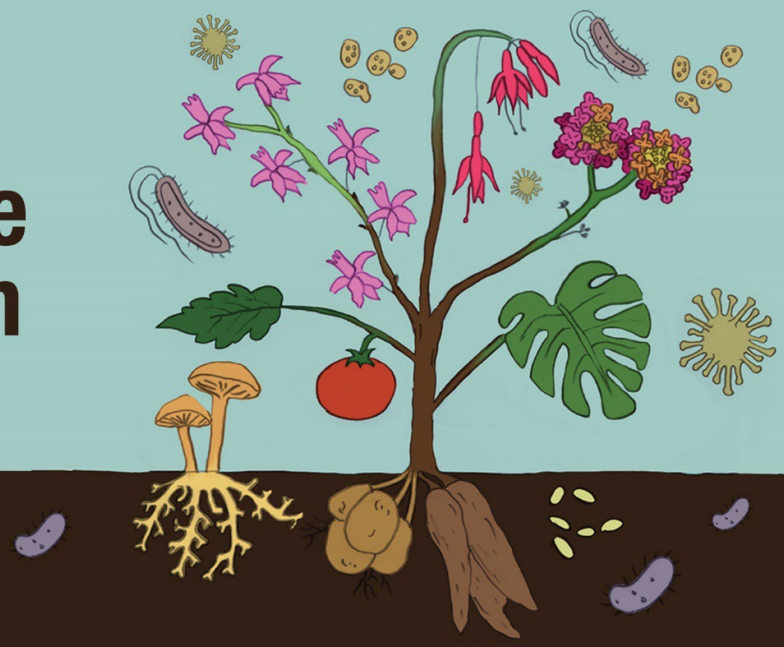
UNIVERSIDAD SAN FRANCISCO DE QUITO

1. Teatro shakespeare
2. 1er piso Hayek
3. Tesorería Campus USFQ
4. Puente entre Hayek y Campus

USFQ UNIVERSIDAD SAN FRANCISCO DE QUITO

4th Plant Microbiome Symposium

Tuesday August 1st

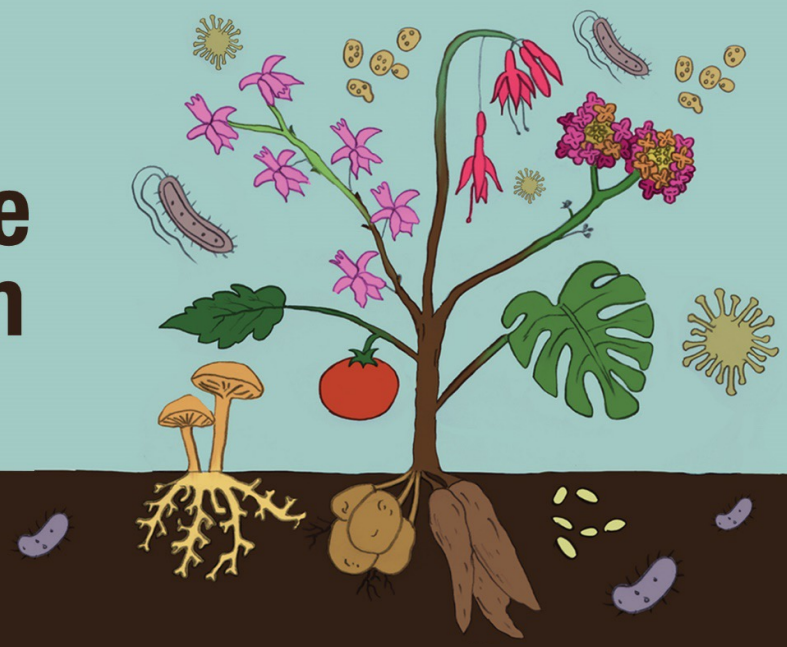


Time	Activity	Speaker
08:00 - 09:00	REGISTRATION	
09:00 - 09:15	OPENING	

Session 1:
Plant microbiome assembly: Control by host and environmental factors

09:15 - 10:00	**KEYNOTE LECTURE** Breaking the witches' spell	**Jos Raaijmakers** *Netherlands Institute of Ecology* *Leiden University* *The Netherlands*
10:00 - 10:15	Effective seedling microbiota engineering using synthetic community inoculation on seeds	**Gontran Arnault** *University of Angers / INRAE* *France*
10:15 - 10:30	Untangling the Effects of Plant Genotype and Soil Conditions on the Assembly of Bacterial and Fungal Communities in the Rhizosphere of the Wild Andean Blueberry (*Vaccinium floribundum* Kunth)	**Milton Gordillo** *Universidad San Francisco de Quito* *Ecuador*
10:30 – 11:00	COFFEE BREAK	LOBBY – SHAKESPEARE THEATER
11:00 - 11:30	**INVITED TALK** The call of the wild: Disentangling the mechanism of green foxtail microbiome for plant health	**Chunxu Song** *China Agricultural University* *China*
11:30 - 11:45	Uncovering Metabolic Interactions Between Bacterial and Fungal Microbial Communities in Arabidopsis root microbiota Using a High-Throughput 3D Printed Multichannel Bioreactor System	**Guillaume Chesneau** *Max Planck Institute for Plant Breeding Research* *Germany*
11:45 - 12:00	The rhizosphere microbiome of wild tomato in its center of origin	**Stalin Sarango flores** *Netherlands Institute of Ecology* *Leiden University* *The Netherlands*
12:00 – 13:45	LUNCH	CAMPUS USFQ

4th Plant Microbiome Symposium



Tuesday August 1st

Session 2: Microbiome-associated plant phenotypes: Abiotic & biotic stress tolerance

Time	Lecture	Speaker
13:45 - 14:30	**KEYNOTE LECTURE** Utilizing *Chlamydomonas* to elucidate bacterial antagonism of plants	**Omri Finkel** *The Hebrew University of Jerusalem Israel*
14:30 - 14:45	Studies on root-associated ACC deaminase Pseudomonas strains under osmotic stresses	**Susan Mosquito** *Rothamsted Research United Kingdom*
14:45 - 15:00	A walk on the wild side: exploring the functional potential of Andean soil microbiomes to enhance tolerance of potato to late blight disease	**Dario X. Ramirez-Villacis** *Netherlands Institute of Ecology Utrecht University The Netherlands*
15:00 - 15:15	Impact of the fungal pathogen *Fusarium oxysporum* on the taxonomic and functional diversity of the common bean root microbiome	**Lucas William Mendes** *Center for Nuclear Energy in Agriculture University of Sao Paulo Brazil*
15:15 - 15:30	Downy-mildew associated resistobiomes	**Jelle Spooren** *Utrecht University The Netherlands*
15:30 – 16:00	**COFFEE BREAK**	**LOBBY – SHAKESPEARE THEATER**
16:00 - 16:30	**INVITED TALK** Identification and characterization of plant biostimulants from amphibians' skin	**Mario Serrano** *Universidad Nacional Autónoma de México Mexico*
16:30 - 16:45	*Pseudomonas brassicacearum* control of the Root rot pathogen *Aphanomyces euteiches* via a novel nitroimidazole antibiotic	**Zayda Morales Moreira** *University of British Columbia Canada*
16:45 - 17:00	Effects of soil conditions on microbial communities associated with native plants in the hyper-arid core of the Atacama Desert	**Jonathan Fortt** *Universidad Católica del Norte Chile*
17:00 - 17:15	Volatile-mediated bacterial recruitment in the rhizosphere of tomato plants under an aboveground herbivory stress	**Muhammad Syamsu Rizaludin** *Netherlands Institute of Ecology The Netherlands*
17:15 – 19:15	**POSTER SESSIONS**	**1ST FLOOR – HAYEK BUILDING**

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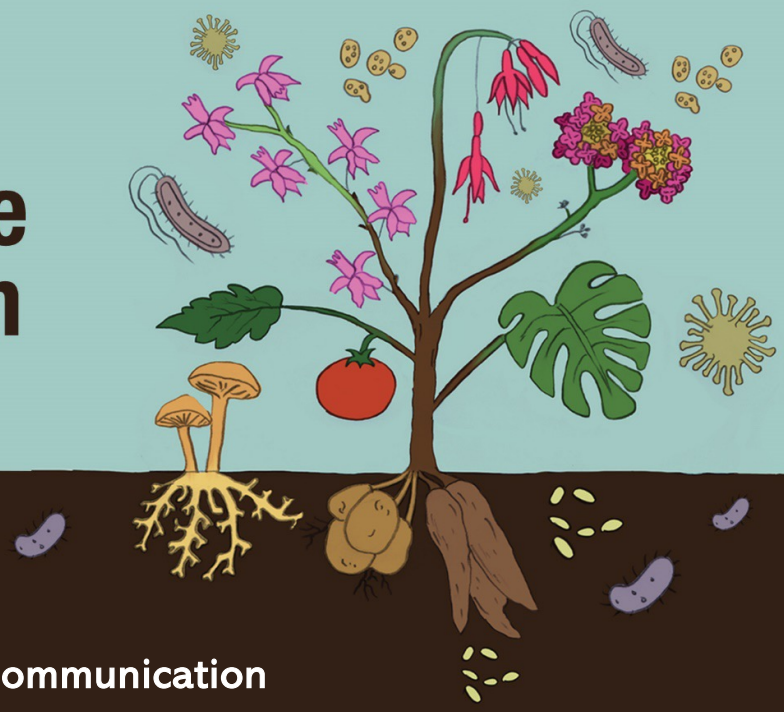
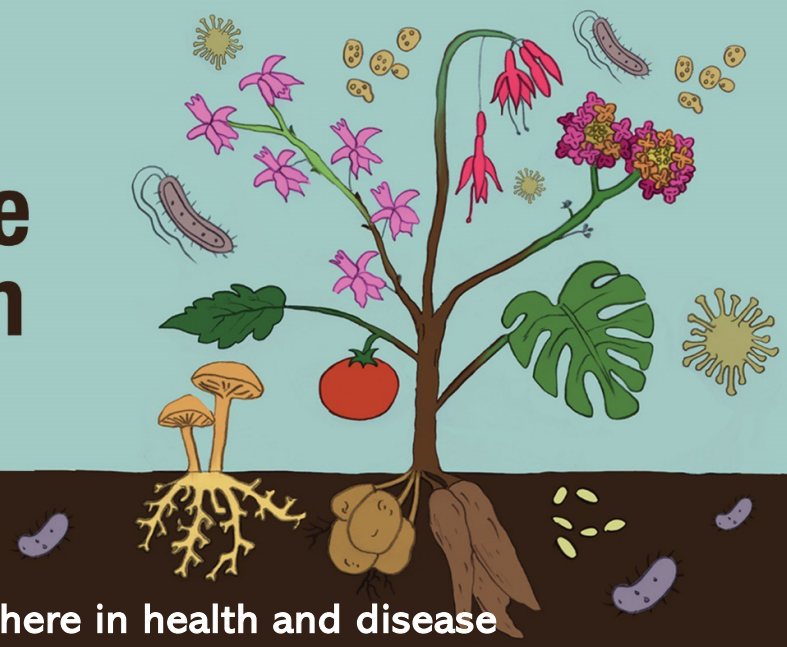


Wednesday August 2nd

Session 3: Plant microbiome communication

Time	Lecture	Speaker
08:30 - 09:15	**KEYNOTE** Coumarin communication along the microbiome-root-shoot axis	**Corné Pieterse** *Utrecht University* *The Netherlands*
09:15 - 09:30	The key role of mannitol and mannitol utilization cluster (*mtl*) genes in biofilm formation and plant root attachment by the plant growth-promoting *Pseudomonas granadensis* CT364	**Eva Cea Torrescassana** *Newcastle University* *United Kingdom*
09:30 - 09:45	Identification of specialized root exudates associated with microbiome assembly of wild and domesticated tomato	**Jie Hu** *Netherlands Institute of Ecology* *NIOO-KNAW* *The Netherlands*
09:45 - 10:00	Impact of Bacillus subtilis eps and TasA genes defective on rhizosphere microbiome assembly of tomato	**Caroline Sayuri Nishisaka** *EMBRAPA Environment / ESALQ /* *Universidade do Sao Paulo* *Brazil*
10:00 – 10:30	**COFFEE BREAK**	**LOBBY – SHAKESPEARE THEATER**
10:30 - 11:00	**INVITED TALK** Microbiome-plant conversation in the rhizosphere	**Rodrigo Mendes** *EMBRAPA Environment* *Brazil*
11:00 - 11:15	Aphid infestation changes metabolic activity and composition of bacterial communities in the wheat rhizosphere	**Sandra Cortés-Patiño** *Rothamsted Research* *The University of Nottingham* *United Kingdom*
11:15 - 11:30	Identification of the conserved iol gene cluster involved in rhizosphere competence in Pseudomonas	**Juan José Sánchez Gil** *Utrecht University* *The Netherlands*
11:30 - 11:45	Bacillus modulates key developmental traits and production of secondary metabolites in response to the plant cell wall polymer pectic homogalacturonan	**Farah Boubsi** *TERRA Teaching and Research Center* *University of Liège* *Belgium*
11:45 – 13:30	**LUNCH**	**CAMPUS USFQ**

4th Plant Microbiome Symposium



Wednesday August 2nd

Session 4: The plant phyllosphere in health and disease

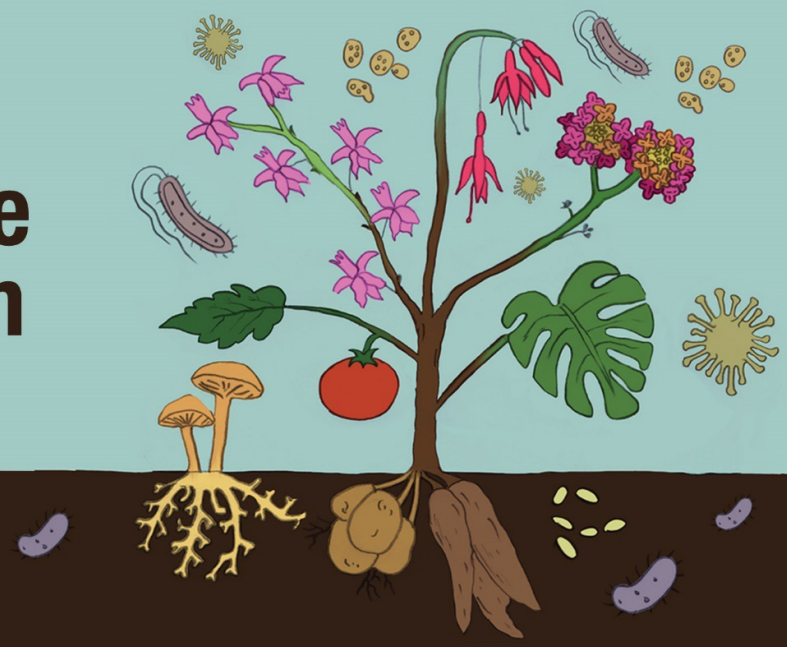
Time	Lecture	Speaker
13:30 - 14:15	**KEYNOTE LECTURE** The plant phyllosphere in health and disease	**Britt Koskella** *University of California, Berkeley* *United States of America*
14:15 - 14:30	Ultra-high resolution amplicon sequencing reveals cross-kingdom antagonists and synergists driving fungal infections in the wheat phyllosphere	**Luzia Stalder** *University of Neuchâtel / ETH Zurich* *Switzerland*
14:30 - 14:45	Production and degradation of indole 3-acetic acid in the phyllosphere microbiome	**Johan Leveau** *University of California, Davis* *United States of America*
14:45 - 15:15	**INVITED TALK** Ecology and functional diversity of phyllosphere yeasts	**Viviane Cordovez da Cunha** *Netherlands Institute of Ecology* *The Netherlands*
15:15 - 15:30	Activity and diversity of prophages harbored by wheat phyllosphere bacteria	**Peter Erdmann Dougherty** *University of Copenhagen* *Denmark*
15:30 - 15:45	Genomics, transcriptomics and metabolomics of phyllosphere yeasts	**Linda Gouka** *Netherlands Institute of Ecology* *The Netherlands*
15:45 – 16:15	**COFFEE BREAK**	**LOBBY – SHAKESPEARE**

Session 5: Defining the ecological rules of plant microbiome

16:15 - 17:00	**KEYNOTE LECTURE** Defining the ecological rules of plant microbiome assembly	**Joana Falcao Salles** *University of Groningen* *The Netherlands*
17:00 - 17:15	Ecological and environmental drivers of virus co-infection in wild plant populations	**Hanna Susi** *University of Helsinki* *Finland*
17:15 - 17:30	Exploring plant invasion in the Galapagos Islands	**Antonio León Reyes** *Universidad San Francisco de Quito* *Ecuador*
17:30 - 17:45	Seed saving and microbiome cycling	**Mason Kamalani Chock** *University of California, Berkeley* *United States of America*
17:45 - 18:15	**INVITED TALK** *To be announced*	**George Kowalchuk** *Utrecht University* *The Netherlands*

4th Plant Microbiome Symposium

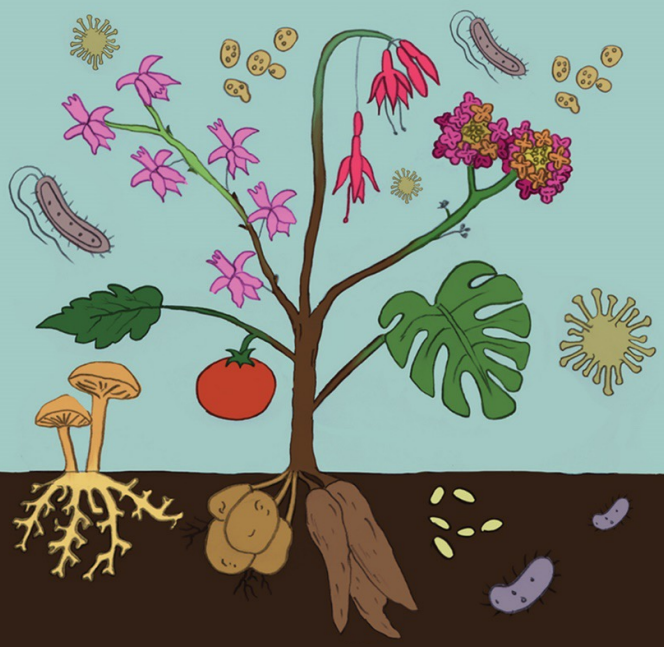
Thursday August 3rd



Session 6: Plant mechanisms to interact with beneficial microorganisms

Time	Lecture	Speaker
08:30 - 09:15	**KEYNOTE LECTURE** From microbiome to molecular analysis of plant microbe interactions	**Philip Poole** *University of Oxford United Kingdom*
09:15 - 09:30	The unsuspected mutualism between *Rhizophagus irregularis* and *Bacillus velezensis* confers enhanced biocontrol functionality	**Adrien Anckaert** *University of Liège Gembloux Agro-Bio Tech Belgium*
09:30 - 09:45	Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests	**Simon Roy Law** *Commonwealth Scientific and Industrial Research Organisation (CSIRO) - Australia*
09:45 - 10:00	The interplay of dual plant colonization by Soybean Mosaic Virus and arbuscular mycorrhizal fungi of field- and greenhouse-grown soybean plants	**Sietske van Bentum** *Utrecht University The Netherlands*
10:00 – 10:30	COFFEE BREAK	LOBBY – SHAKESPEARE THEATER
10:30 - 11:00	**INVITED TALK** Symbionts as filters of plant colonization of islands: Tests of expected patterns and environmental consequences in the Galapagos	**Jessica Duchicela** *Universidad de las Fuerzas Armadas Ecuador*
11:00 - 11:15	*Solanum tuberosum* Group Phureja endophyte microbiome characterization and its bacterial endophyte functionality against phytopathogens	**Estefania Peña-Zuniga** *Universidad San Francisco de Quito Ecuador*
11:15 - 11:30	”Cry for help” upon pathogen attack across the Brassicaceae family	**Melissa Uribe Acosta** *Utrecht University The Netherlands*
11:30 - 11:45	Characterization and biocontrol potential of a new *Bacillus nakamurai* strain isolated in Burundi	**François Nimbeshaho** *Gembloux AgroBio Tech Faculty University of Liège - Belgium*
11:45 - 12:15	**INVITED TALK** Putting microbiology to work: Enabling farmer-led ecosystem restoration through ecological literacy and farmer-led experimentation	**Stephen Sherwood** *Fundacion EkoRural - Ecuador Wageningen University The Netherlands*
12:15 – 14:00	LUNCH	CAMPUS USFQ

4th Plant Microbiome Symposium



Thursday August 3rd

4th PMS - SOCIAL PROGRAM:

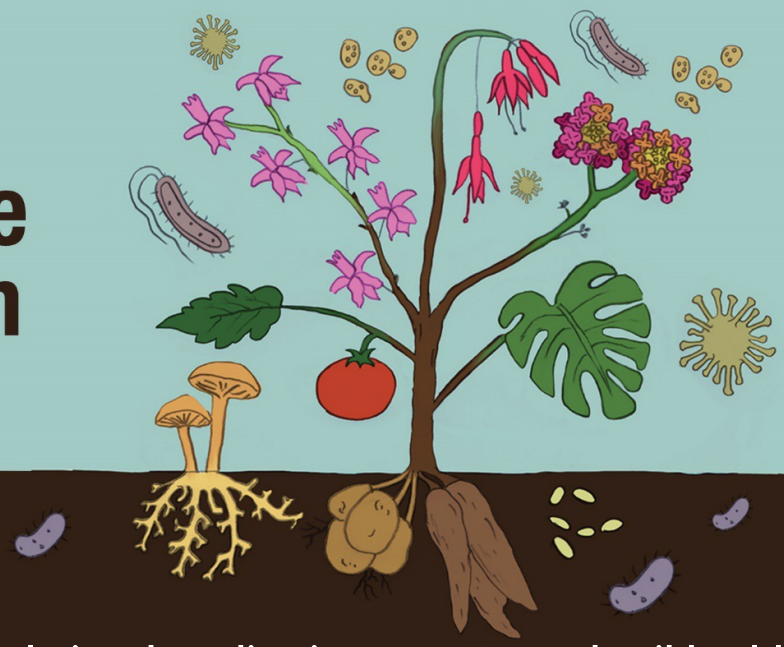
Time	Activity
14:00 - 15:15	Bus transfer to historic centre of Quito
15:15 - 17:30	Guided Quito City tour

17:30 - 18:00	Bus transfer to Social Evening at **PIM'S PANECILLO QUITO**
18:00 - 23:00	Conference Dinner and Social Evening at **PIM'S PANECILLO QUITO**

23:00	Bus transfer to hotels Quito

4th Plant Microbiome Symposium

Friday August 4th

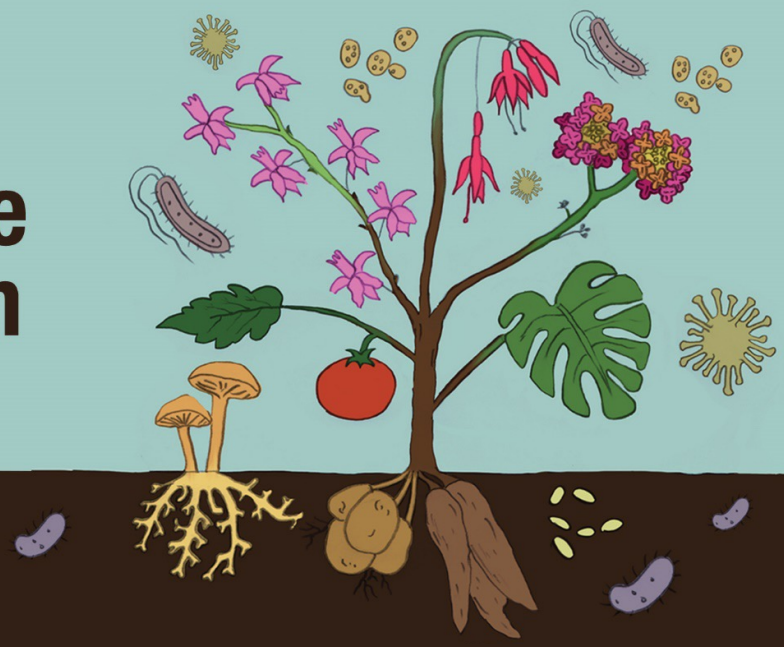


Session 7:
Technological advances and translational application to crops and soil health

Time	Lecture	Speaker
08:45 - 09:30	**KEYNOTE LECTURE** Soil microbiomes as a source of novel biosynthetic gene clusters and plant growth-promoting rhizobacteria	**Mark Liles** *Auburn University* *United States of America*
09:30 - 09:45	Probing the leaf micro-environment with whole cell yeast biosensors to establish principles of microbiome coexistence	**Julian A. Liber** *Duke University* *United States of America*
09:45 - 10:00	Rice straw recycling increased soil microbial functional diversity during the decomposition of rice straw	**Vanessa Otero Jiménez** *National University of Colombia* *Colombia*
10:00 - 10:15	The UK Crop Microbiome CryoBank Resource	**Payton Yau** *Scotland's Rural College (SRUC)* *United Kingdom*
10:15 - 10:30	Investigating the potential roles of plant microbial communities in the differential competitive ability between weedy and cultivated *Oryza sativa*	**Rachel Tavares** *University of Massachusetts Amherst* *United States of America*
10:30 – 11:00	COFFEE BREAK	LOBBY – SHAKESPEARE
11:00 - 11:15	Microbiome-based prediction of potato growth in the field	**Yang Song** *Utrecht University* *The Netherlands*
11:15 - 11:30	Plant-microbe and plant-plant interactions favouring iron content in crop plants	**Barbara Pivato** *Research for Agriculture, Food and Environment - INRAE* *France*
11:30 - 11:45	Grapevine Trunk Disease and the Fungal Mycobiome of Oregon Vineyards (USA)	**Jessie Zimmerman** *Oregon State University* *United States of America*
11:45 - 12:15	**INVITED TALK** Seed Transmitted Microbes are foundational to the Microbiomes of Crop Plants and have Agricultural Potential	**David Johnston-Monje** *Max Planck Tandem Group in Plant Microbial Ecology* *Universidad del Valle* *Colombia*
12:15 – 14:00	LUNCH	CAMPUS USFQ

4th Plant Microbiome Symposium

Friday August 4th



Special Closing Keynotes: *Plant microbiomes in a changing world*

Time	Lecture	Speaker
14:00 - 14:30	***SPECIAL CLOSING KEYNOTE*** *Plant Microbiomes in a changing world*	**Tsai Siu Mui** *Center for Nuclear Energy in Agriculture* *University of Sao Paulo* *Brazil*
14:30 - 15:00	***SPECIAL CLOSING KEYNOTE*** *Plant Microbiomes in a changing world*	**Gilles van Wezel** *Leiden University* *The Netherlands*
15:00 - 15:45	**CLOSING CEREMONY**	

15:45 – 17:00 FAREWELL DRINKS **TO BE ANNOUNCED**

4th Plant Microbiome Symposium

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USFQ Colegio de Ciencias Biológicas y Ambientales

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USFQ Instituto de Microbiología

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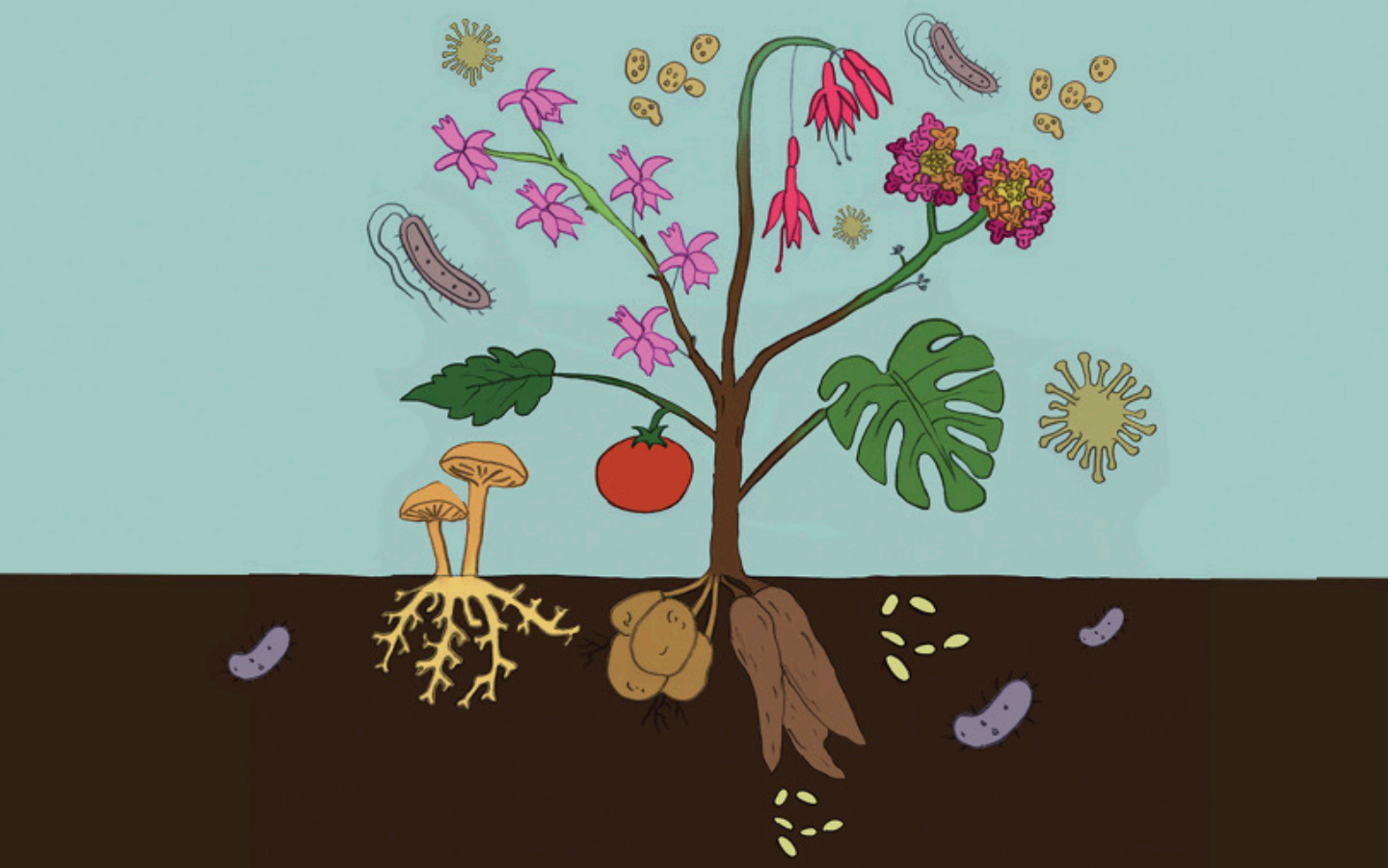

4th Plant Microbiome Symposium

KEYNOTE SPEAKER BIOGRAPHIES

KEYNOTE SPEAKERS

JOS RAAIJMAKERS

Jos Raaijmakers is head of the Microbial Ecology Department at the Netherlands Institute of Ecology (NIOO-KNAW) and Professor at the Institute of Biology at Leiden University. He is a member of the Royal Netherlands Academy of Arts & Sciences and a board member of the PhD graduate School PE&RC. The overall goal of his research program is to unravel the impact of plant domestication on the diversity and beneficial functions of microorganisms associated with plants. In this search for 'missing plant microbes', we work closely together with research institutes and universities in the centres of origin of plant species (Africa, Asia, South America). The functions of the plant microbes studied in detail are protection of plants against infections caused by fungal pathogens, parasitic weeds and insects. Jos teaches BSc and MSc courses at Leiden University and organizes (inter)national PhD courses and conferences, including the International Plant Microbiome conference

BRITT KOSKELLA

Britt Koskella is an Associate Professor of Microbial Ecology and Evolution at the University of California, Berkeley. With a Ph.D. in Ecology and Evolution, her research focuses on plant-microbiome, plant-pathogen, and bacteria-phage interactions. She combines theoretical frameworks with cutting-edge techniques to understand microbiome establishment, within-microbiome interactions, and the role of microbiota and phages in disease. Britt has published notable studies on phyllosphere microbial associations, within-host adaptation, and water stress effects on phyllosphere microbiomes. Her work advances our understanding of ecological and evolutionary principles and informs disease management strategies.

KEYNOTE SPEAKERS

CORNÉ PIETERSE

Corné Pieterse is professor Plant-Microbe Interactions and scientific director of the Institute of Environmental Biology of the Faculty of Science. His research group investigates how the plant immune system protects plants against microbial pathogens and inset herbivores, and how beneficial microbes in the plant root microbiome stimulates plant growth and health. In 2022, Corné Pieterse and his team received the Spinoza Prize. Worldwide, plant diseases and pests cause yield losses of up to 25%. With their research, the Plant-Microbe Interactions group aims to contributes to grand societal challenges, such as food security and sustainable agriculture.

OMRI M. FINKEL

Omri M. Finkel is a Senior Lecturer (Assistant Professor) at the Department of Plant and Environmental Sciences at The Hebrew University of Jerusalem. With a Ph.D. in Environmental Sciences from the Hebrew University of Jerusalem, his research focuses on plant-microbe interactions, microbial ecology, and metagenomics. During his postdoctoral studies in the Dangl lab at UNC Chapel Hill and HHMI from 2014 to 2020, Omri made significant contributions to the field. His research on the role of a single bacterial genus in maintaining root development in a complex microbiome was published in Nature in 2020. He has also investigated the effects of soil phosphorous content on microbiota in relation to the plant phosphate starvation response, which was published in PLoS Biology in 2019. Omri's work on understanding and exploiting plant beneficial microbes was featured in Current Opinion in Plant Biology in 2017. Additionally, he has published studies on bacterial adaptation in the phyllosphere of a salt-secreting desert tree and diversity patterns of phyllosphere bacteria on Tamarix trees across the Sonoran Desert. As a Senior Lecturer at The Hebrew University of Jerusalem, he continues to advance our understanding of plant-microbe interactions and microbial ecology.

KEYNOTE SPEAKERS

JOANA FALCAO SALLES

Joana Falcao Salles is a full professor in Microbial Community Ecology at the Groningen Institute for Evolutionary Life Sciences (GELIFES) at the University of Groningen, the Netherlands. She is also a member of the executive board of the International Society for Microbial Ecology (ISME) since 2020 and an Honorary Professor at the University of Nanjing, China. Her research line uses ecological and evolutionary theory to unravel the causes and the consequences of free-living and host-associated microbial communities. She addresses her research topics in a range of habitats (agricultural soil, salt marshes soils) and hosts (plants, arthropods, birds, mice, and humans) by combining experimental procedures (field, microcosm, mesocosm, manipulative experiments), modeling, microbiological and molecular techniques, metagenomic and bioinformatic approaches, to address both fundamental and applied questions (agriculture, biobased economy). She has coordinated several projects and published over 100 papers in peer reviewed journals

PHILIP POOLE

Philip Poole is Professor of Plant Microbiology in the Department of Biology, University of Oxford and a Senior Research Fellow at Somerville College. Philip's research focuses on bacterial genetics and molecular biology of plant-associated bacteria, exploring the physiology of bacterial growth, survival in the rhizosphere and how bacteria establish symbiotic interactions with plants, including root attachment and colonisation. A further focus of his work is the physiology and biochemistry of nitrogen fixation in legume nodules.

KEYNOTE SPEAKERS

MARK LILES

Mark Liles is an Associate Dean for Research and Graduate Studies, College of Sciences and Mathematics, Auburn University. He has a BS in Biology at Tulane University, PhD in Microbiology at Northwestern University and a Postdoc: University of Wisconsin-Madison, mentors Prof. Jo Handelsman and Prof. Robert Goodman. His research group has an interest in three primary areas: 1) Metagenomic Analysis of Microbial Assemblages. We use a metagenomic approach to study complex microbial assemblages in different environments, especially for natural products (enzymes, metabolites) encoded by environmental metagenomes. 2) Biological control of disease using beneficial microorganisms. They are investigating the natural products produced by these probiotics that can enhance growth performance of the animal or plant host or inhibit the growth of pathogenic microorganisms. 3) Pathogenesis and control of virulent *Aeromonas hydrophila*, thereby helping the worldwide community of aquaculture researchers track the distribution and spread of virulent *Aeromonas hydrophila*

TSAI SIU MUI

Tsai Siu Mui is director of Center for Nuclear Energy in Agriculture CENA/USP. She is a member of the Management Committee of the Agribusiness Sectorial Fund as a representative of the academic-scientific sector of the MCTI-DF. Recipient of the Scientific and Technological Merit Medal, the 2008 Scopus Award and the 2050 Agribusiness Challenge Award (FAO). Elected full member of the Brazilian Academy of Sciences in May 2008. Areas of Study: Agronomy, with emphasis on Microbiology and Molecular Microbial Ecology, working mainly on the following topics: plant-microorganism interaction, symbiosis, molecular markers, genome sequencing, genes of plant defense, microbial biodiversity with emphasis on analysis of microbial community structures, bioindicators of soil quality as a function of land use conversion with a focus on biogeochemical cycles. Studies with common bean focus on the determination of tolerance to water stress in elite genotypes in association with microsymbionts.

KEYNOTE SPEAKERS

GILLES VAN WEZEL

Gilles van Wezel is Professor of Molecular Biotechnology and Director of the Institute of Biology, Leiden University, The Netherlands. He is also Honorary Fellow at the Royal Academy institute NIOO-KNAW in Wageningen. Van Wezel is member of the board of the Netherlands Antibiotic Development Platform (NADP) of the Ministry of Health and of the supervisory board of Netherlands Centre for One Health (NCOH). In 2000, he was awarded a research fellowship from the Royal Netherlands Academy (KNAW) and became assistant professor in 2004. He co-founded the Biotech company Mycobics BV and was the CSO (2001-2010). In 2009 he obtained a VICI fellowship and was appointed full professor in 2010. He received an ERC Advanced grant in 2022 and also coordinates several large research consortia, including the EU H2020 network MARBLES on marine microbes and natural products and NACTAR on novel antibiotics. His laboratory primarily focuses on the Actinobacteria, which are multicellular mycelial bacteria that are widespread in soil and marine environments. Actinobacteria are known as Nature's medicine makers and produce two-third of all known antibiotics and many other molecules with medical application. Aim is to go beyond the known horizons and provide novel insights into the regulatory pathways that control growth, development and antibiotic production of the actinomycetes, and to understand how cells cooperate and differentiate within multicellular systems. An important aspect is the role of Actinobacteria in the microbiome of plants and humans and investigate how they can support health of the host.

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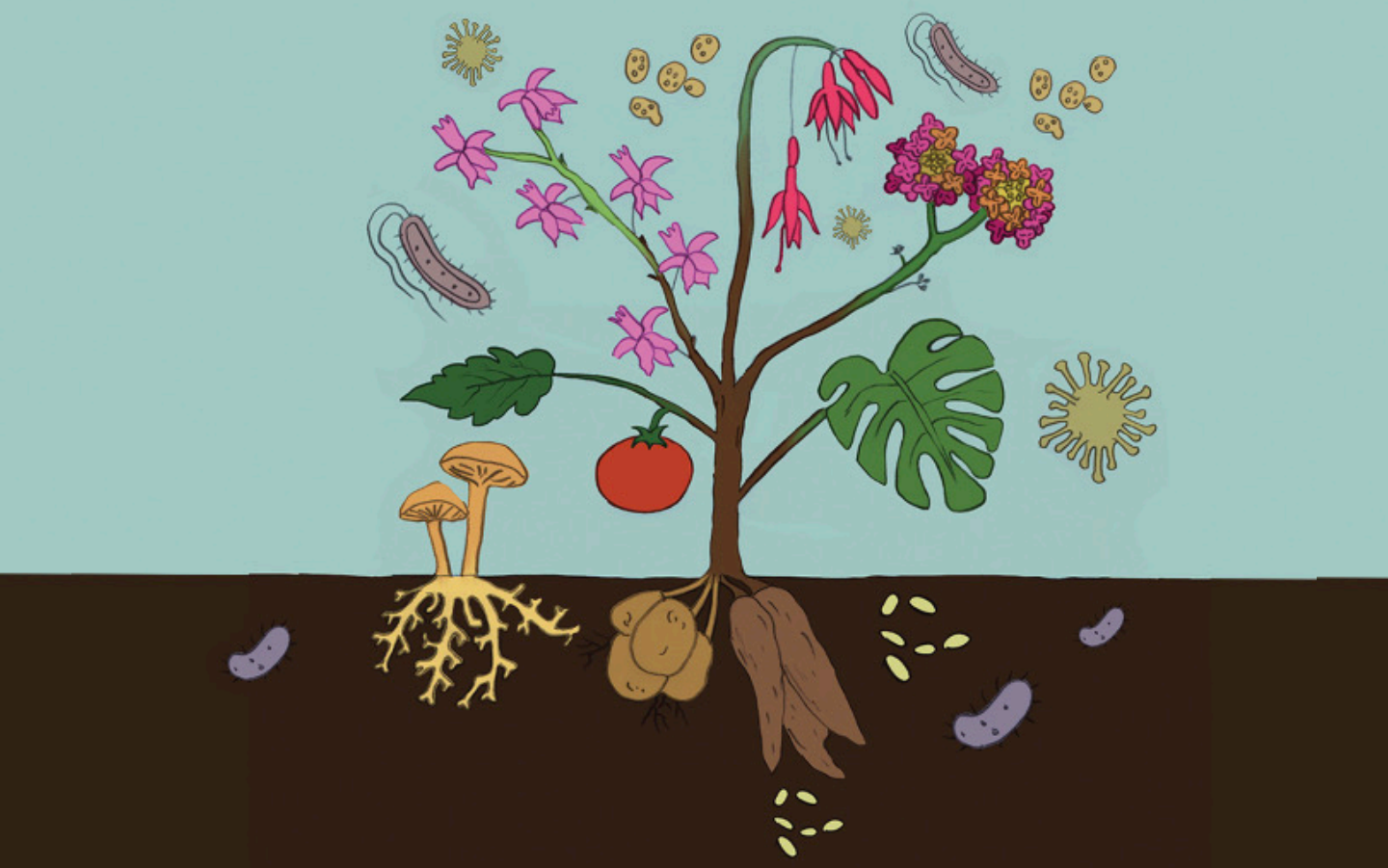
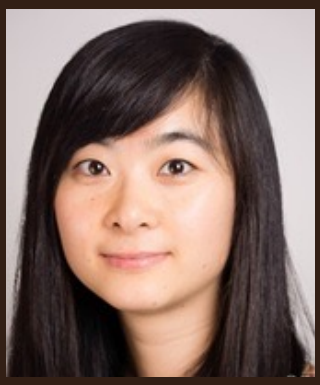


4th Plant Microbiome Symposium

INVITED SPEAKER BIOGRAPHIES

INVITED SPEAKERS

CHUNXU SONG



Chunxu Song is an Associate Professor at China Agricultural University. She has a MSc. iBiochemistry and molecular biology at Huazhong Agricultural University of China and a PhD. in Phytopathology at Wageningen University of the Netherlands. Her main research interest is on deciphering the impact of domestication on foxtail millet microbiome under natural habitat and (a)biotic stresses conditions. Specifically, on how beneficial phyllosphere and rhizosphere microbes can promote plant growth, stimulate plant chemistry, and contribute to plant health.

GEORGE KOWALCHUK

Prof. Kowalchuk heads the Ecology and Biodiversity research group at Utrecht University, which focuses on the development, maintenance and functioning of biodiversity, as determined by ecological processes and interactions with atmosphere, water and soil. His own multifaceted research program is centered around environmental and rhizosphere microbiology in the context of global change. Specific research foci include environmental genomics of ecologically relevant micro-organisms, rhizosphere ecology, molecular community analysis of bacterial and fungal communities, microbial diversity in the rhizosphere, interactions between aboveground and belowground biota, effects of genetically modified plants on soil communities, and roles of plant-microbe interactions in C and N cycling. Much of this work is related to the development and application of novel molecular and genomics approaches to gain insight not only into the diversity, but also the functions, of the largely unexplored soil microbial communities. Via his personal Vici grant “Crossing the frontiers of microbial ecology”, research is conducted to help unravel the fundamental patterns of microbial diversity, by applying emerging genomics toolboxes to the study of microbial diversity at scales from the individual microbe to the globe. In various other projects, more strategic approaches are taken to examine the role of soil microorganisms in a changing world and their potential in help facilitate the biobased economy.

INVITED SPEAKERS

JESSICA DUCHICELA

Jessica Duchicela, Ph.D., is an Associate Professor of Ecology at Universidad de las Fuerzas Armadas - ESPE in Ecuador. Her research focuses on the interaction between arbuscular mycorrhizal fungi (AMF) and vascular plants, studying their role in nutrient uptake and stress response. With an M.S. and Ph.D. in Ecology from Indiana University, she is also a Scientist and Coordinator of Research and Outreach at ESPE's Biotechnology Engineering School. Dr. Duchicela collaborates with government agencies and has published influential studies on mycorrhizal fungi in various ecosystems. Her work sheds light on the diversity of soil microbes and their implications for ecosystem management and restoration. She has received national and international recognition, including the Matilde Hidalgo Junior Scientist Award and Fulbright Faculty Development Grant.

RODRIGO MENDES

Rodrigo Mendes is visiting scientist at Berkeley Lab, University of California Berkeley, research scientist at Embrapa Environment and professor in the Agricultural Microbiology Graduate School at the University of São Paulo. Former Head of Research and Development Department at Embrapa Environment (2015 to 2022). Graduated in Agronomic Engineering with Ph.D. in Genetics and Plant Breeding from the University of São Paulo, Brazil. He worked as a researcher at CanaVialis/Monsanto and at Wageningen University (NWO Postdoctoral Fellow). He was a visiting researcher at the University of Lausanne, Switzerland, at Lawrence Berkeley National Lab, United States, at Rothamsted Research, United Kingdom, and at the Isaac Newton Institute at Cambridge University, United Kingdom. Member of the scientific advisory board of the Promise Program (NIOO-KNAW), Bill & Melinda Gates Foundation, and executive secretary of the International Research Program "Back to the Roots". His research focus on soil and plant microbial communities to understand how the rhizosphere microbiome promotes plant growth and protection

INVITED SPEAKERS

MARIO SERRANO

Mario Serrano is an Associate professor at Centro de Ciencias Genómicas. Universidad Nacional Autónoma de México. Cuernavaca Morelos, México. The line of research of his group is the characterization of innate immunity to the necrotrophic fungus *Botrytis cinerea*. The project is based on the identification and characterization of the molecular elements that link the degradation of the cuticle and the induction of innate immunity in plants. To achieve this goal, the *Arabidopsis thaliana-Botrytis cinerea* interaction model and traditional genomics and chemical genomics tools are used. Likewise, in recent years we have focused on the isolation and molecular characterization of biocontrol of *Botrytis cinerea* from the microbiota of plants and animals

STEPHEN SHERWOOD

Stephen Sherwood (B.Sc. Penn State, M.P.S. Cornell, and Ph.D. Wageningen University) is an external researcher and guest lecturer at Wageningen's Knowledge, Technology, and Innovation Group. His formal academic training is in adult education, plant pathology, and the sociology of change. Previously, he was the Andes Regional Director at World Neighbors. He also has held positions at the International Potato Center (CIP) and Central America Coordinator at the Cornell International Institute for Food, Agriculture, and Development (CIIFAD). Steve's academic contributions center on knowledge in practice, especially in the household, on the streets, and in social movements. Steve has lived and worked in Latin America (Nicaragua, Honduras, Guatemala, Bolivia, Peru, and Ecuador) for 30 years and is co-founder of several agroecology and grassroots development initiatives. Steve and his wife own a family-run organic farm and CSA in Ecuador, Granja Urkuwayku, where they work with members of national and regional grower and consumer food movements. Steve's research addresses the rising uncertainties associated with modernization in agriculture and food, examining people's self-organized, self-harmful organization, as in mass pesticide poisoning, the erosion of seed systems and genetic diversity, overweight/obesity, and the proliferation of associated non-communicable, chronic diseases. Currently, Steve is leading a research program in human-nonhuman inter-subjectivity in soil management and emergent food networks to enable more regenerative agriculture and food in the highland Andes.

INVITED SPEAKERS

VIVIANE CORDOVEZ DA CUNHA

Over the past 10 years, Viviane Cordovez's research has focused on the impact of plant-associated microorganisms on plant growth and health by coupling culturomic, metabolomic and genomic approaches. Currently, she is leading a research project on the diversity and functions of yeasts associated with plant leaves. In particularly, she explores their spatial and temporal distribution, interactions, and genomes to get insight into their ecology as well as their potential for crop protection against pathogens. She is also involved in different international consortia investigating the impact of plant domestication on the microbial community composition and functions.

DAVID JOHNSTON-MONJE

David Johnston-Monje has an undergrad in chemical ecology of medicinal plants with John Arnason at the University of Ottawa, a M.Sc. in wood genetics at the University of British Columbia with the late Carl Douglas and a PhD with Manish Raizada at the University of Guelph in microbial ecology of maize. He has also been a visiting scientist at Biodiversity International, the International Potato Research Institute in Peru, at EMBRAPA Agrobiology in Brazil and most recently at the International Center for Tropical Agriculture in Colombia. His post-doctoral research with George Lazarovits at the company A&L Biologicals focused on discovering what causes an emerging disease called tomato vine decline. Having discovered the most abundant parts of the maize microbiome are transmitted through seed he was recruited to help start the endophyte focused company Indigo Agriculture in Boston, where he lead efforts to bioprospect for beneficial microbes, analyze plant microbiomes, develop inoculant formulations for seeds, and assay plant-microbe interactions in field trials. Most of Indigo Agriculture's patents are based on his research, which laid the foundation for it to become the most well-funded agricultural startup company ever. David currently works as Principle Investigator and Max Planck Tandem Group Leader at Universidad del Valle in Cali, Colombia, cooperating with Paul Schulze-Lefert at the MP Institute for Plant Breeding Research in Cologne, Germany.

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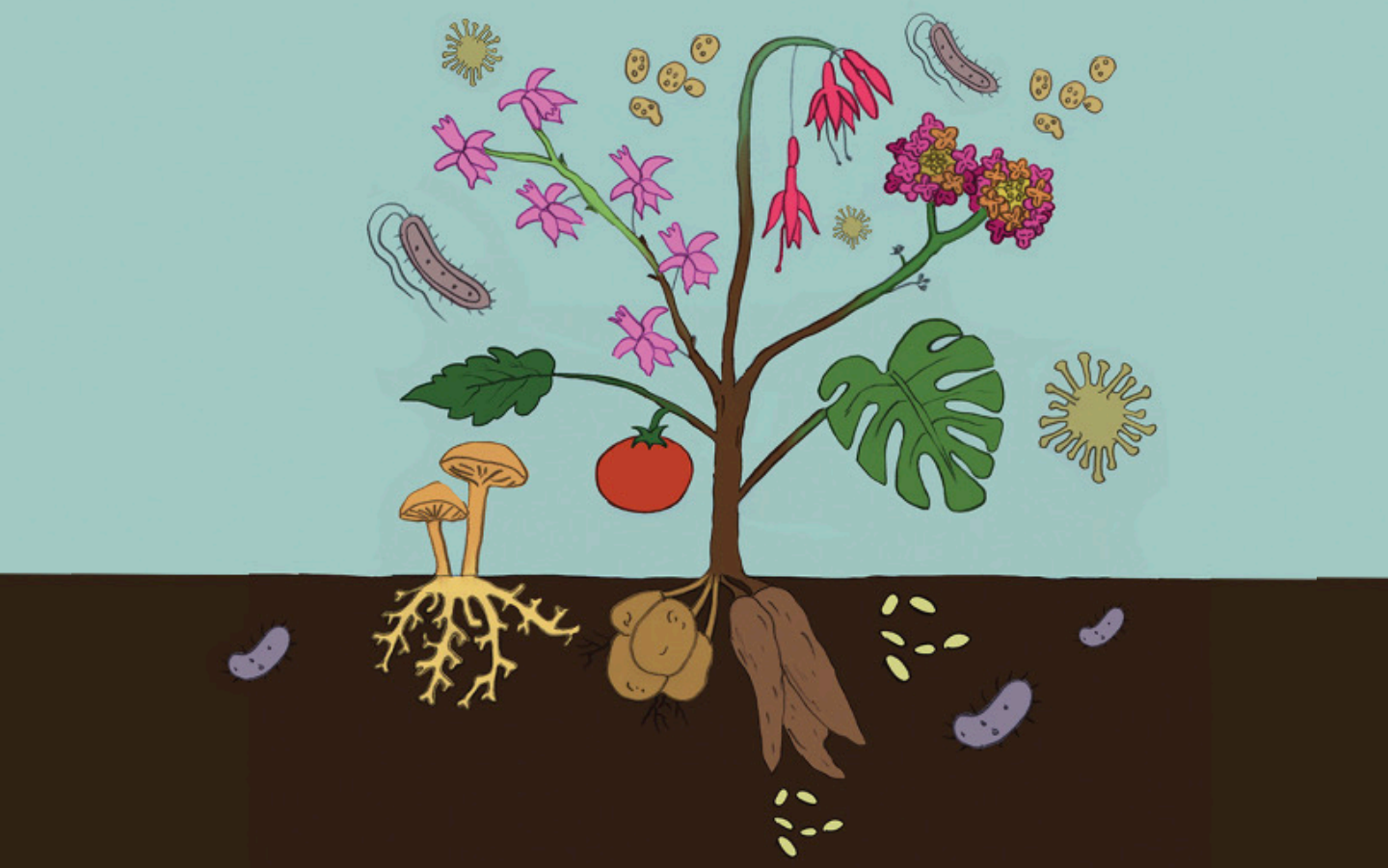

4th Plant Microbiome Symposium

KEYNOTE SPEAKER ABSTRACTS

SESSION 01 - KEYNOTE

Breaking the witches' spell

Raul Masteling[1,7], Dorota Kawa[2], Urgesa Tsega[3], Sewunet Abera-Dinke[3], Getahun Mitiku-Benti[3], Benjamin Thiombiano[4], Mahdere Shimels[1], Desalegn Etalo[1], Luisa Arias-Giraldo[1], Dominika Rybka[1], Somayah Elsayed[7], Mariana Avalos[7], Gilles van Wezel[7], Shelley Lumba[8], Jeroen Dickschat[9], Pedro Crous[5], Lorenzo Lombard[5], Ewald Groenewald[5], Tamera Taylor[2], Marcio Leite[1], Francisco Dini-Andreote[6], Eiko Kuramae[1], Harro Bouwmeester[4], Taye Tessema[3], Siobhan M Brady[2], Wietse de Boer[1], **Jos M Raaijmakers[1,7]**

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[2]Department of Plant Biology and Genome Center, University of California, Davis, USA
[3]Ethiopian Institute of Agricultural Research, Holeta, Ethiopia
[4]Plant Hormone Biology Group, University of Amsterdam, Amsterdam, the Netherlands
[5]Westerdijk Institute of Fungal Biodiversity, Utrecht, The Netherlands
[6]Department of Plant Science, The Pennsylvania State University, Pennsylvania, USA
[7]Institute of Biology, Leiden University, Leiden, the Netherlands
[8]University of Toronto, Toronto, Canada
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Striga is a genus of parasitic plants that pose major limitations on cereal production in Sub-Saharan Africa. This parasite, referred to as witchweed, infects the root system of a broad range of crop species, including sorghum, millet, maize, and upland rice. The development of effective strategies to control Striga has been a major focus of research in the past decades. Among the current approaches with most impact are those based on agricultural practices (e.g., push-pull), resistance breeding and chemistry. To date, however, none of these strategies is singularly effective on different crops and across a diverse range of agroecosystems. In the PROMISE (Promoting Microbes for Integrated Striga Eradication) program, we focused on characterizing microbial communities associated with Striga and the host plant sorghum to understand their role in the life cycle and infection process of this root parasitic weed. More specifically, we studied a diversity of mechanisms by which soil and root-associated microorganisms could diminish the Striga seed bank or interfere with the early stages of root infection to enhance crop productivity. The experimental work ranged from studying the effects of edaphic factors on microbial community diversity and functioning across different Ethiopian agro-ecologies and sorghum cultivars to microbe-mediated changes of host root architecture, root exudation, and induction of Striga resistance. More specifically, we discovered the functional potential of soil and root-associated bacteria and fungi to i) disrupt the early stages of the parasite's life cycle through the production of volatile organic compounds, ii) cause Striga seed decay or suicidal germination, iii) degrade host-derived germination signals and haustorium-inducing factors, and iv) induce structural barriers (aerenchyma, suberin) in the host plant roots. In collaboration with local research institutes, we developed strategies to augment Striga-suppressive activities of indigenous soil microbial communities to achieve Striga suppression in greenhouse and field settings.

SESSION 02 - KEYNOTE

Utilizing Chlamydomonas to elucidate bacterial antagonism of plants

Omri Finkel, Tzlia Vikiniansky, Elad Meilin, Michal Breker

Department of plant and environmental sciences,
The Hebrew University of Jerusalem, Israel

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Keywords: Microbiome, antagonism, model systems

The descent of land plants occurred in a world already populated by microbes. Many of these preexisting microbial taxa adapted to this new reality by forming close, both beneficial and harmful, interactions with plants, thus giving rise to what is known as the plant microbiome. Since land plants are descendants of green algae, it is reasonable to hypothesize that the plant microbiome is similarly descended from the phycosphere microbiome – microbial assemblages typically associated with algae. Therefore, by focusing on the phycosphere microbial milieu, we can (i) identify the modes of interaction at the deep evolutionary root of plant-microbe interactions and (ii) utilize the unicellular green algae Chlamydomonas reinhardtii as a powerful simplified model system for the plant microbiome.

In this study, we aimed to identify evolutionarily conserved mechanisms of bacterial antagonism towards plants. To this end, we implemented multipronged, unbiased approaches we developed or adopted in Chlamydomonas. We screened a collection of approximately 200 diverse bacterial strains isolated from Arabidopsis thaliana roots for antagonism against both Chlamydomonas and Arabidopsis. Our results showed that around 5% of the bacterial strains inhibited Chlamydomonas growth, and of these, 100% were also antagonistic towards Arabidopsis. These strains belonged to three taxonomically diverse bacterial genera: Pseudomonas, Burkholderia, and Paenibacillus. To measure the specificity of antagonism, we tested whether antagonistic strains would also affect Escherichia coli, Bacillus cereus and Saccharomyces cerevisiae. Our findings revealed that the Burkholderia strains are specifically antagonistic towards plants and algae, indicating a plant superkingdom-specific mechanism. Further investigations showed that Burkholderia antagonized algae through a contact-dependent secretion system. By using loss- and gain-of-function mutants in both bacteria and algae, we can pinpoint the exact mechanisms of antagonism.

Soils are home to numerous non-beneficial microbes that, while not causing acute diseases in the host, still hinder plant growth. Studying how such microbes interact with Chlamydomonas will provide a quick way to assess soil health and identify new approaches to enhance it.

SESSION 03 - KEYNOTE

Coumarin communication along the microbiome-root-shoot axis

Corné M.J. Pieterse[1], Shu-Hua Hsu[1], Pim Goossens[1], Alberto Pascale[1], Yang Song[1], Jelle Spooren[1], Max J.J. Stassen[1], Melissa Uribe-Acosta[1], Sietske Van Bentum[1], Gilles Vismans[1], Peter A.H.M. Bakker[1], Roeland L. Berendsen1, Ronnie De Jonge[1], Christian Dubos[2], Ioannis A. Stringlis[1,3]

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[2]BPMP, CNRS, INRAE, Institut Agro, University of Montpellier, Montpellier, France
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Keywords: Coumarins, induced systemic resistance, rhizosphere microbiome, root-shoot signaling

Plants accommodate a large community of microbiota on their roots and shoots, which in turn provide them with essential services, such as enhanced nutrient uptake, growth promotion, and protection against pathogens. Our research is focused on understanding plant-beneficial functions of the plant microbiome and the role of plant genes and traits that recruit these functions. We demonstrated that upon foliar infection by the downy mildew pathogen *Hyaloperonospora arabidopsidis*, Arabidopsis plants recruit a consortium of synergistic microbes to their roots and shoots that in turn provide protection against the foliar pathogen[1,2]. We identified the root-specific transcription factor MYB72 as a central regulator in this process[3]. Metabolomics of root exudates revealed that MYB72 controls the biosynthesis of iron-mobilizing coumarins, such as scopoletin, which are secreted in the rhizosphere where they aid in iron uptake and exert a selective antimicrobial activity[3,4]. Microbiome analysis of coumarin-deficient Arabidopsis mutants revealed that coumarins function in rhizosphere community assembly upon foliar pathogen infection, possibly to promote recruitment of protective microbiota[5]. Previously we demonstrated that coumarin biosynthesis mutant *myb72* and coumarin deglycosylation mutant *bglu42* cannot develop rhizobacteria-induced systemic resistance (ISR)[6]. Conversely, overexpression of beta-glucosidase BGLU42 results in constitutive broad-spectrum ISR. These results suggested that coumarins, which are mainly produced in the roots, may also act as mobile signals that are transported from the roots to the shoots to mediate systemic immunity. Recent data show that coumarins can indeed be transported from the roots to the shoots[7], where they may serve as players in the onset of ISR in the leaves, highlighting coumarins as central players in bi-directional communication along the microbiome-root-shoot axis[8]. Besides coumarins, other chemical and structural root defense barriers have emerged as players in plant-microbiome interactions[9] . Understanding the mechanistic basis of their role in mutually beneficial plant-microbiome interactions provides a firm knowledge basis for the development of future crops that maximize profitable functions from the root microbiome.

SESSION 04 - KEYNOTE

The plant phyllosphere in health and disease

Britt Koskella

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SESSION 05 - KEYNOTE

Defining the ecological rules of plant microbiome assembly

Joana Falcao Salles

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Keywords: Soil microbiome, bacterial invasion, inoculants, community assembly processes.

Soil microbial communities or microbiomes are incredibly diverse, with values ranging from 1000 to 1000000 unique species per gram of soil. These communities of overwhelming diversity are responsible for providing services such as recycling nutrients (carbon, nitrogen, etc.) that sustain soil biodiversity. A large percentage of the soil microbiome lives in close association with plant roots, providing unique functions beyond nutrient cycling – such as disease suppression, improved drought/salinity resistance, or the ability to modify flowering time – highlighting their potential to influence overall plant fitness. However, the increase in food production in the last century has led to the development of plants that rely heavily on external inputs (pesticides/inorganic fertilizers) rather than the soil microbiome. In this talk, I will explore the ecological principles that drive soil microbiomes and how this knowledge can promote plant-microbiome interactions. I will start by talking about principles that regulate the survival of inoculants (biocontrol, biofertilizer, and bioremediation agents) in soil by placing them in the context of bacterial invasions. Next, I will use microcosms and field data to demonstrate how we can use concepts of community assemblage (i.e., which processes regulate bacterial community structure) to improve inoculant survival in soils. Finally, I will explore how we can select crops that are better capable of interacting with the soil microbiome and how this understanding creates opportunities for developing sustainable agricultural practices that reduce agriculture's environmental footprint.

SESSION 06 - KEYNOTE

From microbiome to molecular analysis of plant microbe interactions

Philip Poole*, Beatriz Jorrin, Clare Cocker, Andrez Tkacz, Vinoy Ramachandran

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Colonisation by bacteria of the zone surrounding plant roots (rhizosphere) is crucial to plant productivity, with plants secreting 10-30% of total photosynthate to the rhizosphere. Microarray, RNAseq and metabolic analysis combined with InSeq analysis of growth in the rhizosphere, colonisation of roots, bacteroid formation and regrowth from nodules has been used to dissect the stages in root colonisation and N_2-fixation by *Rhizobium leguminosarum* in its interaction with pea. During infection of legumes the metabolic repertoire of rhizobia is dramatically restricted with a dramatic reduction in metabolic diversity in mature bacteroids (1-4). Here we Examine how nodulation alters the microbiome of legumes, with subtle changes in its composition but large changes in total microbial abundance (5). Next, we consider how large-scale competition experiments can be conducted to identify the rhizobia most competitive for legume nodulation from natural soil populations and a complete soil microbiome (6). This led us to consider how we could mark multiple members of the microbiome to examine root colonization and the dynamics of community assembly. This required the development of a multiple fluorescent marking system for up to six different bacteria that could then be tracked by microscopy or flow cytometry for facile quantification. Ultimately successful root colonisation is driven by root attachment and biofilm formation and in recent work we have established that rhizobia have an exquisitely tuned system for identifying and attaching to the newly emerging root elongation zone of roots. We suggest this is a key step for any plant microbe as the newly emerging elongation zone is probably the only part of the root not already colonised by competitors. Finally, we use the specific example of engineering nodulation in cereals to examine how plants can be engineered to manipulate the microbiome for their advantage and to develop mutualism (7-9).

SESSION 07 - KEYNOTE

Soil microbiomes as a source of novel biosynthetic gene clusters and plant growth-promoting rhizobacteria

Mark R. Liles[1,4], Maria Leticia Pacheco Da Silva[2], Francesco Moen[1], Oluwakemisola E. Olofintila[3], Haley Stephens[1], Zachary Noel[3], Alvaro Sanz-Saez[2], Don Johnson[4], Robb Stankey[4] and David Mead[4]

[1]Department of Biological Sciences, Auburn University, Auburn, AL, USA
[2]Department of Crop, Soil and Environmental Sciences
[3]Department of Entomology and Plant Pathology; [4]Terra Bioforge Corp, Middleton, WI

Key words: soil metagenome, biosynthetic gene clusters, plant growth promoting rhizobacteria, plant pathogens, secondary metabolites

Soil microorganisms encode a vast diversity of bioactive natural products. This presentation will discuss culture-dependent and -independent approaches in accessing diverse soil microbial genomes that can encode biosynthetic gene clusters that produce bioactive metabolites.

Metagenomic approach: A large-insert soil metagenomic clone library (~110kb and 19,200 clones) was constructed from an agricultural soil using a broad host range shuttle BAC vector, pSmartBAC-S. Identification of secondary metabolite biosynthetic gene clusters (BGCs) was conducted using multiple methods. The most inclusive method pooled BAC clones from 384-well plates in plates, rows and columns, and bar-coded DNA sequences from each pool were sequenced. Contigs were assembled from each pool and screened for BGCs using antiSMASH3.0. We identified 884 clones that contained a PKS and/or NRPS cluster among 1,910 total biosynthetic pathways identified. The cloned pathways are very divergent from known pathways, with the %G+C content varying from 34 to 79% and the nearest BLAST hit of keto-synthase domains ranging from 19 to 95% amino acid identity. BGC-containing BAC clones were conjugally transferred to a *Streptomyces coelicolor* M1154 strain engineered for heterologous expression of BGCs and screened for anti-infective activity against multiple multidrug-resistant pathogens. Clones expressing antimicrobial activity were characterized by LC/MS analysis.

(Continue on next page)

SESSION 07 - KEYNOTE

Culture-dependent approach: Plant growth-promoting rhizobacteria (PGPR) can enhance crop productivity, but field studies are highly variable in PGPR efficacy. A comparative genomic analysis of *Bacillus velezensis* PGPR strains found that all strains contained genes for pectin utilization, and could use pectin or a pectin-rich amendment such as orange peel (OP) powder as a carbon source.[1] Inoculation of soybean seeds with 10^6 CFU *B. velezensis* AP193 and 10 mg OP per seed resulted in soybean cultivar-specific responses, with some soybean cultivars having up to a 60% increase in root and shoot growth.[2] Among six *B. velezensis* strains tested in a greenhouse experiment, strains AP191, AP215, and AP216 showed the best results in plant growth promotion when supplemented with OP, and *B. velezensis* AP191 with OP significantly enhanced pod dry weight by 15.8%. A one-time soybean seed inoculation with AP191 and OP showed the greatest yield under field conditions, being the only treatment significantly different from the control treatment ($P < 0.05$; + 0.5 ton/ha), a 9.4% yield increase. Current studies are evaluating formulations of a synbiotic seed treatment to provide growth promotion and disease control activities.

CLOSING KEYNOTE

Plant Microbiomes in a changing world

Tsai Siu Mui

Center for Nuclear Energy in Agriculture, University of Sao Paulo, Brazil

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CLOSING KEYNOTE

Plant-microbe interactions as the basis for our future medicines

Gilles P. van Wezel

Institute of Biology, Leiden University, The Netherlands; Microbial Ecology, NIOO-KNAW, Wageningen, The Netherlands.

E-mail: g.wezel@biology.leidenuniv.nl

Microbes play a key role in the protection of their host against biotic and abiotic stresses. Metagenomic approaches have provided insights into the composition of the microbiomes of plants, humans and animals, with unprecendented detail. The challenge is to translate these enormous data collections into specific functions. Streptomycetes are known as Nature's medicine makers, and produce some two thirds of all known antibiotics and a range of other natural products and enzymes. Their hosts use this property to protect them against a range of diseases and stresses. The treasures that lie hidden in the genomes of streptomycetes and other actinomycetes may well be our final resource in the fight against the rapidly emerging multi-drug resistant pathogens, and at the same time can be harnessed for sustainable crop protection.

Many of the biosynthetic gene clusters (BGCs) for antibiotics are poorly expressed in the laboratory, while they are likely expressed in nature. We harness host-microbe interactions to activate antibiotic production. Where BigPharma has routinely screened bacteria in isolation, in nature bacteria live in complex communities with other organisms, and these often competitive interactions elicit specific responses involving the production of natural products. We discover novel antibiotics by combining multi-omics approaches, such as genome mining, transcriptomics, proteomics and metabolomics. We have discovered a range of chemical elicitors and growth conditions that allow the effective activation of silent BGCs for specialized metabolites.

Thus, understanding the ecological conditions under which antibiotic-producing streptomycetes live is a key factor in approaches to activate their production and discover novel bioactive molecules. This, combined with an efficient paired omics discovery platform, identified several novel bioactive molecules. Most recent advances and an outlook into the future will be presented.

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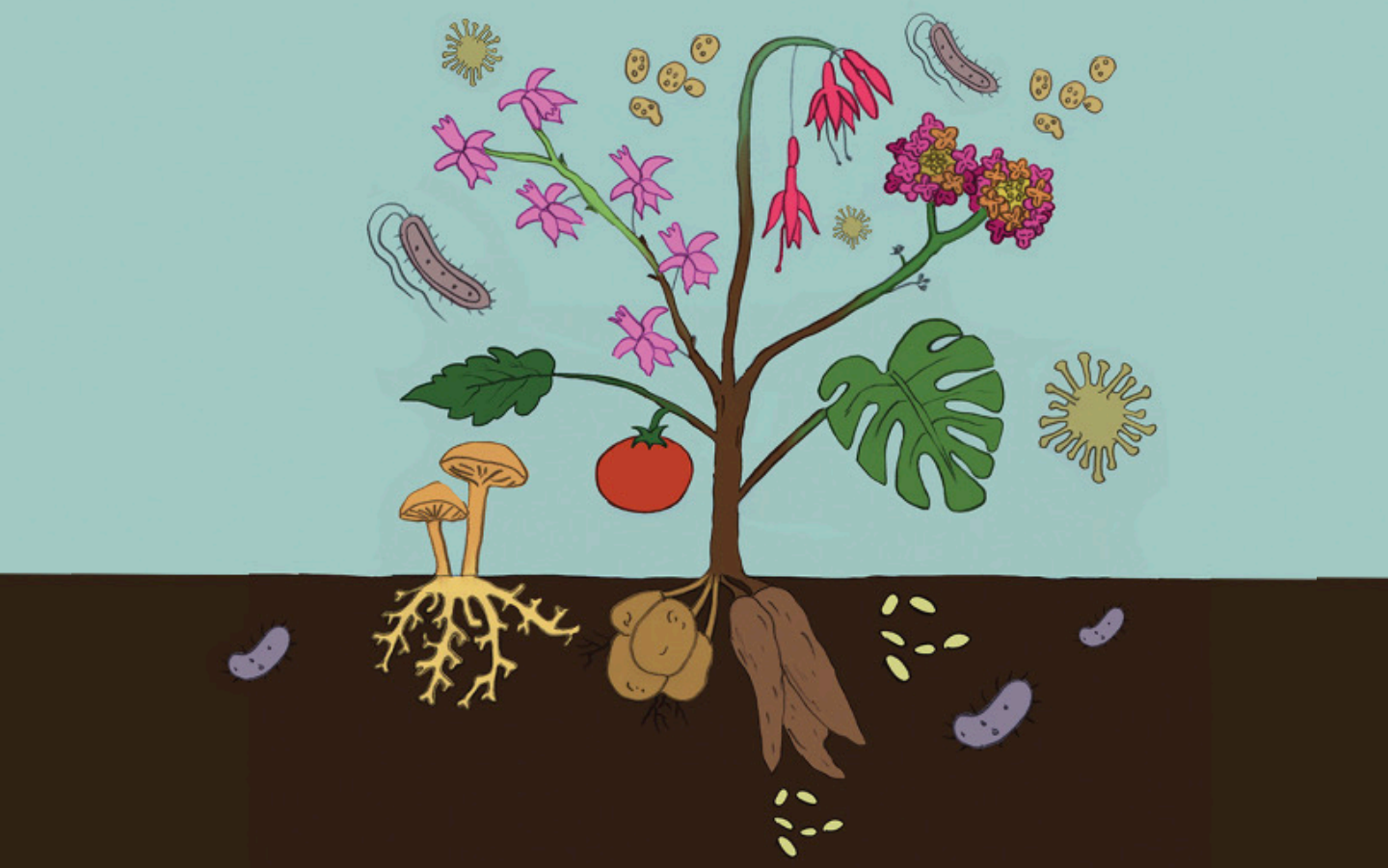

4th Plant Microbiome Symposium

INVITED SPEAKER ABSTRACTS

SESSION 01 – INVITED TALK

The call of the wild: Disentangling the mechanism of green foxtail microbiome for plant health

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Key words: C4 crops, *Setaria*, microbiome assembly, phyllosphere

The microbiome of C4 plants has garnered considerable attention in recent studies, with foxtail millet (*Setaria italica*), and its ancestor green foxtail (*Setaria viridis*) emerging as promising model plants for advancing microbiome research in C4 cereal and biofuel crops. However, the current understanding of their microbiomes, including assembly and functioning, remains limited. In this study, we conducted a comprehensive analysis of the phyllosphere microbial communities of green foxtail plants, the progenitor of foxtail millet, sampled from their natural habitats. Our findings revealed distinct diversity patterns among the phyllosphere microbial communities of green foxtail from different sites. Moreover, we observed variations in dominant taxa across the sites, which displayed correlations with environmental and climatic factors. The ecological dynamics of the phyllosphere bacterial and fungal communities were primarily governed by stochastic processes. Furthermore, we identified keystone/core taxa of bacteria and yeasts in the green foxtail phyllosphere, potentially involved in microbe-microbe interactions and the production of novel secondary metabolites. Lastly, intriguing insights into cross-kingdom collaboration influencing plant health were also observed. Overall, this study sheds light on the underexplored green foxtail microbiome and its ecological dynamics in the phyllosphere. These findings underscore the significance of further investigating foxtail millet for advancing microbiome research in C4 cereal and biofuel crops, presenting opportunities to address both fundamental and applied questions in the field.

SESSION 02 – INVITED TALK

Identification and characterization of biocontrol agents from amphibians' skin against *Botrytis cinerea*

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Key words: biocontrol, *Arabidopsis thaliana*, *Botrytis cinerea*, amphibians

Abstract

Plants are exposed to multiple organisms that can be both beneficial and pathogenic. One of the pathogens to which they are susceptible is the necrotrophic fungus *Botrytis cinerea,* which causes gray rot or gray mold disease. For many years, chemical fungicides have been used as infection control agents. However, their frequent use has been questioned because of their harmful effects on the environment and human health. This has led to the search for new ecological alternatives, such as the use of biological control agents (BCA) or biostimulants that can inhibit the growth and development of plant pathogens. Bacterial communities have been found to exist in the skin of frogs, which can protect them from infections caused by the fungus *Batrachochytrium dendrobatidis*, a pathogenic chytrid fungus implicated in worldwide amphibian declines. However, it is unclear whether these bacteria have the function of preventing and curing diseases caused by pathogenic fungi. In this work, we explored whether neotropical amphibian skin bacteria have the activity to control the development of the pathogen *B. cinerea.* Through dual experiments, we identified 3 potential candidates for biocontrol activity. In addition, the compounds released by the bacteria can inhibit the germination process of manner inhibition in a dose-dependent. We also observed that the bacteria and filtrates confer a protection system in the plants such as A. thaliana and *Solanum lycopersicum.* In addition, we identified that one of the bacteria produces transcriptional changes in growth hormone-related genes in *A. thaliana.* Our results showed that bacteria from amphibian skin may have excellent potential to control diseases caused by phytopathogenic fungi affecting plants.

SESSION 03 – INVITED TALK

Microbiome-plant conversation in the rhizosphere

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Key words: rhizosphere colonization, plant exudates, volatiles compounds, microbial interactions, microbiome assembly.

Complex microbial communities assemble in the surrounding soil of plant roots, where they intimately interact with the host plant. An active selection process is established by the host plant, leading to the enrichment of specific members of the soil microbiome in the rhizosphere. Some of these rhizosphere-competent microorganisms find their way into the inner root tissues, forming the endosphere microbiome. This presentation will focus on the key factors governing chemical communication between the microbiome and the plant. These factors include plant exudates, microbial volatile compounds, and secondary metabolites. The complexity of these interactions will be illustrated by examining how the rhizosphere microbiome protects the root system against soil-borne pathogens. When attacked by the soil-borne pathogen *Rhizoctonia*, sugar beet plants activate a recruited rhizobacterial community, enriching diverse bacterial taxa. The alteration in the microbiome's structure and functions in the presence of the pathogen serves as a shield for the root system, protecting the plant in the soil. Even when the pathogen successfully invades the roots, the endosphere microbiome responds to the invasion by triggering bacterial biosynthetic gene clusters capable of combating the intruder. Understanding the mechanisms underlying communication between the microbiome and the plant is key to enhance beneficial interactions. In conclusion, unraveling the intricate communication between the microbiome and the plant not only sheds light on the complex mechanisms at play in these interactions but also holds the potential to harness beneficial relationships for improved plant health and agriculture.

SESSION 04 – INVITED TALK

Ecology & functional diversity of phyllosphere yeasts

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Keywords: yeasts, phyllosphere microbiome, (a)biotic stresses, microbial interactions

Microorganisms living on and inside plant leaves have a largely unexplored functional potential which can expand the genomic capabilities of their host plant by providing nutrients, protection against pathogens, and enhanced tolerance to abiotic stress, such as drought. Despite the increasing recognition of the importance of the leaf-associated (*i.e.* phyllosphere) microbiome for plant growth and health, the taxonomic and functional diversity of phyllosphere microorganisms is still largely unknown. Yeasts are versatile microorganisms that are abundant on leaf surfaces and inside leaf tissues. Due to their wide metabolic diversity, they are able to withstand several stressful conditions in the phyllosphere, including fluctuating nutrient and water availability, temperature, and UV radiation. In this talk I will highlight ongoing research on the taxonomic and genomic diversity of phyllosphere yeasts as well as their adaptations to the life in the phyllosphere. Knowledge on the ecology and functions of phyllosphere yeasts will provide a fundamental basis for designing microbiome-based strategies for enhanced crop resilience against (a)biotic stresses.

SESSION 05 – INVITED TALK

To be announced

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SESSION 06 – INVITED TALK

Symbionts as filters of plant colonization of islands: Tests of expected patterns and environmental consequences in the Galapagos

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Key words: arbuscular mycorrhizal fungi, habitat filtering, plant–soil feedback, soil aggregate stability, mycorrhizal response, native flora, introduced flora.

The establishments of new organisms that arrive naturally or with anthropogenic assistance depend primarily on local conditions, including biotic interactions. We hypothesized that plants that rely on fungal symbionts are less likely to successfully colonize remote environments such as oceanic islands, and this can shape subsequent island ecology. We analyzed the mycorrhizal status of Santa Cruz Island, Galapagos flora compared with the mainland Ecuador flora of origin. We experimentally determined plant responsiveness and plant–soil feedback of the island flora and assessed mycorrhizal density and soil aggregate stability of island sites. We found that a greater proportion of the native island flora species belongs to families that typically do not associate with mycorrhizal fungi than expected based upon the mainland flora of origin and the naturalized flora of the island. Native plants benefited significantly less from soil fungi and had weaker negative soil feedbacks than introduced species. This is consistent with the observation that field sites dominated by native plant species had lower arbuscular mycorrhizal (AM) fungal density and lower soil aggregate stability than invaded field sites at the island. We found support for a mycorrhizal filter to the initial colonization of the Galapagos. Further exploration of the mycorrhizal status of islands flora reports similar results, however further empirical research is needed in order to better inform to restoration practices into the islands ecosystems.

SESSION 06 – INVITED TALK

Putting biomes to work: enabling smallholder ecosystem restoration

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Key words: Climate change mitigation, ecological literacy, ecosystem restoration

A growing body of literature reveals that planetary-level ecosystem degradation is underway. Not only are we going to fail to reach the Paris Agreement aim of keeping the average global temperature rise this century below 2 degrees Celsius above pre-industrial levels. We are all but assured of reaching that level by 2050. It appears that we are well on our way to reaching a 3 degrees Celsius increase by the end of the Century. Recent research shows that the Earth may be reaching a dangerous tipping point where its biosphere shifts from a net sink to a source of atmospheric carbon in less than a generation. Some argue that at this point, the oxidation of the biosphere may be irreversible. What can be done?

According to the FAO, agriculture presently occupies nearly 5 billion of the 14 billion hectares of the planet's land area. The expansion of farms leads to 90 percent of deforestation, making agriculture the leading cause of biodiversity and habitat loss. Widespread adoption of total tillage, monoculture, and agrochemical use substantially increased production over the last century. Nevertheless, this progress did not come without a cost. Modern agrifood systems do not just produce food. They undermine soil and hydric systems, generate crop pests and diseases, erode genetic resources, and, it appears, undermine the ecosystems on which human survival depends. Arguably, modern food, as a result of production, processing, transportation, and waste, is responsible for a third of the global greenhouse gas (GHG) emissions associated with global warming and climate change. In this keynote address, I explore how placing knowledge of plant-soil microbiomes in the hands of rural people can enable them to continue to feed a growing population, while becoming major actors in climate change mitigation.

Provided present-day ecosystem decline in localities across the planet, the goal of agriculture is no longer sustainability but the fundamental renewal of ecosystem functioning, what Robert Rodale coined in the 1980s as "regenerative agriculture". Both small and large landholders can be part of resource-conserving farming, which can help stabilize farm productivity while reducing farm-related GHG emissions and increasing terrestrial carbon accumulation. A shift from degenerative to regenerative food requires a fundamentally new understanding of how ecosystems emerge, organize, and operate, in particular, I believe, concerning plant-microbial symbiosis.

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About 90% of the 608 million farms on the planet are family-run, and about 80% (or 465 million) work less than 2 ha. Despite having access to just a fraction of the soil and water resources dedicated to agriculture, globally smallholders provide two-thirds of the food that humans consume. How can smallholder family farmers become actors in the transition towards more resource-conserving, regenerative farming?

Most smallholder Andean farmers in Ecuador, where I live and work, eke out a living on highly degraded Andisols, in Kichwa called, cangahua, meaning 'hard, sterile earth.' While healthy highland soils commonly contain over 10% soil organic matter (SOM), following deforestation and erosion, the exposed hardened cangahua subsoil lacks the moisture and plant life to sustain microbial populations. Cangahua is essentially cemented-ash rock that is undergoing continual weathering. Today, exposed cangahua covers about 250,000 ha of northern Ecuador. Composed of rhyodacite ash, rich in silica and low in alkaline metal oxides, it often contains just 1 to 3% SOM. In terms of mineral content, cangahua is rich in the nutrients that plants need for photosynthesis and growth, but these elements are primarily locked into crystals and, provided a general absence of soil life, unavailable to plants. Cangahua is essentially lifeless "dirt."

At EkoRural, we find the rehabilitation of cangahua strategic for at least two reasons. The poorest of the poor Andean farmers are forced to eke out a living on cangahua. Secondly, provided the potential of healthy highland Andisols to accumulate 10% or more of SOM, at just 1-3% SOM, cangahua subsoil covering hundreds of thousands of hectares has a great capacity for increasing atmospheric carbon drawdown.

The bulk of highland agroecological farms are based on cangahua. The agroecology movements have helped to raise awareness of the dangers of synthetic pesticides in food production due to unwanted environmental and human health consequences. Nevertheless, even among these progressive farmers, knowledge of fundamental biological processes, such as photosynthesis, plant physiology, microbial dynamics, and ecological succession, is limited due to the persistence of the sort of human-centered, command-and-control logic that has proven so problematic in modern agriculture.

While certainly a step in the right direction towards healthier more environmentally friendly production, present-day agroecology does not go far enough when we look at soil health. Agroecological farmers continue to practice total tillage, if by hand, and the cultivation of short-term annual crops, such as European vegetables. They use highly soluble, anaerobic, biologically fermented organic amendments ("bioles") and botanic biocides that can undermine plant-microbial symbiosis, thereby limiting essential soil health processes. As a result, agroecological soils fail to accumulate substantial SOM, and farmers continually face pest and disease problems. In the absence of richly bioactive biomes and plant-soil symbiosis, agroecology tends to get stuck in what we sometimes describe as "organic hydroponics" -- an early ecologically successional stage where soil development is precluded, leaving farmers the burden of continually providing crop nutrients, moisture, and weed and pest control. Early successional agroecological farming poses labor and productivity challenges that can place into question the economic viability of the family enterprise.

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Since the COVID-19 pandemic, EkoRural has been working with about 150 pioneers of Andean agriculture in three regions where exposed cangahua is common to help them fill knowledge gaps and innovate for more regenerative agriculture. In the late 1980s, the Food and Agriculture Organization developed in Southeast Asia the Farmer Field Schools (FFS), a knowledge-intensive, action-learning approach typically taking place over a cropping cycle. Over the last 30 years, FFS has enabled tens of millions of farmers from across the globe to sustain or improve their production while reducing dependence on synthetic pesticides and fertilizers. We are applying this approach to help the pioneers advance their ecological literacy in microbiology as it pertains to plant-soil symbiosis and soil health and to apply that knowledge to rehabilitating cangahua.

Through discovery-based learning on the formation of native forests and climax ecosystems to historical analysis of their degradation, FFS participants are challenging common thought in industrial-era agriculture. For example, modern farmers commonly understand that plant nutrition primarily comes from the soil, when, in fact, terrestrial ecosystems are formed the other way around: plant energy primarily derives from sunlight, and plant production of photosynthates effectively 'feed' microbial populations that drive the formation of the "soil sponge" that is at the center of the organization of terrestrial ecosystems. Through their learning experiments, FFS participants come to appreciate the need for urgent change in soil management.

After learning microscopy, farmers gain competence in the identification of general microbial groups (e.g., bacteria, fungi, nematodes, and protozoa), the function of particular species (endophytes, free-living, beneficials, and pests), and their impact on the soil environment (e.g., the promotion of anaerobic or aerobic conditions) vis-à-vis different management histories and successional stages of plant-soil communities – from lifeless "dirt" to productive farming soils to climax forests. Participants learn, for example, how to conduct systematic sampling and determine the bacterial-to-fungal ratio by weight of a particular sample. They learn how to manipulate functional groups, for example, through the production of aerobic, diverse compost and the application of soil drenches and foliar teas that favor certain populations and communities over others. Subsequently, participants conduct studies on existing Andean "chakras" and design means of increasing the biodiversity of plant genera and families for greater soil health, for example, through increasing alternative cropping associations, green manure/covercrop mixtures, and commonly underutilized auxiliary crops, such as flowers, medicinal plants, traditional Andean vegetables. Participants come to appreciate the importance of increasing the profile of perennials on their farms, such as grasses, bushes, and trees that can help them limit the need for soil movement while maximizing on-farm photosynthesis and carbon accumulation.

The pioneers have learned basic experimental design and are encouraged to continually conduct and share experiments. The emergent study groups have organized around improving the quality and efficiency of composting, the production of extracts, covercrop mixtures, and the development of tools and technologies for limited tillage, micro-irrigation, and the integration of animals.

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In addition, we are working with researchers and their students from three public universities – Universidad Técnica del Norte, Universidad Técnica de Cotopaxi, Escuela Politécnica Superior de Chimborazo – to identify and test soil health indicators and protocols and to set up soil health laboratories. Students are beginning to provide technical backstopping to help us critically assess the most promising farmer experiments.

While there is still much work to do, we already find that helping farmers build workable knowledge of the plant-soil biome holds great promise. Through a clearer understanding of soil life and soil health processes, participants gain greater awareness of the urgency of a transition towards more regenerative agriculture and opportunities for farmer-based carbon draw-down. Due to their vested interest in improving soils and their ability to mobilize local microbial food sources such as tree bark, seeds, water, and other resources, families commonly do not need to be paid for this activity. Nevertheless, sometimes subsidies can help accelerate progress, for example, in financing an FFS process, gaining access to seeds or plants or a microscope and soil tests, and logistical support in breaking up cangahua and finding soil amendments. While there is certainly cost involved in enabling smallholder farmers to become knowledgeable about microbiology and capable of working with microbiomes for climate change mitigation, we also see the potential for tremendous benefits.

We find that a basic understanding of how plant-soil microbiomes organized and operate can help farmers open up pathways to regenerative agriculture, enabling them to become prominent actors in climate change mitigation while securing their farm production and livelihoods. Despite the carbon-sequestering potential of hundreds of millions of family farmers who work well over a billion hectares, we do not know a single program anywhere that strategically invests in smallholders as promising agents of carbon drawdown. Provided the persistence of hunger, the urgency of global warming, and the potential arrival of a species-threatening tipping point, can we afford to continue to keep the scientific insights of plant-soil microbiome out of the hands of the families that work the land and who provide our food?

SESSION 07 – INVITED TALK

Seed Transmitted Microbes are foundational to the Microbiomes of Crop Plants and have Agricultural Potential

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Bioprospecting for beneficial bacteria within plant microbiomes offers much potential to develop inoculants for sustainably improving plant productivity, mitigating stress, and controlling diseases. With the goal of finding beneficial endophytes for maize agriculture, I discovered that seeds were a rich source of endophytes, especially belonging to the genus *Pantoea, Enterobacter*, and *Burkholderia*, and that some of these had the ability to systemically move through adult plants, exit through the roots and colonize the rhizosphere. Some examples of these beneficial seed bacteria were the strongly plant growth promoting *Burkholderia phytofirmans* isolated from seeds from a giant Mexican landrace, root growth enhancing *Enterobacter asburiae* isolated from seeds of a wild variety of Nicaraguan swamp grass and the fungal biocontrol strain *Burkholderia gladioli* isolated from seeds of a Mexican desert popcorn. I went on to find that seeds are more important than soil in the formation of young maize endospheres, and likewise the rhizospheres of young maize plants are dominated by seed transmitted Proteobacteria, primarily *Burkholderia* and *Enterobacter*. Expanding the study to include 16 other species of angiosperm plant including *Arabidopsis, Brachypodium*, wheat, tomato, rice and coffee, I found evidence that the seeds, spermospheres, shoots, roots and rhizospheres of angiosperms are all dominated by taxonomically similar strains of *Pantoea, Enterobacter* and *Pseudomonas*. Shared by dicots and monocots alike, this core microbiome perhaps hints at an important and ancient relationship between seed transmitted Proteobaceria and angiosperm plants. Patents related to these discoveries, helped launch the company Indigo Agriculture, which is the best funded agriculture startup in world history.

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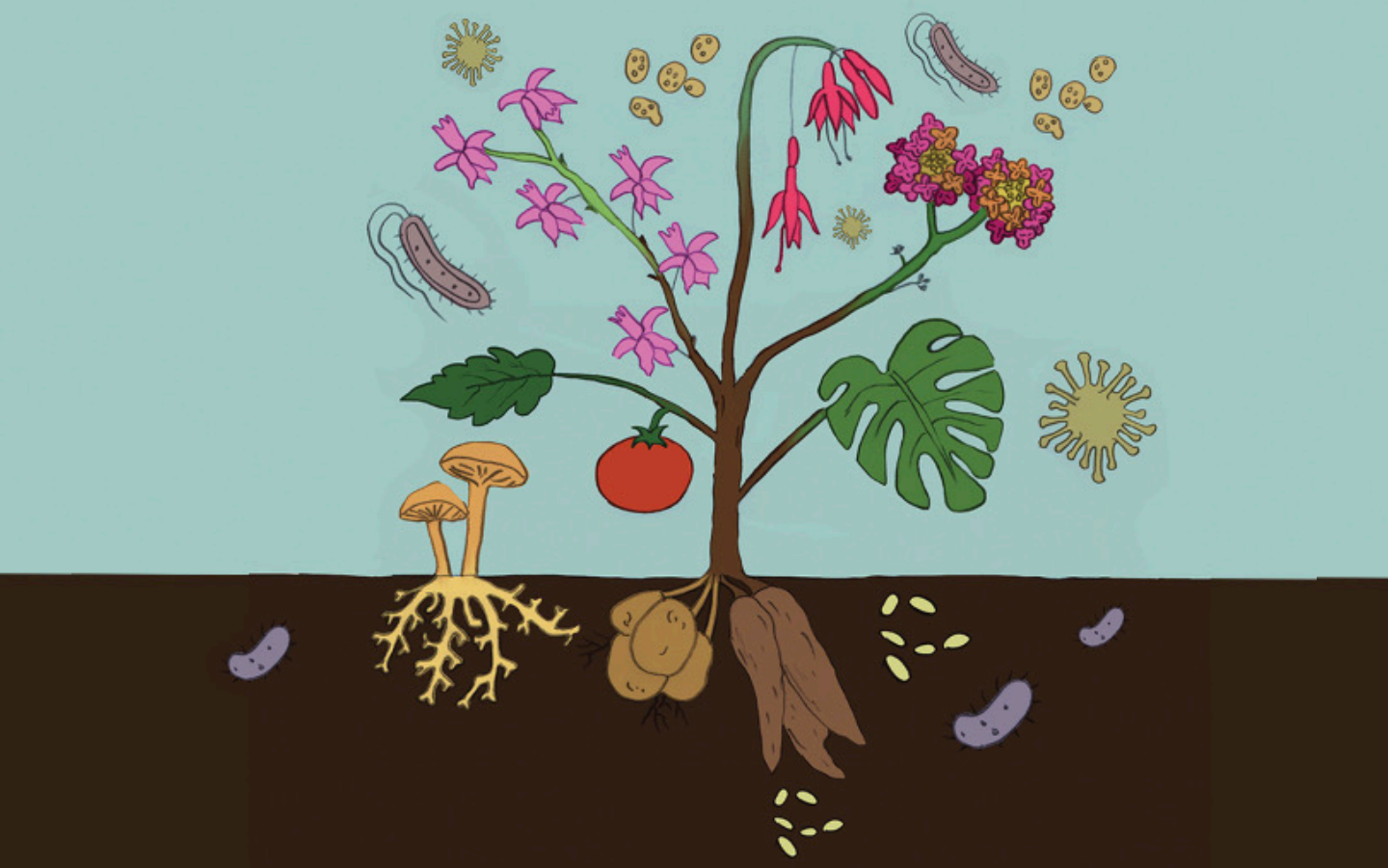

4th Plant Microbiome Symposium

SHORT TALK ABSTRACTS

SESSION 01 - SHORT TALK

1-A

Effective seedling microbiota engineering using synthetic community inoculation on seeds

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Key words: synthetic community, microbiota engineering, seed microbiota transmission

Microbiota engineering through inoculation of synthetic communities (SynComs) is gaining attention as a potential way to improve plant growth and health. Seeds represent a vector of dissemination of plant-associated microorganisms. Hence, inoculation of SynComs on seeds could be a relevant way to improve plant protection and yield using a limited amount of inoculum. However, many questions are to be answered before a possible application of SynComs on seeds: What is the influence of SynCom (1.1) concentration, (1.2) species richness and (1.3) phylogenetic diversity on its stability and ability to colonize seeds and seedlings? And finally, (2) what is the impact of the SynComs on seedling phenotype?

To answer these questions, a collection of 1250 bacterial strains isolated from bean seeds and seedlings has been obtained. A total of 43 SynComs were designed to study the impact of SynCom (1.1) concentration, (1.2) richness and (1.3) phylogenetic diversity. A metabarcoding approach was performed to track our bacterial strains in the inocula, seeds and seedlings. We showed that SynCom concentration but neither richness nor phylogenetic diversity influence SynCom capacity to colonize seeds and seedlings. On average, SynComs are representing 97% of the relative abundance of the seed microbiota and 80% of the seedling microbiota, even in a coalescence context with the natural microbiota of the potting soil. We showed that strains identity and biotic interactions were the main drivers of strain and SynCom ability to colonize seeds and seedlings. (2) Also, the 43 SynComs showed contrasted effects on seedling phenotype related to seed vigor (emergence and abnormal seedling rates). Three SynComs with beneficial effects were further investigated for their impact on plant metabolome and microbiome assembly dynamics.

To conclude, our SynCom inoculation approach on bean seeds is a promising method to manipulate plant microbiota and phenotype for future agricultural applications.

SESSION 01 - SHORT TALK

1-B

1-B Untangling the Effects of Plant Genotype and Soil Conditions on the Assembly of Bacterial and Fungal Communities in the Rhizosphere of the Wild Andean Blueberry (*Vaccinium floribundum* Kunth)

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Keywords: *Vaccinium floribundum,* rhizosphere microbiome, edaphic factors, Ecuadorian Highlands.

Microorganisms in the rhizosphere play a crucial role in nutrient acquisition and stress management for plants. However, the impact of environmental and biological factors on the plant microbiome in the wild remains largely unexplored. To address this, we examined the effects of soil type and plant genetics on the rhizosphere microbiome of *Vaccinium floribundum*, an Andean species that has not been cultivated or domesticated. Our analysis of 39 rhizosphere samples from four genetic clusters of *V. floribundum* in two soil regions in the Ecuadorian Highlands, using high-throughput sequencing of the 16S rRNA and ITS region, revealed that Proteobacteria and Acidobacteria were the dominant bacterial phyla, while fungal communities showed no predominant taxonomic groups. Bacterial alpha diversity was mainly influenced by soil type, with phosphorous and lead being the most influential edaphic factors. The fungal community, on the other hand, was mostly determined by the interaction between plant genotype and altitude. Our study provides valuable insight into the various factors that contribute to the assembly of the rhizosphere microbiome of wild plants. While soil conditions largely influence bacterial communities, plant genetics are more critical in determining fungal community composition. By examining plant-microbe associations, we have gained a better understanding of the factors driving their diversity in the paramo, a unique ecosystem of the Ecuadorian Andes.

SESSION 01 - SHORT TALK

1-C

Uncovering Metabolic Interactions Between Bacterial and Fungal Microbial Communities in Arabidopsis root microbiota Using a High-Throughput 3D Printed Multichannel Bioreactor System

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Key words: microbe-microbe interactions, 3D printed bioreactor, synthetic community, targeted metabolomics, root microbiota

Plants are colonized by diverse multi-kingdom microbial communities whose interactions leading to a healthy plant phenotype are poorly understood. For instance, studying microbe-microbe metabolic interactions in a natural context is challenging due to the lack of suitable experimental systems. To address this issue, we developed a high throughput 3D printed multichannel bioreactor system that can be fed with natural extracts, and run 96 complex combinations of microbial communities in parallel. We couple this system with targeted metabolomics, quantitative community profiling, and a synthetic community (SynCom) approach, using a representative Mini SynCom of the *Arabidopsis thaliana* root microbiota composed of 11 bacterial isolates and 4 fungal isolates.

In result, we identified a strong metabolic signature in the multi-kingdom SynCom, characterized in part by high consumption of sugar alcohols (mannitol and sorbitol) and high production of Arginine and Lysine. We demonstrated that this signature is mainly driven by the bacterial members of the multi-kingdom SynCom. To gain further insight into this metabolic signature, we screened the carbon consumption profile and community composition of both the single and multi-kingdom SynCom in 190 different carbon sources. Our results confirmed our initial findings and revealed the specific metabolization of 3-O-Methyl-Glucose, a plant "non-metabolized" carbon source, only by the multi-kingdom SynCom. Through single strain drop-out experiments, we identified one fungal strain, *Plectosphaerella cucumerina*, and several members of the bacterial SynCom belonging to *Agrobacterium* and *Pseudomonas* species, as key contributors to this strong metabolization.

In conclusion, the specific metabolism of 3-O-Methyl-Glucose by the multi-kingdom SynCom, represents an important source of carbon, which is made available to the plant through its microbiota. The overall results of this study have important implications for the understanding of metabolic interactions between microbial kingdoms at the community level in natural systems and their potential impact on plant health and development.

SESSION 01 - SHORT TALK

1-D

The rhizosphere microbiome of wild tomato in its center of origin

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Key words: wild tomato, rhizosphere, microbiome profile, native habitat, Ecuador

Abstract

Domestication and breeding have substantially changed the genetic and phenotypic traits of plant species. How domestication affected the taxonomic and functional diversity of microorganisms living on and inside plant tissues is largely unknown for most species. To investigate if domestication of plants impacted the association with specific microbial taxa and beneficial microbial traits, we took a BackToRoots approach to first determine the taxonomic and functional microbial composition of wild tomato *S. pimpinellifolium* rhizosphere growing in its center of origin in southern Ecuador. We specifically focused on taxonomic profiling of bacteria and fungi associated with tomato roots in three sites in Loja province (South of Ecuador). Bulk and rhizosphere soil samples of wild tomato were collected from 1400 to 200 masl (meters above sea level). The sites resulted to be significantly different based on their physicochemical soil properties (r2 = 0.18048, p = 0.0112). Beta diversity analysis showed that the microbial community in bulk soil samples was significantly different among sites (bacteria: r2 = 0.0820, p = 2e-04; fungi: r2 = 0.0853, p = 1e-04). However, the rhizosphere community composition of the wild tomatoes grown in each of these three distinct sites was similar, sugesting similar selective forces of the wild tomatoes on microbiome assembly. The wild tomato rhizosphere in its center of origin was shown to be dominated by *Enterobacter*, *Rhizobium, Lactococcus*, *Lechevalieria*, unidentified fungi, *Fusarium, Aspergillus, Acrocalymma, Torula* and *Papiliotrema*. Subsequent metagenome analyses also revealed similarities among the different sites with signaling and cellular processes, carbohydrate metabolism, membrane transport and amino acid metabolism as the most dominant functional categories. It can be concluded that even though there are variations among tomato genotypes, soil properties, and soil microbiomes, wild tomatoes still recruit similar bacterial communities and microbial functions in the rhizosphere, while exhibiting different fungal communities.

SESSION 02 - SHORT TALK

2-A

Studies on root-associated ACC deaminase Pseudomonas strains under osmotic stresses

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Keywords: ACC deaminase, *Pseudomonas*, osmotic-stress, wheat

Stressful conditions such as high salinity or drought increase the production of 1-aminocyclopropane-1-carboxylate (ACC), the precursor of ethylene, in higher plants. ACC deaminase, an interkingdom enzyme, catalyses the deamination of ACC into alpha-ketobutyrate, and root associated bacteria which produce this enzyme have been implicated in the regulation of plant stress. In plant-associated pseudomonads, this enzyme has been shown to influence root elongation.

In this work, three ACC deaminase (*acdS* gene) positive *Pseudomonas* strains (Roth83, Roth91 and Roth93) previously isolated and genome-sequenced from the wheat root microbiome isolate collection at Rothamsted, Harpenden, UK were selected. We generated an *acdS* knock-out mutant for each strain and quantitative ninhydrin ACC consumption tests confirmed the inability of the three knock-out mutants to breakdown ACC, while the complemented mutants showed a partial recovery of function.

The bacterial survival was compared after growing for three days under no-stress vs. high salinity (0.5mM NaCl, 0.8mM NaCl) and no-stress vs. sugar-osmotic stress conditions (0.2mM Sorbitol and 0.4mM Sorbitol). At 0.8mM NaCl and 0.4mM Sorbitol a decrease in the survival of all strains was observed. In Roth83, the *acdS*-mutant survival decrease was the most marked with respect to the wild-type, as it presented a three-fold decrease in 0.8mM NaCl and two-fold decrease in 0.4mM Sorbitol. Roth 91 and Roth 93 *acdS*-mutants only presented one-fold decrease in 0.4mM Sorbitol respect to the wild type.

Pseudomonas wheat (cv. Cadenza) inoculation studies, for testing the wild-type vs. *acdS* knock-out mutant effects on plant growth under no-stress as well under osmotic pressures, NaCl (150mM) and Sorbitol (300mM) are on-going. We will evaluate the effect of the bacterial inoculants on the root length (WinRHIZO™) and shoot length, dry weight, chlorophyll concentration, and root image analysis. Further analysis of secondary metabolites from the recovered root exudates of stressed and non-stressed plants will be also performed.

SESSION 02 - SHORT TALK

2-B

A walk on the wild side:

Exploring the functional potential of Andean soil microbiomes to enhance tolerance of potato to late blight disease

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Key words: Soil microbiome, Induce resistance, *Solanum tuberosum*, Late-blight.

Plant domestication is a complex process affecting plant genetics, plant phenotype and habitat relocation, collectively referred to as the domestication syndrome. However, the impact of these changes on the microbiome and its functions is largely unknown for most plant species. In this study, we investigated the impact of plant domestication on the potato microbiome and its tolerance to late blight disease caused by *Phytophthora infestans*. For the experimental work, we collected native and agricultural soils from 14 sites along the Ecuadorian Andes and grew potato plants (var. Superchola) in these soils. After challenging the plants with *P. infestans*, we found that those grown in native soil often exhibited enhanced tolerance to late blight compared to those grown in agricultural soils. Using heat-treated soils and transplant experiments, we differentiated the contribution of the microbiome from the edaphic factors. We found that only the plants grown in treatments supplemented with 10% live native soil exhibited the induced-resistance phenotype. These results demonstrate the potential of the native soil microbiome in enhancing crop resilience to a specific disease. Currently, we are analyzing the composition of the soil and root microbiome, which will be presented at the meeting.

SESSION 02 - SHORT TALK

2-C

Impact of the fungal pathogen *Fusarium oxysporum* on the taxonomic and functional diversity of the common bean root microbiome

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Keywords: rhizosphere, endosphere, metagenome, metatranscriptome, plant-microbe interaction

Plants rely on their root microbiome as the first line of defense against soil-borne fungal pathogens. The abundance and activities of beneficial root microbial taxa at the time prior to and during fungal infection are key to their protective success. If and how invading fungal root pathogens can disrupt microbiome assembly and gene expression is still largely unknown. Here, we investigated the impact of the fungal pathogen *Fusarium oxysporum* (*fox*) on the assembly of rhizosphere and endosphere microbiomes of a *fox*-susceptible and *fox*-resistant common bean cultivar. Integration of 16S-amplicon, shotgun metagenome as well as metatranscriptome sequencing with community ecology analysis showed that *fox* infections significantly changed the composition and gene expression of the root microbiome in a cultivar-dependent manner. More specifically, *fox* infection led to increased microbial diversity, network complexity, and a higher proportion of the genera *Flavobacterium*, *Bacillus*, and *Dyadobacter* in the rhizosphere of the *fox*-resistant cultivar compared to the *fox*-susceptible cultivar. In the endosphere, root infection also led to changes in community assembly, with a higher abundance of the genera *Sinorhizobium* and *Ensifer* in the *fox*-resistant cultivar. Metagenome and metatranscriptome analyses further revealed the enrichment of terpene biosynthesis genes with a potential role in pathogen suppression in the *fox*-resistant cultivar upon fungal pathogen invasion. Collectively, these results revealed a cultivar-dependent enrichment of specific bacterial genera and the activation of putative disease-suppressive functions in the rhizosphere and endosphere microbiome of common bean under siege.

SESSION 02 - SHORT TALK

2-D

Downy-mildew associated resistobiomes

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Key words: resistobiome, soil-borne legacy, downy-mildew, *Arabidopsis thaliana,* resistance

Plant microbiomes can be dynamically manipulated by the plant in response to pathogen attack to enhance plant resistance. As downy mildew pathogens are obligate biotrophs, they populate living plant hosts where they co-occur with other leaf microbiota. In the laboratory, the downy mildew of *Arabidopsis thaliana*, *Hyaloperonospora arabidopsidis* (*Hpa*), is cultured by successive weekly passaging of spores from diseased to healthy host plants. We hypothesized that this leads to the selection of a disease-associated microbiome that mediates the interaction between the plant and the pathogen. Here we show that plants infected by *Hpa* recruit specific beneficial bacteria that accumulate in *Hpa* cultures, reduce disease and can be inherited as a soil-borne legacy. We found that distinct *Hpa* cultures, derived from multiple isolates maintained separately in British, German and Dutch laboratories, were dominated by isogenic bacteria that negatively affect pathogen proliferation. Moreover, we demonstrated that plants, upon infection, specifically promote this *Hpa*-associated microbiome and that the promoted microbes can form a soil-borne legacy that protects a subsequent plant population. Finally, we showed that a plant-beneficial *Xanthomonas* isolate that is consistently associated with *Hpa* cultures can colonize the root endosphere, and that its colonization of both root and shoot tissue is promoted by *Hpa* infection. Our results indicate that specific beneficial microbes are recruited by *Hpa* infected plants and that repetitive infections with *Hpa* results in the build-up of conserved 'resistobiomes' that improve plant resistance.

SESSION 02 - SHORT TALK

2-E

Pseudomonas brassicacearum control of the root rot pathogen *Aphanomyces euteiches* via a novel nitroimidazole antibiotic

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Key words: Peas, root rot, *Pseudomonas*, nitroimidazole.

Pseudomonas fluorescens and related species are broadly plant-associated bacteria that can contribute to pathogen control. Root rot diseases are a major problem for crops worldwide. In peas (*Pea sativum*), for example, the *Fusarium-Aphanomyces* root rot complex causes significant losses each year including the largest producer in the world, Canada. In our study, genome-sequenced isolates of *P. fluorescens* were used in a high-throughput phenotyping approach coupled with a comparative genomics pipeline to identify genes involved in the control of the root rot pathogen *Aphanomyces euteiches*. A nitroimidazole biosynthetic operon, previously reported in Streptomyces, was identified in one of the strains that exhibited biocontrol activity in vitro, *Pseudomonas brassicacearum* DF41. The antibiotic production in DF41 was quantified using liquid chromatography–mass spectrometry (LC-MS). To confirm if the antibiotic was responsible for the control of *Aphanomyces*, a nitroimidazole DF41 mutant was generated. We found that the mutant was no longer able to inhibit the root rot pathogen growth. We are currently testing DF41 wild type and mutant in peas to evaluate the effectiveness of this nitroimidazole *in planta*. Similarly, we are analyzing how the soil oomycete community shifts in the presence of bacteria producing this compound. Our research represents an important step toward the identification of strains and novel mechanisms to control a wide range of important root rot pathogens in a sustainable way.

SESSION 02 - SHORT TALK

2-F

Effects of soil conditions on microbial communities associated with native plants in the hyper-arid core of the Atacama Desert

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Key words: Atacama Desert – Microbial communities – Rizhosphere – Environmental conditions

The hyper arid core of the Atacama Desert in northern Chile has been described as the driest region in the world. Despite the extreme environmental conditions this area is colonized by a large microbial diversity and few species of major organisms such as plants. Furthermore, the effects of environmental stress over the microorganisms have pressured them to develop particular tolerance mechanisms. Native plants that grow at low precipitation and high salt concentration environments, can benefit by establishing symbiotic relationships with bacterial properties or products to tolerate abiotic stress. Therefore, we proposed that soil conditions such as lack of water, salinity and pH modulated the diversity of these rhizospheric microbial communities of native plants in Yungay Oasis, contributing to aid plants tolerate abiotic stress conditions. Additionally, we described and compared the taxonomic composition of rizhospheric microbial communities with physicochemical parameters of two native plants rizhosphere from the Yungay Oasis, *Suaeda foliosa* and *Distichillis spicata.* Indeed, parameters such as pH and electrical conductivity (EC) were significant differences between both rizhospheric soil of Yungay native plants. We analyzed the both plant rhizosphere microbiomes through Illumina high-throughput sequencing of 16s rRNA gene fragments. In the rhizosphere of *S. foliosa* and *D. spicata* the microbiota differs in composition and structure. Finally, our study contributes new insights into the microbial ecology of the hyper-arid core of the Atacama Desert, particularly to understand the bacterial mechanisms to resist extreme environmental conditions in a region affected by climate change scenario which expected to negatively impact the physiology of desert microbial communities.

SESSION 02 - SHORT TALK

2-G

Volatile-mediated bacterial recruitment in the rhizosphere of tomato plants under an aboveground herbivory stress

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Keywords: root volatiles, *Solanum lycopersicum*, insect herbivory, olfactometer, belowground plant-microbe interaction

Apart from soluble compounds, roots continuously release a plethora of volatile organic compounds (VOCs) important for belowground chemical communication. External stress stimuli such as pathogen and herbivory attacks can locally or systemically change the quantity and profile of root volatiles. Such stress-induced volatiles can have direct defensive effects, while others act as chemical cues attracting specific beneficial (micro)organisms for additional protection. However, if and how volatile emissions from roots of plants under stress attract specific microbial community is largely unknown. Our *in-vitro* study showed that tomato plants (Solanum *lycopersicum* cv Moneymaker and *Solanum pimpinellifolium)* under aboveground herbivory stress (*Spodoptera exigua*) exhibited a different root volatilome than non-stressed plants[1]. Furthermore, we applied belowground olfactometer system to investigate if and how tomato plants exposed to the leaf herbivorous insect can recruit, from a distance, a specific subset of soil bacteria via root volatiles. Significant changes in the root volatilome of *S. lycopersicum* cv Moneymaker upon *Spodoptera* stress and a concomitant change in the taxonomic composition of the recruited rhizobacterial communities were observed. We further elucidate the functional importance of this volatile mediated- belowground 'cry for help' by performing targeted isolation and testing the recruited isolates on planta, to validate their protective functions against the herbivory stress.

SESSION 03 - SHORT TALK

3-A

The key role of mannitol and mannitol utilization cluster (*mtl*) genes in biofilm formation and plant root attachment by the plant growth-promoting *Pseudomonas granadensis* CT364.

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Key words: Biofilm formation, Mannitol, *Pseudomonas*, Colonization, Plant Growth-Promoting Rhizobacteria.

Biofilm formation is the first step of bacterial plant pathogenesis and a limiting feature for competent root colonisation by plant growth-promoting rhizobacteria (PGPR) and endophytes. A deeper molecular and genetic understanding of bacterial biofilm development and regulation is therefore important to understand bacterial colonisation of plants. Moreover, this knowledge may enable the creation of enhanced biocontrol strategies and biofertilizer agents. *Pseudomonas granadensis* CT364 is a plant growth-promoting endophyte recently isolated from the rhizosphere of olive (*Olea europea L.*) plants. In this work, we describe the role of mannitol and the mannitol utilisation cluster (*mtl*) in biofilm formation and its carbon source-mediated regulation by mannitol and other sugars. Mannitol is a sugar alcohol present in the exudates of many plants, and it is especially high in the exudate of olive trees. Here we show that mannitol enhances biofilm formation and root attachment to *Arabidopsis thaliana* roots. Further, using a combination of *in vitro* biofilm assays, confocal microscopy and genome editing of the *P. granadensis* genome we show that the *mtl* cluster is required for biofilm formation in response to mannitol and that the response is affected by the presence or absence of other sugars.

SESSION 03 - SHORT TALK

3-B

Identification of specialized root exudates associated with microbiome assembly of wild and domesticated tomato

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Key words: specialized root exudates, microbiome assembly, plant domestication

Domestication of plant species has significantly impacted on the rhizosphere microbiome composition, but the underlying chemistry of microbiome assembly in wild and domesticated plant species remains largely elusive. Here, we collected soluble root exudates from 4 wild and 4 domesticated tomato plants, and analyzed their chemical composition via Quadrupole Time-of-Flight LC-MS/MS. Secondly, we repeatedly inoculated the extracted root exudates into soils from the center of origin and from the center of tomato production to determine specific shifts in the soil microbiome. First, we showed that the different genotype tomato plants have distinct rhizosphere microbiome composition and diversity when growing in greenhouse soils and native soils. Moreover, root exudate composition was distinctly different between wild and modern tomato plants, with specific mass features significantly more abundant in the root exudates of the 4 wild tomato species. Collectively these results suggest that tomato plant specialized metabolites might be an important driver for recruiting specific microbial taxa. By integrating ‘metabolomics’ and ‘microbiomics’, we are now investigating and validating which specialized metabolites are key compounds in tomato domestication and microbiome assembly.

SESSION 03 - SHORT TALK

3-C

Impact of *Bacillus subtilis eps* and *TasA* genes defective on rhizosphere microbiome assembly of tomato

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Keywords: PGPR, *Bacillus subtilis,* eps, rhizosphere microbiome, mutant, soil diversity

Bacillus subtilis holds significant agricultural and ecological importance as one of the most extensively studied plant growth promoters. To better understand *Bacillus* genetic traits associated with plant fitness, we used a mutant gene-defective model to analyze itsimpact on tomato development and on rhizosphere microbiome under a gradient of soil microbial diversity. We used *B. subtilis* strain UD1022 and its mutant (UD1022eps-TasA-) defective for biofilm formation. Control treatments and plants inoculated with wild or mutant Bacillus strains were used in the bioassay. Soil DNA isolation was followed by qPCR targeting *B. subtilis gyrB* gene, and 16S rRNA and ITS amplicon sequencing. Data analysis included comparisons of plant growth performance, *gyrB* quantification, and amplicon sequence variants processing using Dada2 pipeline, followed by exploratory, permutational variance, and covariance analysis. UD1022 strain significantly increased shoot and root dry masses when tomato was grown in soils with lower microbial diversity. UD1022 inoculation significantly changed soil bacterial and fungal communities' assembly in low microbial diverse soil (autoclaved soil), compared to UD1022eps-TasAand control in the same soil. On the other hand, in high microbial diversity (natural soil) the rhizosphere microbiome is less affected by the inoculants. Bacterial network analysis showed that the UD1022 inoculation also impacted the relationship among bacteria phyla, by increasing the network's modularity and number of nodes, compared to control and UD1022eps-TasA- treatments. For fungal network, the UD1022eps-TasA- inoculation caused higher changes on network's modularity, number of nodes and edges, compared to control and UD1022 treatments. In conclusion, knocking down genes associated with biofilm formation in *Bacillus*, impacts not only the ability of plant colonization, but also the assembly of the rhizosphere microbiome during plant development.

SESSION 03 - SHORT TALK

3-D

Aphid infestation changes metabolic activity and composition of bacterial communities in the wheat rhizosphere

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Keywords: Plant defence, plant volatiles, community-level metabolism

Plant-microbe interactions are fundamental to plant defence against herbivores, which cause significant losses in food production worldwide. This project aims to study the effect of aphid feeding on the plant system and its effect on bacterial communities in the wheat rhizosphere. In the first part of this project, we designed a microcosm experiment consisting of two treatments (wheat plants with and without aphid infestation). Rhizosphere samples were taken before infestation and two weeks post-infestation. We analysed bacterial community profiles at taxonomical (16S rRNA gene sequencing) and physiological levels (Ecoplates, Biolog). Moreover, aboveground volatiles were collected to characterise their chemical composition. After two weeks of infestation, bacterial diversity was reduced in the rhizosphere of aphid-infested plants in comparison with the non-infested, but a higher abundance of Actinobacteria and Firmicutes was observed. The physiological profiling showed a higher microbial metabolic activity in the rhizosphere of aphid-infested plants, particularly in response to D-Xylose, N-acetyl D-glucosamine, and some amino acids ($p < 0.05$). Unsurprisingly, we detected aboveground volatiles involved in herbivory response (e.g., limonene, α-cubebene, β-Ocimene) in aphid-infested plants, which validated that plant chemistry changed under aphid feeding. Following these results, we are currently conducting another experiment to characterise changes in soil microbial communities (taxonomical and physiological) associated with two cultivars from the ancestral wheat Triticum monococcum under aphid herbivory. These cultivars have been previously identified as resistant (MDR049) and susceptible (MDR037) to aphid feeding. We hope that the results of this experiment will increase our understanding of the role of soil microbial communities in the plant response to herbivory and will help design future strategies to increase plant resistance to pests that threaten food security.

SESSION 03 - SHORT TALK

3-E

Identification of the conserved *iol* gene cluster involved in rhizosphere competence in *Pseudomonas*

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Keywords: *Pseudomonas*, inositol, rhizosphere competence, root colonization, microbial genomics

The *Pseudomonas* genus has shown great potential as a sustainable solution to support agriculture through its plant-growth promoting and biocontrol activities. However, their efficacy in the field is limited by unpredictable colonization in complex natural conditions. To effectively support plant health with beneficial microbes, a deeper knowledge is required on the underlying molecular mechanisms of superior root colonization in natural scenarios. Here, we assessed the ability of a set of plant-associated pseudomonads to colonize Arabidopsis roots in natural soil. A comparative genomic analysis identified the *iol* locus, a gene cluster in *Pseudomonas* involved in catabolism of inositol, a plant-derived compound, as a feature enriched among superior root colonizers. Further characterization revealed that the *iol* locus increases competitiveness by inducing swimming motility and fluorescent siderophore production in response to inositol. Public data analyses indicate that the *iol* locus is broadly conserved in the *Pseudomonas* genus and linked to diverse host-microbe interactions. Our findings suggest the *iol* locus as a relevant driver of root colonization by pseudomonads in natural conditions and a potential target for developing more effective microbial inoculants for sustainable agriculture.

SESSION 03 - SHORT TALK

3-F

Bacillus modulates key developmental traits and production of secondary metabolites in response to the plant cell wall polymer pectic homogalacturonan

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Key Words: *Bacillus*, homogalacturonan, biofilm, sporulation, bioactive secondary metabolites.

As common members of the so-called rhizosphere, some soil-dwelling bacteria typically associate with plants, providing benefits to their host in terms of health and growth. Among them, *Bacillus velezensis* represent one of the most promising biocontrol agent already commercialized by leading agrochemical companies. The biocontrol activity of these plant-beneficials primarily relies on efficient establishment at threshold populations in the rhizosphere. In that context, the impact of small chemicals exuded by roots on chemotaxis and bacterial phenotype has been widely reported. However, the possible outcomes resulting from the interaction occurring upon contact with root tissues are still poorly described but crucial to consider. Here we focused on the potential effect of pectin, the first and most abundant cell wall polysaccharide supposedly sensed by *B. velezensis* upon contact with root cells. More precisely, we have identified the homogalacturonan (HG) pectin backbone as molecular pattern retaining a key role in the plant-*Bacillus* interaction. We show that upon HG sensing, *B. velezensis* stimulates key developmental traits via a dynamic process involving two conserved pectinolytic enzymes. HG perception by the bacterium causes some transcriptional reprogramming leading to a multifaceted phenotypic response at the community level which integrates the switch from planktonic to sessile cells, a strong increase in biofilm formation and an accelerated sporulation dynamic while conserving the potential to efficiently produce key specialized secondary metabolites such as polyketides and lipopeptides, with important ecological functionalities. We anticipate that this global response of *Bacillus* to cell wall-derived host molecular patterns contributes to its efficient establishment and persistence in the competitive rhizosphere niche but also *in fine*, to its activity as biocontrol agent. Our work thus unveils new aspects in the interkingdom molecular interactions between plants and their bacterial associates.

SESSION 04 - SHORT TALK

4-A

Ultra-high resolution amplicon sequencing reveals cross-kingdom antagonists and synergists driving fungal infections in the wheat phyllosphere

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Keywords: *Pseudomonas*, *Zymoseptoria tritici*, PacBio, wheat, biocontrol

Plant-associated microbiomes promote plant health in natural environments and can confer resistance to pathogens. Within these microbial networks, plant-beneficial and plant pathogenic strains are often closely related. Hence, monitoring pathogenic and plant beneficial microbes at the strain level is critical for our understanding of microbiome functions. However, high-resolution strain level monitoring is hindered by the available barcoding loci. Here, we introduce multiple 3-kb highly polymorphic bacterial and fungal amplicons to be sequenced in 10,000-multiplex pools on the PacBio Sequel II system. We analyzed large sets of high-quality genomes covering the phylogenetic breadth of *Pseudomonas* bacteria and the major fungal wheat pathogen *Zymoseptoria tritici* to define highly robust amplicon sets. Pseudomonads include synergistic and antagonistic species of *Z. tritici* in the wheat phyllosphere. We complemented the sequencing with the full-length 16S and fungal ITS loci to generate deep insights into crop microbiomes. We apply our set of amplicons to a hierarchical set of 500 wheat samples spanning the growing season, different plant genotypes, as well as replicated leaf and root compartments. The deep sequencing revealed highly granular structures of both the focal pathogen and the co-existing *Pseudomonas* diversity. We used evidence for co-occurrence and exclusion of individual genotypes to investigate synergistic and antagonistic microbiome interactions. A comprehensive strain collection from the same field allowed us to validate the predicted interaction network under controlled conditions. We build a model of biotic and abiotic factors determining the ecological niche of the crop pathogen and reveal broad principles of competitive exclusion and persistence. Overall, our work introduces a powerful new approach for ultra-deep amplicon analyses to interrogate plant microbiome interactions.

SESSION 04 - SHORT TALK

4-B

Production and degradation of indole 3-acetic acid in the phyllosphere microbiome

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Keywords: phyllosphere, IAA, auxin, phytomicrobiome

Production of the plant hormone indole 3-acetic acid (IAA) is a common property among leaf surfaceassociated bacteria, but the function and fate of this IAA in the phyllosphere microbiome are not well understood. A time-course analysis of the changes in microbial community composition on the foliage of field-grown lettuce showed 1) an increase over time in the relative abundance of bacterial species belonging to the order Enterobacterales, 2) a higher proportion of isolates with the ability to produce IAA later in the season, and 3) an overrepresentation of high-IAA producers among isolates from the species Pantoea, Erwinia, and Morganella (all Enterobacterales). While these findings suggest that the ability to produce IAA is necessary for successful leaf surface colonization, it is not sufficient, as was demonstrated through leaf inoculation experiments with IAA-producing and non-producing, but otherwise isogenic, strains of E. coli. A GFP-based bacterial bioreporter that responds to IAA in a dose-dependent manner was used to show that IAA is indeed produced in vivo by Erwinia bacteria after inoculation onto leaf surfaces. When supplemented with tryptophan, such IAA production was significantly higher, suggesting that the availability of tryptophan is a limiting factor for IAA production in the phyllosphere. Two possible fates of bacterially produced IAA in the phyllosphere will be discussed: 1) destruction by sunlight, and 2) degradation by bacteria such as Pseudomonas putida 1290, which can use IAA as a source of carbon, nitrogen and energy. P. putida 1290 was originally isolated from pear tree foliage and its genes underlying the utilization of IAA for growth have been identified and characterized.

SESSION 04 - SHORT TALK

4-C

Activity and diversity of prophages harbored by wheat phyllosphere bacteria

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Key words: Prophages, bacterial warfare, phyllosphere

The plant microbiome harbors an enormous diversity of fungi, bacteria, and viruses, but little is known on the diversity and function of prophages lying within plant-associated bacteria. Using VIP-Seq (Virion Induction Profiling Sequencing), a novel method based on supernatant sequencing, we identified and quantified the activity of 120 spontaneously induced prophages in a collection of 63 *Erwinia* and *Pseudomonas* strains, all isolated from wheat flag leaves collected from the same field. Many bacterial strains exhibited high levels of spontaneous prophage induction, with some producing > 10^8 virions/mL in overnight culture. Significant induction *in planta* also occurred from a lysogenic *Erwinia* strain inoculated on wheat seedlings. The potential of these active prophages in bacterial warfare was exhibited by their widespread killing of rival bacterial strains. Evidence of transduction was also observed, and the prophages were shown to contribute a majority of the non-core genome of *E. aphidicola* isolates. Many additional prophages were predicted by bioinformatic tools, and we found the presence of IS-annotated genes in prophages was significantly negatively correlated with spontaneous activity.

Our results suggest that the spontaneous induction of prophages may represent an unknown but wide-spread competition mechanism involved in phyllosphere microbiome assembly and function. and may have implications for the design and resilience of synthetic bacterial communities used as biocontrol for certain plant diseases.

SESSION 04 - SHORT TALK

4-D

Unravelling the volatile-mediated suppression of *Fusarium* growth by phyllosphere yeasts

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Key words: Yeast, Volatiles, *Fusarium*, Mycotoxins, transcriptomics, wheat phyllosphere

Volatile compounds are low molecular weight compounds which play a role in numerous biological processes, including (inter)species-communication and modulation of growth and development of other (micro)organisms and plants. Most studies on microbial volatiles have focused on soil and rhizosphere microorganisms, whereas volatile production by phyllosphere microorganisms has been largely overlooked, especially phyllosphere yeasts. Previously, we have established and screened a diverse collection of phyllosphere yeasts for antagonistic activities against plant pathogens through the production of volatile compounds. We identified isolates that strongly inhibit the growth of the mycotoxin-producing pathogen *Fusarium graminearum.* However, the molecular mechanisms underlying the volatile-mediated effects on pathogen growth, more specifically *F. graminearum*, is still largely unknown. To identify suppressive volatile compounds and the molecular mechanisms mediating this yeast-pathogen interaction, we coupled yeast volatile profiling and transcriptomic analysis of *F. graminearum* exposed to yeast volatile compounds. We found that specific volatiles, applied individually or as a mix, downregulated the expression of the mycotoxin genes *TRI5* and *TRI11*. These results demonstrate the potential of volatile compounds in combating *Fusarium* infection and decreasing mycotoxin contamination in grains.

SESSION 05 - SHORT TALK

5-A

Ecological and environmental drivers of virus co-infection in wild plant populations

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Keywords: Viruses, community assembly, landscape, co-occurrence networks.

Viruses are a vastly underestimated component of biodiversity that occur as diverse communities across hierarchical scales from the landscape level to individual hosts. Virus co-infections, i.e., two or more viruses infecting the same host individual, may have profound impact on disease evolution and epidemiology, yet we know very little about the drivers of virus community assembly in wild. Here, we investigated virus communities in *Plantago lanceolata* populations in spatially variable landscape in the Åland Islands, Finland. We found that the plants hosted diverse virus communities that are characterized by diverse, non-random coinfections. Using a novel graphical network modelling framework, we demonstrate how environmental heterogeneity influences the network of virus taxa, and how the virus co-occurrence patterns can be attributed to non-random, direct statistical virus-virus associations. Moreover, we show that environmental heterogeneity changed virus association networks especially through their indirect effects. Our results highlight a previously underestimated mechanism of how environmental variability can influence disease risks by changing associations between viruses that are conditional on their environment.

SESSION 05 - SHORT TALK

5-C

Seed Saving and Microbiome Cycling

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Key words: Agroecology, climate resilience, ecology, phytobiome

Plant microbes can be transferred from maternal tissue, to seed, and eventually partition into various seedling organs in the next generation. Although vertically transmitted seed microbes have been found to play critical roles in early plant development, interactions with the surrounding soil community is largely understudied. In our study, we use Hopi Beans (*Phaseolus vulgaris*), that have been saved for over 25 years, to test 1) how seed and soil microbes interact with each other during early plant development (dynamics of seed and soil microbial community coalescence), 2) which microbes are consistently transferred from one generation to the next, and 3) how these microbial compositions/dynamics affect plant health. To test these questions, we perform a cross-combination experiment, by sterilizing seed, soil, or both. We find that 1) the removal of soil microbes have the largest effect on plant health, but seed microbes may play integral roles in reproductive related plant traits, 2) various bacterial taxa are consistently transferred to the next generation across treatments, and 3) various bacterial taxa are associated with increased plant vigor and health. We believe the findings of this study not only illustrate a poorly understood dynamic of seed-soil microbiome coalescence but also understand how local seed saving practices may allow farmers to develop locally-adapted microbiomes for their crops.

SESSION 06 - SHORT TALK

6-A

The unsuspected mutualism between *Rhizophagus irregularis* and *Bacillus velezensis* confers enhanced biocontrol functionality

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Key words: Biocontrol, *Bacillus velezensis*, Mycorrhiza, interaction, mutualism

Bacillus velezensis is a model species for plant-associated bacilli and its biocontrol potential relies on secretion of secondary metabolites playing crucial roles in direct pathogen inhibition and/or in the stimulation of host systemic resistance. Arbuscular Mycorrhizal Fungi (AMF) are symbionts also providing benefits to the host not only by facilitating nutrient acquisition but also by helping the plant to deal with (a)biotic stresses. The concept that AMF recruit and interact with some bacteria in its hyphosphere is nowadays well established. However, it mainly concerns phosphate solubilizing bacteria and the interaction has been mostly studied for reciprocal beneficial exchange of nutriments, leaving the molecular basis underpinning communication between the two microbes almost unknown. In this work, we demonstrate the compatibility of the interaction between *Rhizophagus irregularis*, an AMF, and *B. velezensis* which was a priori questionable due to the potential of the bacterium to produce strong antifungal compounds. Time-laps microscopy imaging combined with specific histochemical staining revealed a prompt and robust biofilm formation by *Bacillus* along hyphae but without detrimental effects on AMF viability and vitality. Additional data from metabolomics revealed that the observed compatibility is due to a dampened production of the toxic fengycin lipopeptide upon interaction. We anticipate that the high hyphosphere fitness of *Bacillus* may reflect some adaptation of the bacterium to an AMF-associated lifestyle. Being hosted in the nutrient-rich hyphosphere niche and using the AMF as highway to considerably enhance its soil invasion potential are clear ecological benefits for the bacterium. In turn, as the potential to produce most of the other BSMs is conserved while dwelling in the hyphosphere, the bacterium would provide some protection to the fungus against its microbial enemies. Finally, data from first greenhouse trials shown a synergic effect of the combination of these two microbes on the stimulation of plant systemic resistance.

SESSION 06 - SHORT TALK

6-B

Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests

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Keywords: Metatranscriptomics, mycorrhizae, assembly

Carbon storage and cycling in boreal forests—the largest terrestrial carbon store—is moderated by complex interactions between trees and soil microorganisms. However, existing methods limit our ability to predict how changes in environmental conditions will alter these associations and the essential ecosystem services they provide. To address this, we developed a metatranscriptomic approach to analyze the impact of nutrient enrichment on Norway spruce fine roots and the community structure, function, and tree–microbe coordination of over 350 root-associated fungal species. In response to altered nutrient status, host trees redefined their relationship with the fungal community by reducing sugar efflux carriers and enhancing defense processes. This resulted in a profound restructuring of the fungal community and a collapse in functional coordination between the tree and the dominant Basidiomycete species, and an increase in functional coordination with versatile Ascomycete species. As such, there was a functional shift in community dominance from Basidiomycetes species, with important roles in enzymatically cycling recalcitrant carbon, to Ascomycete species that have melanized cell walls that are highly resistant to degradation. These changes were accompanied by prominent shifts in transcriptional coordination between over 60 predicted fungal effectors, with more than 5,000 Norway spruce transcripts, providing mechanistic insight into the complex molecular dialogue coordinating host trees and their fungal partners. The host–microbe dynamics captured by this study functionally inform how these complex and sensitive biological relationships may mediate the carbon storage potential of boreal soils under changing nutrient conditions.

SESSION 06 - SHORT TALK

6-C

The interplay of dual plant colonization by Soybean Mosaic Virus and arbuscular mycorrhizal fungi of field- and greenhouse-grown soybean plants

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Keywords: Soybean, Rhizosphere, Arbuscular mycorrhizal fungi, Soybean Mosaic Virus, DNA amplicon sequencing

Microbes can significantly affect plant health, and plants have been shown to modulate their rhizosphere microbiome in response to pathogen attack. The model plant species *Arabidopsis thaliana* was previously found to recruit a consortium of disease resistance-inducing microbes upon downy mildew infection. We are interested whether such a phenomenon also applies to agricultural crops. Here, we study changes in the soybean (*Glycine max* L.) rhizosphere upon pathogen infection to identify candidate plant-beneficial microbes associated with this economically-important crop. In 2020, soybean plants growing in two commercial fields in the Netherlands showed symptoms of Soybean Mosaic Virus (SMV) infection. The presence of SMV was confirmed in leaf material of infected plants, presenting the first official occurrence of this virus in the Netherlands[1]. Based on 16S and ITS2 amplicon sequencing, both bacterial and fungal rhizosphere communities were distinct between healthy and SMV-infected plants in both fields. A taxonomically diverse set of 20-28 bacterial ASVs per field was differentially abundant between healthy and SMV-infected plants with no clear enrichment of particular phylogenetic groups in the rhizosphere of SMV-infected plants. In the fungal rhizosphere communities, arbuscular mycorrhizal (AM) ASVs were enriched in healthy plants in both fields. We are currently performing greenhouse experiments testing whether AM and SMV affect each other's ability to colonize a soybean plant. Preliminary results suggest that SMV does not affect AM root colonization under greenhouse conditions, while AM fungi alleviate SMV-induced shoot growth reduction. Additional experiments with early (pre-mycorrhizal root colonization) and late (post-mycorrhizal root colonization) virus inoculation should reveal more of the interplay between SMV and AM fungi simultaneously colonizing a soybean host.

SESSION 06 - SHORT TALK

6-D

Solanum tuberosum Group Phureja endophyte microbiome characterization and its bacterial endophyte functionality against phytopathogens

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Landrace potatoes, such as *Solanum tuberosum* Group Phureja, are known for their natural resistance to phytopathogens like *Phytophthora infestans*, making them essential candidates for breeding programs. In this study, two varieties of *S. tuberosum* Group Phureja were grown in native soil and heat-treated soil to simulate the loss of diversity associated with modern agricultural practices. The microbial community structure and diversity of the soil and tubers were analyzed using DNA high-throughput sequencing. The results showed that the microbial community of the tubers had less diversity than the soil, and the community composition of the tubers grown in native soil versus heat-treated soil was reduced as expected, indicating that the soil is the primary source of endophytes. The analysis also revealed a reduction in the bacterial community composition in potatoes grown in heat-treated soil, with the dominant bacterial phylum being Proteobacteria in all cases, but its abundance varied greatly in samples after heat treatment. The predominant phylum of fungi was Saccharomycetales in all cases. The β diversity of bacteria differed significantly depending on the variety of potatoes in native soil, but the samples clustered together after heat treatment. The β diversity of fungi showed no evident variation due to the potato variety or after heat treatment. Further analysis of the cultured endophytic bacteria showed great potential for these bacteria to act as antagonists to highly important phytopathogens such as *Rhizoctonia solani* and *Phytophthora infestans*. Overall, this study provides valuable knowledge about the microbial community composition of a landrace potato variety and the potential for endophytic bacteria to act as a biological control against phytopathogens.

SESSION 06 - SHORT TALK

6-E

“Cry for help” upon pathogen attack across the Brassicaceae family

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Keywords: Brassicaceae, root microbiome, defense hormones

Following infection, *Arabidopsis thaliana* recruits beneficial rhizobacteria that stimulate plant immunity against the pathogen, a phenomenon termed “cry for help”. It is unknown whether this pathogen triggered recruitment is conserved. To test this, we treated 23 species from the *Brassicaceae* plant family with the defense hormones methyl jasmonate (MeJA) and salycylic acid (SA) as mimics for pathogen attack, and collected roots for microbiome analysis. Then we identified microbial taxa recruited following treatment by performing 5 differential abundance analyses on each plant species comparing the control with the treated group. We designated Amplicon Sequence Variants (ASVs) detected by at least 2 of these analyses as the consistent set of responsive ASVs. In the bacterial communities 5.5% and 7.3% of the total ASVs were responsive to MeJA and SA respectively, while these proportions were 2.7% and 3.8% for the fungal ASVs. Next, we compared the ASVs at the taxonomic level by selecting microbial orders overrepresented in the set of responsive ASVs compared to the total community. In the MeJA treatment, the order Hypocreales was significantly overrepresented as responsive to MeJA, but no fungal group was detected in the SA treatment. Contrarily, in the bacterial communities several bacterial orders were commonly responsive accross different plant species. In particular, Burkholderiales, Xanthomonadales and Rhizobiales were shared between at least 2 plants in both hormone treatments while Sphingomonadales only in the MeJA treatment. Other 21 bacterial orders were responsive only in single plant species. These results show that most of the microbial recruitment is plant species specific, but particular bacterial orders are commonly recruited, potentially showing a stronger and distinct evolutionary relationship. Now we are analyzing whether there is a phylogenetic signature between the plants and these responsive microbial orders.

SESSION 06 - SHORT TALK

6-F

Characterization and biocontrol potential of a new *Bacillus nakamurai* strain isolated in Burundi

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Keywords: Burundi, *Bacillus*, biocontrol potential, plant pathogens

In response to the deleterious effects of chemical pesticides to the environment in general, searching for safe and eco-friendly alternatives has become a worldwide trend since some decades. *Bacillus* strains among other microorganisms already proved their biocontrol potential. Sixteen *Bacillus*-like bacterial isolates were isolated from arable soil samples collected from two different agro-ecological locations in Burundi. These isolates were first evaluated for their antimicrobial activities against a range of bacterial and fungal phytopathogens including three species isolated from infested leaves samples collected from Burundi. One particular isolate BDI-IS1 displayed a broad and strong antimicrobial activity comparable to the commercial strain *B. velezensis* QST713. Greenhouse biocontrol experiments carried out on tomato infested by *Alternia solani* revealed that the treatments with BDI-IS1 reduce the disease incidence by 35%. The 16S rRNA gene sequencing of this isolate showed that it belongs to *Bacillus nakamurai* species. Our data indicated that the active compounds are soluble secondary metabolites (SMs). Chemical analyses of culture supernatants by LC/Q-TOF mass spectrometry showed that this *B. nakamurai* strain produces a vast array of SMs including cyclic lipopeptides (surfactins and iturins A), polyketides (bacillaene), siderophores (bacillibactin), the dipeptide bacilysin and the ribosomally synthesized and post-translationally modified peptide plantazolicin. Furthermore, genome mining with Antismash predicted the biosynthesis of amylocyclicin as additional bacteriocin. In vitro confrontation tests with metabolite depleted mutants evidenced the role of these SMs in the observed antimicrobial activities. Adaptability of this strain to abiotic stresses (pH, temperature, etc.) and in planta experiments are the forefront activities to be carried out for in-depth physiological characterisation and efficacy assessment. These findings suggest that Burundi soils are a reservoir of interesting plant beneficial bacteria and that the rare species *B. nakamurai* is worth to be exploited in the biocontrol strategies to reduce plant diseases.

SESSION 07 - SHORT TALK

7-A

Probing the leaf micro-environment with whole cell yeast biosensors to establish principles of microbiome coexistence

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Keywords: Biosensors, phyllosphere microbiome, trait-based ecology

The aboveground organs of plants host a diverse and highly functional community of microorganisms, known as the phyllosphere microbiome, yet we lack knowledge of the mechanisms involved in the assembly and maintenance of this complex community. Ecological models of species coexistence may allow for predicting which microbes can persist in the phyllosphere, given the traits of the organisms and the characteristics of the environment. However, application of such models as niche partitioning depends on detailed observation of the environment, including variations across time and space. Whole-cell biosensors are genetically-engineered microorganisms expressing fluorescent proteins which can relay changes in conditions within and surrounding the microscopic habitat, such as the concentration of metabolites, nutrients, ions, reactive oxygen species, or other conditions. We are developing native phyllosphere yeasts within the Microbotryomycetes, including novel taxa, to express these biosensor proteins with the goal of observing multiple characteristics of the microenvironments experienced by microbes on the leaf surface with high spatial and temporal resolution. These yeasts, when applied to the model host plant *Arabidopsis thaliana*, can consistently obtain high cell densities of at least 10^5 colony-forming units/cm^2 on leaves 15 days post inoculation, and express detectable fluorescence. Optimization of this system requires genetic alterations to the yeast, formulation of inoculation medium, and tuning of the expression system, as well as validation of biosensor function. A similar approach can be employed to observe how different members of the phyllosphere microbiome, such as pathogens vs. mutualists or bacteria vs. fungi experience the leaf environment. Combined with microbial trait data, a map of the leaf environment across host, space, and time may facilitate the construction of predictable and functional plant microbiomes.

SESSION 07 - SHORT TALK

7-B

Rice straw recycling increased soil microbial functional diversity during the decomposition of rice straw

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Key words: rice straw, biogeochemical cycles, metagenomics, enzyme activities, agronomic parameters.

Agricultural residues are precursors of soil organic matter, its decomposition in the field allows the entry of carbon and other nutrients into the system. However, it can also favor the proliferation of pathogens, converting it into a great challenge for producers. Among the alternatives to waste management are, burning of rice straw and/or its incorporation into the soil. However, the knowledge of the impact of these strategies on the microbial community and especially in their functionality is limited. This study sought to determine the effect of the application of four rice straw management strategies, on the structure and function of the microbial communities associated with the biogeochemical cycles of carbon (C), nitrogen (N), and phosphorus, those strategies are: 1. Leave rice straw as a mulch; 2. Rice straw as a mulch with the addition of microorganisms; 3. Rice straw plus microorganism inoculum followed by incorporation into the soil; 4. Burning of rice straw followed by ashes incorporation into the soil). A field trial was implemented with a random incomplete block design, sampling soil three times during a cultivation cycle. The soil was characterized by physicochemical and enzymatic analyzes, the microbial communities were described using shotgun metagenomics. Productivity and phytosanitary status of the rice crop were determined. The results showed differences in pH, enzyme activities, and microbial community at initial and degradation time compared to final time. Genes related to diverse processes of the N cycle as nitrogen fixation, nitrification, denitrification among others were identified. Regarding the C cycle, glycosyl hydrolases with action on hemicellulose increased especially at degradation times. This study suggests that the strategies of using rice straw, either as mulch or incorporated in the soil with microorganisms, are an adequate option for the final disposal of the rice straw, as agricultural practice to improve sustainable agricultural systems.

SESSION 07 - SHORT TALK

7-C

The UK Crop Microbiome CryoBank Resource

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Key words: crop; microbiome; cryopreserve; sequencing; database

The UK Crop Microbiome CryoBank is a biological and bioinformatics resource funded by the Biotechnology and Biological Sciences Research Council (BBSRC). It contains cryopreserved and characterised crop microbiomes and intends to underpin national and international crop research. Three different soil types (clay, silt, and sandy) from various regions across the United Kingdom were used to cultivate six major US crops – barley, oats, oilseed rape, sugar beet, faba bean, and wheat – in a greenhouse setting to investigate the growth and rhizosphere microbiota of these crops, which were harvested at the onset of flowering. The resource includes conserved culturable isolates and microbiomes with a focus on crop rhizospheres and sequence data, plus relevant metadata for crops and soils. The full and integrated resource for the ongoing project is currently under construction and the current information can be accessed through an online database: AgMicrobiomeBase.org. Microbiomes from crop rhizospheres were sequenced for taxonomic groups, including bacterial (16S), and fungal communities (ITS – wheat only). The overall community structure of wheat and faba bean are on the way for shotgun metagenomic sequencing. Culturable isolates will be applied for *de novo* whole-genome sequencing. Sequence data analysis pipelines were developed for the state-of-the-art data outputs. The involvement with MGNify from the European Bioinformatics Institute has actively served to improve microbiome datasets' utility. The main sequence data analysis aims to: **(i)** provide an accessible dataset with complete metadata, **(ii)** compare the soil and crop sample type communities, and **(iii)** establish standardised protocols for use with inherently complex soil microbiota communities. The key objective of the project is to establish a legacy, making the datasets and resources openly accessible for academic, policy, and industry interests in sustainable development towards achieving zero hunger and a net zero food production system.

SESSION 07 - SHORT TALK

7-D

Investigating the potential roles of plant microbial communities in the differential competitive ability between weedy and cultivated *Oryza sativa*

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Keywords: Plant-growth promoting; Endophytic; Microbial community composition; Competitive ability

Domesticated rice (*Oryza sativa*) is a nutritional staple for over half of the world's population (Durand-Morat et al., 2018). There are continuous efforts to enhance rice production to meet the growing needs of the human population. One major obstacle in this effort is the devastation caused by invasive weedy rice (*Oryza sp.*) in cultivated rice paddies. This weedy type of rice is capable of causing yield losses within a cultivated rice paddy of over 50% when weedy rice plant density is a mere 8 plants/m2 (Xu et al., 2017). One of the most detrimental weedy rice traits is the ability for these plants to grow quickly and have enhanced nutrient use efficiency than cultivated rice. In this work, I studied the potential roles of plant microbial communities in the differential competitive ability between closely related weedy and cultivated rice. Beneficial plant-microbe relationships, termed plant-growth promoting (PGP), are known to contribute to plant fitness (Pérez-Jaramillo et al., 2015). However, the potential role of PGP microbial communities in contributing to weedy rice success is not yet known. I used next-generation sequencing (NGS) approaches to characterize the root endophytic microbial community composition of several genotypes of weedy and cultivated rice. Preliminary results show differential community composition between weedy and cultivated rice. Work is in progress to taxonomically identify the culturable seed endophytic microbes of these weedy and cultivated genotypes to quantify their ability to perform PGP activities. Preliminary results show more diversity of culturable endophytic microbial members from weedy rice seed than cultivated rice. This research will produce a bank of microbes with demonstrated PGP ability in this system. This is particularly important for future studies that focus on the creation and study of synthetic microbial communities and bioinoculants, which could, in turn, function in increasing plant growth and health in crop species when applied (de Souza et al., 2020).

SESSION 07 - SHORT TALK

7-E

Microbiome-based prediction of potato growth in the field

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Key words: potato, microbiome, machine learning, prediction, growth

Potato is one of the world's most important food crops, but potato production also requires high quantities of agrochemicals. The microbial communities that pervade and surround plants are known to carry out important functions for plant health and performance. The plant microbiome therefore has generated great interest as an integral part of plant biology with great new opportunities for microbiome-assisted agriculture as a biological alternative for chemical fertilizers and pesticides. In this study, we combined high-throughput microbial sequencing with drone imaging data to generate a novel microbiome-based prediction model for the performance of seed potatoes. We investigated the microbiome of seed potatoes derived from more than 240 Dutch fields and subsequently assessed the performance of the emerging potato plants in trial field in the subsequent growing season. We observed a strong influence of the field of production of the seed potato tubers on potato vitality. This indicates that potato vitality is a trait that is imprinted in the seed potato tubers by local biotic and abiotic conditions in the production field and is transferrable from one potato generation to the next. Using advanced bioinformatics and machine learning approaches, we show that sequence-based potato analysis of microbiome of seed potato tubers can be used to predict the growth of the potato crop that emerges from them. Furthermore, we were able to identify microbial signatures that are predictive for the vitality of the seed potato tuber and can thus be developed as potential biomarkers for vitality by analysing microbiome fingerprints of seed potato tubers.

SESSION 07 - SHORT TALK

7-F

Plant-microbe and plant-plant interactions favouring iron content in crop plants

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Keywords: Pea, iron dynamics, siderophore, pea-wheat intercropping

Legumes reduce the use of nitrogen inputs and the high protein content of their grains allows replacing a part of animal proteins in diet. Regarding possible risk of anaemia associated with this partial replacement, attention is given to the iron content in legume grains. It is worthwhile to note that plant iron-nutrition is known to be promoted by rhizosphere fluorescent pseudomonads and in legume-cereal intercropping.

Our goal was to identify additional microbial groups and siderophores able to increase iron content and modulate the expression of related genes in pea plants, when cultivated in sole-cropping or intercropping with wheat.

Two pea varieties, with different susceptibility to chlorosis, were cultivated in three soils. Bacterial communities in the rhizosphere (R) and the root tissues (RT) were compared for their susceptibility to iron stress, including *Pseudomonas* spp. fluorescens and their siderophores. The abundance of the bacterial groups the most resistant to iron stress, thus the most likely to contribute to iron dynamics, was further quantified in a wider range of pea varieties, in sole or intercropping in field conditions. Representative siderophores were tested for their impact on plant growth, iron content and expression of 18 genes known to mediate iron homeostasis and plant defence reactions.

Thirteen bacterial families with low susceptibility to iron stress were identified; their abundances varied upon the plant genotype but were always higher in RT than R. One family with a very low susceptibility to iron stress significantly increased iron content in wheat. The two most abundant siderophores increased pea iron content, and modulated the expression of six related genes.

Positive effect of pea-wheat intercropping on iron nutrition was confirmed. New bacterial families able to promote iron content were identified. These new bacterial families are currently further characterized to identify traits mediating the improved iron nutrition.

SESSION 07 - SHORT TALK

7-G

Grapevine Trunk Disease and the Fungal Mycobiome of Oregon Vineyards (USA)

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Keywords: Grapevine Trunk Disease Fungi GTD Metabarcode

Grapevine Trunk Diseases (GTDs) are a group of fungal pathogens that attack mature vines worldwide. In the past 30 years, their incidence has increased, both in emerging grape-producing regions, as well as those with an extended history of viticulture. In the same time span, our understanding of GTDs as a whole has shifted. Once considered a small handful of independent diseases, diseases such as Eutypa dieback, esca, and Botryosphaeria dieback, have been grouped into the GTD complex due to a core set of symptoms, all resulting from affected xylem tissue. At the same time, inconsistent symptom expression, and an ever-growing list of GTD-associated species implies there is complexity in this system that relates to fungal communities more broadly than was once considered. To better understand GTDs in the state of Oregon we conducted an amplicon metabarcoding study, amplifying the ITS1 region of fungal rDNA extracted from vine stem tissue sampled from 28 vineyards in the Rogue and Willamette valleys of Oregon. More specifically, our goals are to (1) characterize GTD species composition, examine trends in GTD distribution, and (3) compare results of culture-based and sequencing-based methods for GTD research. We found over 2000 OTUs, mostly in the Ascomycota. Visual examination of NMDS (non-metric multidimensional scaling) plots indicates that origin valley is likely the best predictor of fungal community dissimilarity. Blocked MRPP indicates that sampling position relative to the graft scar does not predict clustering of sub-samples ($A = -0.002$, $p = 0.767$). Further analysis will focus on examining how fungal communities and GTD distribution vary in relationship to vineyard age, climatic conditions, and cultivars grown.

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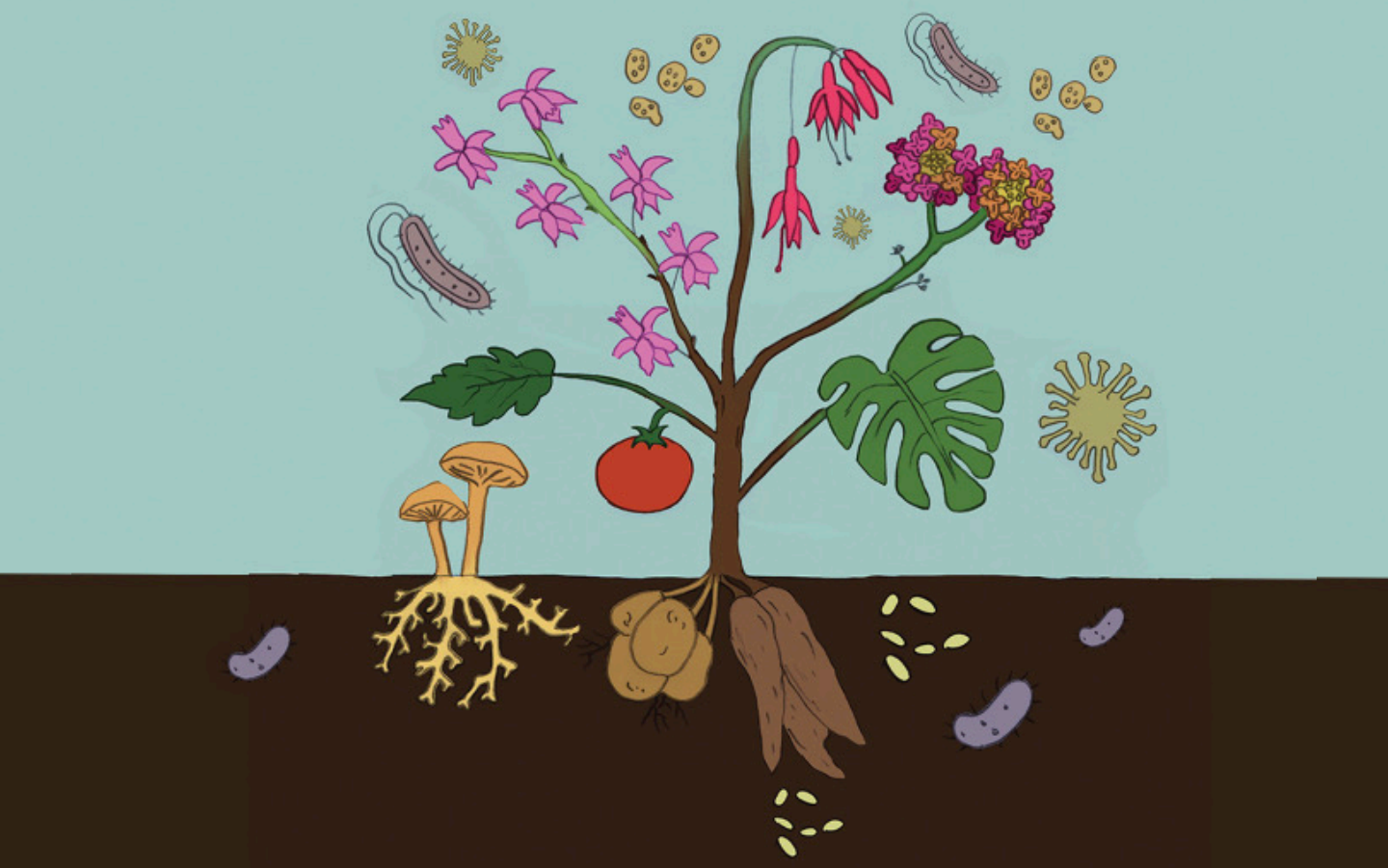

4th Plant Microbiome Symposium

POSTER ABSTRACTS

POSTER ABSTRACT

P-01

Towards a positive plant-soil feedback model as a driver for restoration of Amazonian degraded pasture soils

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Keywords: Amazonian Dark Earths, Biogeochemical cycles, Microbiome,

Removal of primary forest leads to losses of soil surface layers and decreases in soil nutrient contents available to the remaining trees, in addition to the risks of clearings caused by falling trees. In this work, we tested the plant-soil feedback to shape microbial communities for conditioning the plant host for positive interaction at rhizosphere level, enhancing the aboveground biomass of plant trees for restoration of degraded pasture soils. Amazonian Dark Earths (ADE) were applied to plant species aiming to find key microbes that can improve plant development and be suitable for biotechnological approaches. We performed a controlled experiment in greenhouse with four treatments with a pre-conditioning of 60 days with *Urochloa brizantha.* At the second phase, the treatments were: (a) Control bulk soil (C), (b) conditioned with 20% of *U. brizantha* (C+CS), (c) conditioned with 2% of ADE (C+ADE) and (d) conditioned with both *U. brizantha* and ADE (C+CS+ADE). Four species (*Cecropia pachystachya*, *Schizolobium amazonicum*, *Acacia mangium* and *Handroanthus avellanedae*) were tested for all treatments with five replicates. After 180 days, data were collected from plant and root biomasses, soil parameters and 16S rDNA sequencing from the soil rhizosphere, for taxonomical and functional diversities. These data were analyzed in R software. Our results showed that C+CS+ADE decreased the growth of *C. pachystachya*, and C+CS decreased *H. avellanedae*. These data were also similar for both root and shoot dry mass. However, the microbial communities from both C+ADE and C+CS+ADE pots showed higher abundance of bacteria with potential to control plant pathogens. Our data suggested that ADEs after *U. brizantha* conditioning does not directly promote plant growth, but have the potential for plant maintenance under adverse situations with the potential modulation of antagonists to the host microbiome. These findings can lead to possible biotechnological solutions for ecological succession in ecosystem restorations.

POSTER ABSTRACT

P-02

The role of seed transmitted endophytes in the quinoa tolerance to cadmium stress

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Keywords: Microbiome, heavy metal stress, plant growth promotion

Quinoa (*Chenopodium quinoa*) is an important crop due to its nutritional characteristics and resistance to many environmental challenges including soil salinity and drought stress. This crop is also highly tolerant to heavy metals like cadmium (Cd), though these metals can accumulate in quinoa grains putting consumers at risk. Quinoa seeds host a diverse assortment of microorganisms that are vertically transmitted from their parent plants. These seedborne microbes have been found to play a critical role in helping quinoa seeds germinate under high salt concentrations. They also have potential to help quinoa plants tolerate Cd stress and influence the uptake and translocation of this heavy metal to developing grains. Consequently, learning more about the types and functional capabilities of these microbes, as well as factors that influence their composition and activity, could help improve quinoa productivity and reduce the challenge of Cd accumulation. We suspect that quinoa genotype and exposure to different soil Cd concentrations are two critical factors influencing these communities. To test this hypothesis, we characterized the composition and functional capabilities of endophytes in the seeds of two quinoa genotypes (Pasankalla and QQ74) that varied in Cd accumulation and were grown in soils containing 0 or 10 ppm Cd. The composition and potential functional capabilities of the seedborne endophytes were determined using next-generation sequencing and bioinformatic programs. Cultural endophytes were also isolated using semi-selective media, identified via sequencing, and subject to laboratory assays to quantify their plant growth promoting properties such as capacity to produce indole-acetic acid (IAA) and 1-aminocyclopropane-1-carboxylate (ACC) deaminase, and reduce Cd stress. Nine unique culturable isolates were obtained in total, most of them from the Pasankalla genotype, and *Bacillus sp.* were the most representative. One fungal isolate was a high ACC deaminase producer and one yeast was a high IAA producer. Two bacterial isolates increased root length under Cd exposure, though the effect varied among quinoa genotypes. Culture-independent assays of quinoa seed microbiomes are still underway. Results to-date from this study provide further evidence that the quinoa seed microbiomes can influence critical root characteristics, and help mediate tolerance to abiotic stress.

POSTER ABSTRACT

P-03

Establishing a well-characterized microbial culture collection from diverse plants species under siege

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Keywords: Isolation, microbial collection, characterization, pipeline, storage system

Culture collections play a crucial role in microbiome research. Establishing microbial cultures from microbiome samples is essential to identify and catalogue the diversity of microbes from a specific environment. Moreover, having the collection at hand is highly instrumental in validating specific hypotheses generated by the microbiome analyses. Furthermore, culturing microbes allows the study of their growth and metabolic characteristics, providing insight into their functional roles. Maintaining a microbial culture collection serves as a repository of microbial genetic and metabolic information, preserving the microbial heritage for future generations. In this context, a pipeline encompassing targeted and untargeted isolation is key to guarantee representative microbial taxa and long-term preservation of valuable microbial genetic material. In this study, we applied a systematic and rigorous method to create a culture collection of diverse plant species under biotic and abiotic stresses. We isolated a broad range of microorganisms, including bacteria, fungi and yeasts that are actively recruited by plants exposed to herbivorous insects, plant pathogenic fungi, phosphate and drought stress. Each microorganism was thoroughly studied using culture-based (general and semi-selective media) and molecular methods, and documented using a name-code system that includes information on media requirements, incubation time and temperature, morphological characteristics, and taxonomic classification. Currently, the entire microbial collection is being genome-sequenced.

POSTER ABSTRACT

P-04

Metagenomic analysis reveals differential network structures in soil microbial communities associated with different Urochloa cultivars

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Key words: *Brachiaria*, soil microbial communities, P-cycling abilities, functional diversity, bioinformatics.

The rhizosphere microbiome plays a crucial role in plant growth and nutrient cycling. This study aimed to investigate the effects of *Urochloa* plant breeding on soil microbial communities and their phosphorus (P)-cycling abilities in *Urochloa* genotypes: *U. brizantha* cv. Marandu (UM), *U. brizantha* BRS Paiaguás (UP), *U. ruziziensis* (UR), and the hybrid BRS Ipyporã (UI). Soil samples were collected at three depths and short-read metagenomic sequencing was performed to analyze the taxonomic and functional composition of microbial communities. Data were analyzed in R using the "*microeco*" package, microbial networks were calculated using the *SparCC* method. The results showed that microbial communities associated with different *Urochloa* genotypes had different compositional characteristics, with network hubs and module hubs differing between the genotypes. Although, the relative abundance of microbial communities was similar across all treatments and depths, significant differences were observed in the beta-diversity of microbial communities associated with the rhizosphere of different genotypes. The phyla *Acidobacteria* and *Proteobacteria* were prominent in all treatments, with several genera of *Proteobacteria* such as *Pseudomonas* and *Halomonas* playing major roles in the networks. The UM cultivar exhibited the highest values for network diameter, clustering coefficient, and centralization, indicating a highly connected community, while the UP showed the lowest values for most network properties, yet had one more module than other genotypes, indicating a more compartmentalized network. Our findings suggest that plant-specific traits can influence the rhizosphere microbial community structure and function. In addition, functional analysis showed *Urochloa* genotypes prefer distinct genes related to phosphatase production (*pho*D, *pho*A and *pho*B) and P mobilization (*pit*, *ppa* and *phy*) and these genes correlated positively with phosphorus fractions. These differences in P-cycling abilities could affect soil nutrient dynamics and plant growth. This study highlights the importance of considering plant-microbe interactions in the selection of *Urochloa* genotypes for plant breeding programs.

POSTER ABSTRACT

P-05

Identification of ecological determinants of rhizosphere microbiome assembly of wild plant species from semi-arid Inner Mongolia

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Key words: plant niche, wild plant species, microbiome assembly, precipitation niche.

Plants actively recruit microbes from the soil, forming species-specific root microbiomes. However, their relationship with plant adaptations to temperature and precipitation remains unclear. Here we examined the host-selected and conserved microbiomes of 13 native plant species in the Xinlingol steppe, Inner Mongolia, a semi-arid region in China. Through calculating plant global precipitation and temperature niches, plant phylogenetic distances, and functional traits, we found all these factors significantly influenced rhizosphere microbiome assembly. We further quantified the strength of host selection and observed that plants with wider precipitation niches exhibited greater host selection strength in their rhizosphere microbiome assembly and higher rhizosphere bacterial diversity. In general, the rhizosphere microbiome showed a stronger link to plant precipitation niches than temperature niches. *Haliangium* exhibited consistent responsiveness to host characteristics. Wild plant species have a small set of highly connected conserved amplicon sequence variants (ASVs), with unclassified Isosphaeraceae as cores in the hub. Seven out of the total 25 genera in the conserved network are found in the human gut microbiota. Our findings offer novel insights into host selection effects and ecological determinants of wild plant rhizosphere microbiome assembly, with implications for steering the root microbiomes of wild plants and understanding plant-microbiome evolution.

POSTER ABSTRACT

P-06

Slime Time in the Rhizosphere: mucilage release and root cap development as microbe selection factors in Arabidopsis root colonization

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Plants naturally modify the chemical, physical, and biotic environment of the soil by exuding a complex polysaccharide mixture called root mucilage. Mucilage can sequester ions, aggregate soil, and store water due to its charge, adhesive, and hygroscopic properties. Several Arabidopsis thaliana genes have described functions in mucilage processes, and in crops, mucilage phenotypes can vary across strains with different tolerances to stress. But current studies have not fully bridged the functions of mucilage genes with their physiological impact. My research uses microscopy and root cap mutants available in A. thaliana to explore whether root mucilage contributes to abiotic stress tolerance, how mucilage processes are regulated, and how changes in mucilage and root cap regulation might affect microbe associations.

POSTER ABSTRACT

P-07

Assessing the impact of water-soluble fertilization concentration on the rhizosphere and endosphere microbiome of Petunia × hybrida

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Key words: floriculture, endosphere, rhizosphere, petunia, peat

Petunia is the most popular flowering potted plant in the US. Flowering potted plants are cultivated in containers filled with soilless substrates. High levels of fertilization are required to produce high-quality plants. However, increasing concerns exist regarding fertilizer affordability, availability, and environmental impact. The root microbiome (endosphere and rhizosphere) can provide additional functions to enhance nutrient availability for plant uptake. While the root microbiome has been studied extensively in soil-based crop production, less is known about the microbiome of flowering crops grown in peat-based substrates. The objective of this study was to analyze the rhizosphere and endosphere microbiome of two *Petunia* × *hybrida* cultivars ('Picobella Blue' and 'Wave Purple') grown under limited, optimal, and excess chemical fertilization. We will characterize the core root microbiome of *Petunia* × *hybrida*, and the unique microbial taxa associated with each cultivar. In addition, we will investigate the impact of various fertility levels on microbial community composition and diversity. Our goal is to understand how fertilization levels, and subsequent pore-water mineral nutrient availability, alter the root microbiome and how this in turn quantitively changes plant mineral nutrient uptake. Our results will contribute to the development of microbial biostimulants targeted to improve plant mineral nutrition in soilless production systems.

POSTER ABSTRACT

P-08

Characterization of native algae-bacteria consortia from Ecuador with potential wastewater remediation capacities

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Keywords: algae-bacteria consortia, wastewater, metabolic pathways

The proper treatment, remediation, and management of wastewater is of great importance, but conventional strategies are costly and have pollutant removal constraints. Microalgae-bacteria consortia have been explored to overcome such limitations, due to the synergy between the metabolic capacities of these organisms. The biodiversity potential for wastewater management remains unexplored and unreported in Ecuador. The present study aimed to characterize the composition and remediation capacity of native consortia from the Amazon, Highlands, and Galapagos Islands in wastewater. Laboratory experiments were performed where the consortia were subjected to synthetic wastewater for 12 days, under light and dark conditions, and data were collected on days 0, 6 and 12. Shotgun metagenomic analysis was carried out to characterize microbial composition. Diversity indexes were calculated to assess diversity between and among consortia. Functional analyses were performed to correlate metabolic pathways to remediation capacity. Preliminary results show that the microbial composition primarily includes 12 phyla, where Proteobacteria and Chlorophyta are the most abundant in each sample. In terms of diversity (effective number of species and evenness) and composition, the Amazon consortia was the most diverse. Under dark conditions, the Highlands and the Amazon consortia show a clear pattern of lower abundance of photosynthetic microorganisms on day 12. In contrast, no clear trends were found for the Galapagos samples. Preliminary functional analysis identified 1,844 metabolic pathways that need to be further analyzed to correlate microbial composition and remediation capabilities. The present study is a first step towards the application of novel and efficient biological remediation strategies for wastewater treatment and management in Ecuador.

POSTER ABSTRACT

P-09

Deciphering the impact of soil conditions on the composition and potential plant growth promoting activity of the rhizosphere microbiota of wheat and maize agroecosystems in Morocco

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Keywords: rhizosphere microbiota, plant growth promoting activity, wheat, maize, soil characterization

The plant-soil interface, the rhizosphere, is inhabited by microbial communities with potential beneficial functions for plant growth. These communities constitute the rhizosphere microbiota, and its members originate majorly from the surrounding soil. We hypothesize that soil nutrient availability contributes to modulate the rhizosphere microbiota composition and function. We follow a three-pronged experimental approach thorough soil characterization, phylogenetic profiling of microbial communities and functional screening of the readily culturable microbiota.

Wheat and maize are important crops grown in Morocco, across a variety of soils and agroclimatic conditions. To represent the wheat and maize Moroccan agroecosystems, seven regions were selected, comprising four fields per region with five random sampling points each containing a pooled sample of five plants and nearby unplanted soil. In total 140 samples, from 28 fields of 7 regions were collected for each cropping system.

Extensive soil physical and chemical characterization, with a focus on nutrient content, was used to group soils according to their similarities. Illumina generated 16S rRNA gene bacterial profiles will be interrogated to determine the impact of soil condition on the rhizosphere and unplanted soil taxonomic composition. Regions of interest for high throughput microbial isolation were selected according to microbial and soil profiling information. Plant growth promoting activity of isolates are currently being determined, and these will be used to construct bacterial synthetic communities for plant inoculation.

This framework will allow us to obtain mechanistic understanding, linking soil conditions with microbiota structure and functional capabilities of microbial isolates, facilitating experimental testing of hypothesis and the selection of suitable consortia for crop inoculation. The final objective is to put to work the bacterial genetic diversity of Morocco to alleviate crop's nutrient and environmental stresses. This research is supported by the OCP group.

POSTER ABSTRACT

P-10

Application of biochar and compost to mining soil reduces lead (Pb) and zinc (Zn) toxicity to plants and induces changes in soil microbial communities in a long-term study

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Keywords: bioavailability, heavy metals, microbial community, soil health, biochar

Heavy metals (HMs) are the most frequent contaminants in soil. At elevated concentrations, HMs can be toxic, impairing soil functioning and reducing soil productivity. Organic amendments such as biochar and compost have been proposed as sustainable alternatives to stabilize HMs in soil. These amendments can immobilize pollutants by different chemical and physical mechanisms, reducing HM toxicity towards plants and soil microorganisms, which may then enable restored land to be reused. Nonetheless, the long-term effects of these amendments on HM stability and soil health are not fully understood. This study explores the ability of wheat straw biochar alone or in combination with green waste compost to reduce HM toxicity in an outdoor pot experiment using a mining soil highly polluted with Pb and Zn. The experiment was conducted over an 18-month period after which soil samples were used for chemical analysis. Community composition and relative abundance of soil microbes (bacteria and fungi) were studied by high-throughput sequencing. Half of the pots were planted with *Lolium perenne* to assess the impact of the amendments on plant performance over two harvesting seasons. Results demonstrated that biochar and green waste compost significantly reduced the concentrations of bioavailable HMs and limited plant uptake over an 18-month period. No additional benefit was identified from the combined application of biochar and compost. Both amendments modified the soil microbial community composition and relative abundance. These changes were correlated with reduced HM toxicity and an increase in soil pH and organic matter. The microbial groups that increased with the addition of the amendments were associated with nutrient cycling, suggesting enhanced soil functioning. Overall, this study confirms the potential of biochar and compost to reduce the long-term ecological risk of sites highly contaminated with heavy metals.

POSTER ABSTRACT

P-11

From Susceptibility to Resilience: Uncovering the Rhizosphere Microbial Contributions to Drought Tolerance in Common Bean

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Keywords: Microbial ecology, Drought tolerance mechanisms, flux balance analysis, network analysis

Climate change has intensified drought-related events in agricultural production, adversely affecting economic stability, societal well-being, and food security. While genetic advancements in crops and soil microorganisms have shown promise in enhancing resistance to abiotic stressors, our understanding of the rhizosphere microbiome remains limited, especially in tropical regions. In this study, four common bean (*Phaseolus vulgaris* L.) genotypes underwent 96 hours of drought stress. Two genotypes are renowned for their drought susceptibility (SC) (IAC-Carioca 80SH and IAC Milenio), and the other two for their drought tolerance (TL) (BAT477 and Sea5). Using short-read metagenomic sequencing, we analyzed the rhizosphere microbial composition across these genotypes throughout the experiment. Based on the community structure analysis, we found that rhizosphere communities in all genotypes were similar before water stress exposure. However, after 96 hours of drought, SC plants' microbial structure remained largely unchanged, while the rhizosphere community of TL plants underwent significant alterations. Network analysis revealed an increase in the number of edges for SC plants compared to the control, suggesting an increase in the complexity of microbial interactions under stress. In contrast, TL plants exhibited a decrease in edges compared to the control, indicating a reduction in the complexity of microbial interactions and potential selection of specific stress-tolerant microorganisms. These results imply that TL plants might favor a distinct community compared to SC plants, thus enhancing their ability to cope with such challenges. Flux balance analysis of rhizosphere microbial communities suggested that chemical flux of compounds involved in the regulation of stomatal closure, osmotic balance, and protection of cellular membranes, as well as affecting membrane fluidity and permeability, could contribute to drought resistance in TL plants. Our study illustrates the effects of abiotic stress on plants and highlights the role rhizosphere microbial communities play in fostering stress tolerance in the context of climate change.

POSTER ABSTRACT

P-12

Study of soil fungi and bacteria diversity associated with tillage systems and cultivated plant species

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Key words: no-till, PCR amplification, soil DNA next-generation sequencing, bioinformatics analysis, soil microbial diversity

The abundance and diversity of microorganisms allow inferring about soil health and fertility, which are associated with agricultural management practices. The objective of this research was to establish a baseline of the fungi and bacteria diversity and abundance in a soil under two tillage systems and two plant species, which will allow determining the dynamics of these microorganisms in the long term. The trial was established on agricultural soil from Pichincha under a split plot design; where the large plot contains the crop rotation scheme with corn and beans, and the small plot has the tillage systems (no-till and conventional tillage). Soil was sampled from the first 10 cm of the surface, from which DNA was extracted. The DNA quantity and quality was determined with spectrophotometry. The 16S ribosomal gene V3 and V4 regions and the 18S ribosomal gene ITS1 and ITS2 were PCR amplified, DNA next-generation sequencing was performed using the MiSeq Illumina PE 2x250 bp platform, and bioinformatics analysis was conducted using Quime software. The results indicate that the abundance and diversity of fungi (Chao1=273-380, Shannon=5.20-6.17) and bacteria (Chao1=1412-1443, Shannon: 8.74-9.17) are slightly higher on the soil under no-tillage in the case of corn, the opposite occurs with beans. The most abundant genus of fungi in all the plots is Penicilliun (30-47%), followed by Fusarium (1 and 6%). In bacteria, the genera present in percentages between 1-3% are: Rhodoplanes, Kaisobacter, Candidatus, Bacillus, Balneimonas, Nitrospira, while between 73 and 79% are unclassified. In conclusion, the present research allows us to infer that there is a direct effect of the tillage and cultivation system on the soil fungi and bacteria abundance and diversity.

POSTER ABSTRACT

P-13

Comparison of fall armyworm microbiota fed on different plant diets

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Keywords: fall armyworm, bacterial microbiome, maize, sorgum, millet

Insect gut microbiota plays important roles in many physiological processes of the host including digestion, protection, detoxification, and development of immune responses. Moreover, it has been hypothesized that gut bacteria play an important role in insects´ ability to adapt to different foods. Diet has received considerable attention due to its strong effect on the composition of the microbial community. Fall armyworm FAW *Spodoptera frugiperda* feeds on approximately 350 different species of plants, but prefers certain cultivated plants (maize, millet, sorghum and rice). So far, no one study has been published on the microbiome of FAW larvae fed with different plant diets. In this study we investigated the microbiome composition (bacterial abundance and diversity) of FAW gut larvae fed with leaves of maize (a hybrid and a landrace), sorghum (two varieties) and millet (one variety). We extracted DNA for FAW gut larvae and made 16S rDNA amplification and sequencing. We found that *Sphingomonas* were more abundant in larvae guts from sorghum Andiwo and maize Nyamula, and less abundant in guts from sorghum Gadam, pearl millet and maize Duma. Enterococcus was equally abundant in larvae guts from sorghum Gadam, maize Nyamula and maize Duma, whereas this genus was scarce in guts from sorghum Andiwo and pearl millet. The highest diversity of bacteria was found in larvae guts from sorghum Gadam (H = 3.2) and pearl millet (H = 3.1). We found that all the members of the bacterial communities are present in the guts from all diets. However, bacterial microbiota from pearl millet guts varied slightly comparing with the other plant diets. Our study provides first insights into the bacterial community composition of FAW larvae fed with different plant diets. Further studies can contribute to understand how certain gut bacteria species may aid FAW to adapt to feed on certain hosts plants species.

POSTER ABSTRACT

P-14

Molecular and chemical cues in the endophytic microbiome

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Keywords: Endophytes, TnSeq, disease suppression

We recently discovered that plants under attack by fungal root pathogens can actively recruit endophytic microbes inside their root tissues (endosphere) for protection. We showed that *Cupriavidus* and *Stenotrophomonas* species were significantly enriched in the root endosphere of sugar beet upon *Rhizoctonia solani* infection. In addition, metagenomic analyses of the endosphere showed a high abundance of biosynthetic gene clusters (BGCs) encoding for phenazines, non-ribosomal peptide synthetases (NRPSs) and lanthipeptides associated with these taxa, but their functional roles in plant colonisation and protection are yet unknown. To characterise the taxonomic, genomic, and functional traits of *Cupriavidus* and *Stenotrophomonas,* we established a collection of 45 *Cupriavidus* and 310 *Stenotrophomonas* isolates from sugar beet root endosphere and selected five unique isolates after dereplication based on BOX-PCR and 16S sequences. Genome sequencing, *in vitro* and *in vivo* antagonistic activity and metabolomics experiments are ongoing to investigate their functional potential and to resolve the role of the identified BGCs in endophytic colonisation and plant protection. We also analysed the genomic sequences in MicroLife, a new bioinformatic pipeline to identify specific genomic features associated with the endophytic lifestyle of bacteria. Our initial results from MicroLife showed a large degree of genomic variation among the endophytic *Cupriavidus* isolates and those isolated from other environments. Random-barcode transposon-site sequencing (RB-TnSeq, BarSeq) experiments with endophytic bacteria are underway to complement MicroLife results and identify genetic factors involved in endophytic lifestyles. In conclusion, our results and ongoing experiments will shed light on microbiome assembly in the endosphere and which genes and metabolites are expressed in plants under siege.

POSTER ABSTRACT

P-15

Factors governing attachment of Rhizobium leguminosarum to legume roots

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Keywords: Rhizobia, pea roots, bacterial attachment, pH

Primary attachment of rhizobial bacteria to host legume roots, the first physical interaction during nitrogen-fixing symbiosis, depends on pH. We have used genome-wide insertion sequencing (INSeq), together with luminescence-based attachment assays, and demonstrate that primary attachment of Rhizobium leguminosarum biovar viciae 3841 to Pisum sativum (pea) roots is more complex than was previously thought [1]. In total, 115 genes are needed for initial attachment under one or more of the conditions (acid, neutral or alkaline pH) investigated, with 22 required under all conditions. These include those encoding a cell-surface filamentous hemagglutinin adhesin (RL4382) and its transporter (RL4381), transmembrane protein RL2400, RL3752 (PssA, glycosyl transferase) affecting capsular polysaccharide and transcriptional regulator RL4145 (PckR). The 54 genes required for attachment at pH 7.0 were investigated for the effect mutation has on the ability to form a nitrogen-fixing nodule.

Unsurprisingly, the bacterial cell surface plays a key role in attachment to roots, but environmental conditions influence genetic requirements which are therfore not necessarily constant. For example, glucomannan biosynthesis protein A (GmsA, RL1661) is required to attach to roots at pH 6.5 but not at pH 7.5 [2]. We demonstrate by INSeq and attachment assays using Lux-labelled bacteria a requirement for gmsA at pH 6.5. and pH 7.0, while it is not required at pH 7.5.

Our results demonstrate the complexity of primary root attachment and diversity of mechanisms involved in the initial reaction between bacteria and plant roots on their pathway to successful symbiosis.

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POSTER ABSTRACT

P-16

Bioreactors, carbon sources and diazotrophic microbial communities: key elements for the production of nitrogenous biofertilizers and reuse of agroindustrial wastes

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Key words: short chain fatty acids, plant-growth-promoting; batch; continuous culture

Today's agriculture uses about 100 million tons of nitrogenous fertilizers per year to sustain world food demand; the production of these fertilizers and their application in the field have caused considerable environmental effects. On the other hand, food production is also associated with the production of more than 900 million tons of agro-industrial residues per year. Alternative solutions have been proposed for these problems based on: the ecological theory of microbial communities, bioprocess engineering and the recovery of agro-industrial waste in order to produce biofertilizers. The objective of this work was to integrate the aforementioned solution alternatives to propose and test a novel method to cultivate diazotrophic microbial communities by enriching a soil sample in bioreactors that supply N2 by air pumping and are operated with different carbon sources. The results show in the first instance an increase in diversity when the soil sample is cultivated in the reactors using citrate as a source of C and also show that tomato plants inoculated with the effluent achieve a growth equal to that obtained with synthetic fertilizers. On the other hand, it was possible to demonstrate that short-chain fatty acids from pig wastes can be used as a source of C to feed the reactors and that inorganic forms of nitrogen can even be obtained in the supernatant in concentrations that can match a commercial nutrient solution. Reactor microbial biomass also have the capacity to colonize rizhosphere of tomato roots and contribute to plant growth. We demonstrate the potential of the methodology that we have called directed bioprospecting to grow a complex diazotrophic microbial community for agricultural purposes. The simplicity of operation of the reactor and the ability to operate with carbon sources from agro-industrial waste treatment makes its application promising for developing countries with low technological progress.

POSTER ABSTRACT

P-17

Maize microbiome: A key ally in the fight against drought

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Drought is abiotic stress that limits plant growth and crop production. Several scientific studies have demonstrated the close relationships between plants and coexisting microorganisms, helping to stimulate early defense pathways and preparing plants to cope with stress. Recently, it has been observed that plants under stress change in root microbiome diversity. Maize is a threatened crop since irrigation is limited in the Andean region. This study describes the microbiome of two Ecuadorian Andean maize varieties (PEPA and INIAP-122) under drought stress. We found significant differences between the diversity of microorganisms in the rhizosphere and root endosphere, and we identified the presence of taxa highly related to drought tolerance, allowing us to infer that after an arduous adaptation of the soil and maize to drought, only taxa with the ability to induce drought tolerance were recruited. Thanks to the climatic characteristics (low precipitation) of the parish of Malchinguí, in the canton Pedro Moncayo (Province of Pichincha-Ecuador), we could experiment with the plants in soil with a history of drought. Once we described the microbiome of the Malchinguí soil and intended to analyze the impact of the microbiome on plant growth under drought stress, we planted maize in sterile soil in contrast with plants with a preserved microbiome. Plants grown in sterile soil showed signs of stress after two days with a stomatal conductance below 100 mmol-2s-1. The physiological response shows that plants grown without microorganisms are less tolerant to drought. Plants grown in soil with a conserved microbiome tolerated more than seven days of absolute drought, maintaining turgor. Plant genetics play an important role in drought tolerance, as we observed that plants of the INIAP-122 variety grown in sterile soil were more significant than those grown in soil with a conserved microbiome. The next step will be to describe the microbiome associated with more resistant plants and unravel plant defense mechanisms.

POSTER ABSTRACT

P-18

Exploration and identification of the rhizosphere microbiome of the genus Inga in the Ecuadorian Amazon

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Key words: Amazon, Ecuador, Inga, Microbiome, Tiputini Biodiversity Station, biodiversity.

The Amazon rainforest is one of the most megadiverse ecosystems in the world. At USFQ's Tiputini Biodiversity Station (TBS) in the Ecuadorian Amazon, we have studied two main Ecosystems, the Várzea Partially Flooded Forest, and the Terra Firme Forest, which has relatively well-drained soils. In both environments it has been identified that the trees of the genus Inga are predominant. This genus belongs to the *Fabaceae* family, which is characterized by forming symbiotic associations with both mycorrhizal-forming fungi and nitrogen-fixing bacteria. This research aims to generate information on the biodiversity, composition and abundance of microorganisms associated with the rhizosphere of Inga seedlings in the Ecuadorian Amazon. A physicochemical analysis of the soil samples associated with the rhizosphere of Inga seedlings was carried out, and through staining and evaluation of Inga seedling roots, it was possible to identify mycorrhizal structures. Subsequently, the ITS and 16S regions were sequenced for subsequent analysis of respectively fungi and bacteria using the QIIME2 platform. The mycobiome was mainly made up of 68.67% fungi from the Ascomycota phylum, 18.59% from the Basidiomycota phylum, and 1.42% of the sequences belonged to the Glomeromycota phylum, which includes arbuscular mycorrhizal fungi. In the bacterial community, the predominant phyla were Proteobacteria, Acidobacteria and Actinobacteria. The present study describes for the first time the microbiome including arbuscular mycorrhizae associated with the rhizosphere of seedlings of the genus Inga at the Tiputini Biodiversity Station in the Ecuadorian Amazon. In addition, it is possible to identify that abiotic factors such as soil edaphic conditions and environmental climatic conditions, and biotic factors in the soil affect the diversity of microbial communities.

POSTER ABSTRACT

P-19

The rhizosphere microbiome of wild tomato in its center of origin

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Key words: wild tomato, rhizosphere, microbiome profile, native habitat, Ecuador

Domestication and breeding have substantially changed the genetic and phenotypic traits of plant species. How domestication affected the taxonomic and functional diversity of microorganisms living on and inside plant tissues is largely unknown for most species. To investigate if domestication of plants impacted the association with specific microbial taxa and beneficial microbial traits, we took a BackToRoots approach to first determine the taxonomic and functional microbial composition of wild tomato *S. pimpinellifolium* rhizosphere growing in its center of origin in southern Ecuador. We specifically focused on taxonomic profiling of bacteria and fungi associated with tomato roots in three sites in Loja province (South of Ecuador). Bulk and rhizosphere soil samples of wild tomato were collected from 1400 to 200 masl (meters above sea level). The sites resulted to be significantly different based on their physicochemical soil properties (r2 = 0.18048, p = 0.0112). Beta diversity analysis showed that the microbial community in bulk soil samples was significantly different among sites (bacteria: r2 = 0.0820, p = 2e-04; fungi: r2 = 0.0853, p = 1e-04). However, the rhizosphere community composition of the wild tomatoes grown in each of these three distinct sites was similar, sugesting similar selective forces of the wild tomatoes on microbiome assembly. The wild tomato rhizosphere in its center of origin was shown to be dominated by *Enterobacter*, *Rhizobium, Lactococcus*, *Lechevalieria*, unidentified fungi, *Fusarium, Aspergillus, Acrocalymma, Torula* and *Papiliotrema*. Subsequent metagenome analyses also revealed similarities among the different sites with signaling and cellular processes, carbohydrate metabolism, membrane transport and amino acid metabolism as the most dominant functional categories. It can be concluded that even though there are variations among tomato genotypes, soil properties, and soil microbiomes, wild tomatoes still recruit similar bacterial communities and microbial functions in the rhizosphere, while exhibiting different fungal communities.

POSTER ABSTRACT

P-20

Mining the soybean microbiome for disease-suppressive microbes

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Plant-associated microorganisms can exert beneficial effects on the host, offering possibilities for the improvement of agronomical traits in crops through the manipulation of their microbiomes. Among these traits, resistance to pathogens is of major relevance for agriculture. In this work, we investigated how infection of soybean with Asian Soybean Rust (ASR) affects the leaf and root/rhizosphere microbiome. We hypothesize that leaves infected with ASR present an altered bacterial community that is enriched in strains with the ability to antagonize the fungus *Phakopsora pachyrhizi*, the causal agent of ASR. We also hypothesize that soybean plants exposed to aboveground infections can modulate the rhizosphere microbiota and recruit beneficial microbes via root exudates. To test these hypotheses, we evaluated the bacterial communities that colonize healthy and infected field-grown soybean leaves and roots via high throughput sequencing of the 16S ribosomalgene. We found remarkable differences in the bacterial populations inhabiting these leaves and identified taxa that show either higher or lower relative abundance in infected leaves. These results confirm that ASR affects the soybean leaf microbiome. In the roots/rhizosphere, however, we did not detect significant differences between healthy and infected plants. We also isolated bacteria from soybean leaves and roots to assemble a culture collection of 'soybean-associated bacteria'. This collection (named *Soybiome*) currently consists of 3,038 strains and constitutes a valuable resource for the identification of microorganisms that can exert any kind of beneficial effects on plants. Indeed, initial screenings have revealed strains that can antagonize a set of 6 soybean pathogens, including *Phakopsora pachyrhizi*. The characterization of such strains will pave the way for the development of biofungicides effective against one of the most important plant diseases in soybeans plants.

POSTER ABSTRACT

P-21

Influence of Grafting on Rootstock Rhizosphere Microbiome Assembly in Rosa sp. 'Natal Brier'

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Keywords: rose; Rosa spp.; microbiome; grafting; rootstock; scion; Natal Brier; ExplorerTM; FreedomTM

The root microbiome is vital in plant development and health and is highly influenced by crop cultural practices. Rose (Rosa sp.) is the most popular cut flower worldwide. Grafting in rose production is a standard practice to increase yield, improve flower quality, or reduce root-associated pests and diseases. 'Natal Brier' is a standard rootstock used in most commercial operations in Ecuador and Colombia, leading countries in producing and exporting ornamentals. It is known that the rose scion genotype affects root biomass and the root exudate profile of grafted plants. However, little is known about the influence of the rose scion genotype on the rhizosphere microbiome. We examined the influence of grafting and scion genotype on the rhizosphere microbiome of the rootstock 'Natal Brier.' The microbiomes of the non-grafted rootstock and the rootstock grafted with two red rose cultivars were assessed using 16S rRNA and ITS sequencing. Grafting changed microbial community structure and function. Further, analysis of grafted plant samples revealed that the scion genotype highly influences the rootstock microbiome. Under the experimental conditions, the rootstock 'Natal Brier' core microbiome consisted of 16 bacterial and 40 fungal taxa. Our results highlight that the scion genotype influences root microbe's recruitment, which might also influence the functionality of assembled microbiomes.

POSTER ABSTRACT

P-23

Rice straw recycling increased soil microbial functional diversity during the decomposition of rice straw

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Key words: rice straw, biogeochemical cycles, metagenomics, enzyme activities, agronomic parameters.

Agricultural residues are precursors of soil organic matter, its decomposition in the field allows the entry of carbon and other nutrients into the system. However, it can also favor the proliferation of pathogens, converting it into a great challenge for producers. Among the alternatives to waste management are, burning of rice straw and/or its incorporation into the soil. However, the knowledge of the impact of these strategies on the microbial community and especially in their functionality is limited. This study sought to determine the effect of the application of four rice straw management strategies, on the structure and function of the microbial communities associated with the biogeochemical cycles of carbon (C), nitrogen (N), and phosphorus, those strategies are: 1. Leave rice straw as a mulch; 2. Rice straw as a mulch with the addition of microorganisms; 3. Rice straw plus microorganism inoculum followed by incorporation into the soil; 4. Burning of rice straw followed by ashes incorporation into the soil). A field trial was implemented with a random incomplete block design, sampling soil three times during a cultivation cycle. The soil was characterized by physicochemical and enzymatic analyzes, the microbial communities were described using shotgun metagenomics. Productivity and phytosanitary status of the rice crop were determined. The results showed differences in pH, enzyme activities, and microbial community at initial and degradation time compared to final time. Genes related to diverse processes of the N cycle as nitrogen fixation, nitrification, denitrification among others were identified. Regarding the C cycle, glycosyl hydrolases with action on hemicellulose increased especially at degradation times. This study suggests that the strategies of using rice straw, either as mulch or incorporated in the soil with microorganisms, are an adequate option for the final disposal of the rice straw, as agricultural practice to improve sustainable agricultural systems.

POSTER ABSTRACT

P-24

Deciphering Microbial Cross-kingdom Carbon Consumption in Plant Roots

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Key words: Microbe-microbe interactions, synthetic community, Carbon reallocation, 3-O-Methyl-glucose, root microbiota

Plants are colonized by diverse multi-kingdom microbial communities whose interactions lead to a healthy plant phenotype. However, the metabolic interactions that facilitate the coexistence of these microbes within plants remain poorly understood. Given the significance of resource availability in microbiome assembly, we investigated the dependencies of carbon (n=190) consumption between microbes, focusing on cross-kingdom interactions. To address this knowledge gap, we conducted a comprehensive screening of carbon source consumption, involving 11 bacterial and 4 fungal strains representative of the Arabidopsis thaliana root microbiota. In addition, we performed community profiling experiments using Bacterial Synthetic Community (SC) (n = 11), Fungal SC (n = 4), or the full SC (n = 15). Through a combination of microbiology, plant assays, and the SC approach, we deciphered the complex multi-kingdom consumption of 3-O-Methyl-Glucose.

Our findings revealed a predominantly additive effect of carbon consumption at the community level, with only a few instances of multi-kingdom dependencies among the 190 carbon sources tested. Notably, one such dependency involved the consumption of 3-O-methyl-glucose (3OMG), a carbon source present in soil that is taken up by plants but remains unmetabolized by both plants and microbes. We attribute this meaningful consumption of 3OMG to the high abundance of Plectosphaerella cucumerina in the presence of three specific bacterial strains associated with the genera Pseudomonas sp., Agrobacterium sp., and Mesorhizobium. Intriguingly, inoculation of 3OMG in a plant-gnotobiotic system colonized with the fungal fraction of our SynCom resulted in the complete reduction of the pathogenic effects typically observed in natural soil.

In conclusion, the unique metabolism of 3-O-Methyl-Glucose by the multi-kingdom SynCom represents a crucial source of carbon that becomes available to the plant through its microbiota. This study's overall results hold significant implications for comprehending metabolic interactions between microbial kingdoms at the community level in natural systems and their potential impact on plant health and development.

POSTER ABSTRACT

P-25

Unravelling the volatile-mediated suppression of *Fusarium* growth by phyllosphere yeasts

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Key words: Yeast, Volatiles, *Fusarium*, Mycotoxins, transcriptomics, wheat phyllosphere

Volatile compounds are low molecular weight compounds which play a role in numerous biological processes, including (inter)species-communication and modulation of growth and development of other (micro)organisms and plants. Most studies on microbial volatiles have focused on soil and rhizosphere microorganisms, whereas volatile production by phyllosphere microorganisms has been largely overlooked, especially phyllosphere yeasts. Previously, we have established and screened a diverse collection of phyllosphere yeasts for antagonistic activities against plant pathogens through the production of volatile compounds. We identified isolates that strongly inhibit the growth of the mycotoxin-producing pathogen *Fusarium graminearum.* However, the molecular mechanisms underlying the volatile-mediated effects on pathogen growth, more specifically *F. graminearum*, is still largely unknown. To identify suppressive volatile compounds and the molecular mechanisms mediating this yeast-pathogen interaction, we coupled yeast volatile profiling and transcriptomic analysis of *F. graminearum* exposed to yeast volatile compounds. We found that specific volatiles, applied individually or as a mix, downregulated the expression of the mycotoxin genes *TRI5* and *TRI11*. These results demonstrate the potential of volatile compounds in combating *Fusarium* infection and decreasing mycotoxin contamination in grains.

POSTER ABSTRACT

P-27

Small things matter: the contribution of the microbiome to induced systemic resistance along the root-shoot axis

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Keywords: Induced systemic resistance; coumarins; *Pseudomonas*; microbiota assembly

In nature, plants harbor myriads of microbes. Microbes like *Pseudomonas simiae* WCS417 (WCS417) are beneficial as they enhance plant growth and defense. Upon colonization of Arabidopsis roots, WCS417 activates an induced systemic resistance (ISR) in different plant compartments including the shoot. Key components of WCS417-induced ISR, MYB72 and BGLU42, are also required for production and exudation of coumarins in the rhizosphere. Coumarins can shape the root microbiome, e.g. by favoring beneficial and repelling detrimental microbes. Ongoing work in our group suggests that root colonization by WCS417 induces coumarin accumulation not only in roots but also in leaves where ISR is expressed. Therefore, we hypothesize that coumarins can have a role in ISR by regulating the phyllosphere microbiome. To study the contribution of the plant microbiome on ISR, we grew Arabidopsis in natural soil with its resident microbiome and tested for ISR against the leaf pathogen *Pseudomonas syringae*. Our findings revealed that root colonization by WCS417 significantly affects microbiome assembly along the root-shoot axis. To what extend changes in the phyllosphere microbiome contribute to ISR is under investigation. Furthermore, to understand the role of coumarins in microbiome assembly on roots and shoots of ISR-expressing plants, we currently explore microbiome assembly on roots and shoots of WCS417-colonized Arabidopsis mutants *myb72, f6'h1,* and the overexpressor line ox-BGLU42.

POSTER ABSTRACT

P-28

Mechanisms of drought stress tolerance by the root-colonizing beneficial bacterium Pseudomonas simiae WCS417

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Keywords: rhizobacteria; abiotic stress; drought-stress tolerance; *Pseudomonas*; SynCom

Abiotic stresses, such as soil salinity and drought, have severe detrimental impacts on plant growth, health and crop productivity. According to the Food and Agriculture Organization of the United Nations, global economic costs associated with droughts are estimated at $34 billion annually. Microbial biostimulants, such as those containing beneficial rhizobacteria, are a promising and eco-friendly solution to addressing the negative impacts of water scarcity in agriculture. However, the exact mechanisms by which rhizobacteria promote drought stress tolerance remain unexplored. Using the *Arabidopsis thaliana* plant model and *in vitro* screening assays, we identified the strain *Pseudomonas simiae* WCS417 as a plant growth promoter under osmotic stress conditions in mono-association. Inoculation of WCS417 significantly rescued plants from drought stress and led to the enhancement of shoot and root biomass, compared to non-inoculated mock plants. We are currently performing directed-reverse and forward genetic screens using a random-barcoded transposon (RB-Tn) library to identify key genes responsible for the observed phenotype. Using a 34-member bacterial synthetic community (SynCom), we will determine if WCS417-observed growth promotion can be recapitulated in a soil-based system and a bacterial community context with *A. thaliana* and *Solanum lycopersicum*. Furthermore, the 34-SynCom members will be tested in mono-association and as a community to determine similarities and differences in drought stress tolerance promotion mechanisms by coupling phenotyping with comparative transciptomic analyses, 16S rRNA amplicon sequencing and plant mutants compromised in phytohormone signaling and biosynthesis. Understanding key processes of abiotic stress tolerance in plants is essential for advancing and guiding the development and adoption of microbial inoculants in agriculture, especially considering climate change and the associated global warming effects on crop productivity.

POSTER ABSTRACT

P-29

Exploring the Biotechnological Potential of Anaerobic Microbiomes

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Keywords: sulfate-reduction, metabolism, cooperation, fitness

Anaerobic microbiomes refer to diverse microbial communities that thrive in environments devoid of oxygen. These communities exist in a variety of habitats, such as gut, soil, sediments, wastewater, and bioreactors. Anaerobic microbiomes provide several advantages, including the ability to facilitate bioremediation processes, such as the precipitation of metals via sulfate-reduction. Additionally, they can improve soil fertility and nutrient availability, as well as be utilized to produce biofuels, bioplastics, and biopharmaceuticals, among other applications. We have primarily focused on characterizing the prokaryotic microbiomes of various anaerobic environments, including freshwater sediments, acid mine drainages, sludge from sulfate-reducing bioreactors, and cultured colonies. We sought to understand the genetic and functional traits of these microbiomes through the use of classical culture techniques, high-throughput sequencing, and bioinformatic tools. Our assessments included the analysis of microbial community structure, compositional changes in response to abiotic factors, and functionality inference. We have found that microbial communities under sulfate-reducing conditions exhibited reduced diversity, with interactions leading to syntrophic associations. Thus, a top-down enrichment may direct the evolution of these communities, increasing their fitness for specific applications by adapting to changes in the environment, competing with other microorganisms, and maintaining or even expanding the population size. In addition, we observed that metabolic interactions play a critical role in driving the assembly of microbial communities, promoting coexistence in both natural and engineered environments. This experimental approach holds the potential to generate novel insights into the understanding of anaerobic microbiomes and their potential applications in biotechnology.

POSTER ABSTRACT

P-30

Forest fungal litter community as a crucial indicator of ecological restoration in the Atlantic Forest

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Keywords: Ecosystem restoration; Deforestation; Forest ecology; Biodiversity; Forest Functionality; Brazil.

Ecological restoration of Atlantic Forest aims to reverse environmental impacts of sugarcane and pastureland degradation. Litterfall is crucial for nutrient cycling, biodiversity services, and carbon storage in newly restored forests. However, many soil studies remove litter, thereby discarding a critical above-to-belowground interface together with key microbial diversity and ecosystem functions. Our study evaluates how nine natural second-growth Atlantic Forests during 11–48 years of regeneration recover litter quantities, quality, and fungal communities toward native healthy forests. Three degraded pastures and three native forests were used as the start and endpoints for restoration, respectively. Litter biomass, carbon and nitrogen isotopes ($\delta^{13}C$ and $\delta^{15}N$), and nutrients composition were used as indicators of litter quality. Fungal community was evaluated through ITS region sequencing. Our results showed that after four decades of regeneration, the litter quality of secondary forests became similar to primary forests. Additionally, there was a positive correlation between restoration time and accumulation of $\delta^{13}C$ and $\delta^{15}N$ in the forest litter, which was also found in all soil depths (0–10, 10–20, 20–30 cm). In contrast, pastures exhibited lower litter biomass, containing poorer nutrient contents, resulting in lower quantity and quality. The older the forest growth, the higher the litter $\delta^{15}N$, which are efficient indicators of the progress of ecological restoration. Fungal alpha-diversities were similar when comparing primary forest, secondary forest, and pasture, indicating a stable fungal community that drives litter decomposition. Beta-diversity was higher in primary and secondary forest, and positively correlated with litter nutrient content. Basidiomycota and Ascomycota were the most abundant phyla in all sites, while *Trichoderma*, *Penicillium*, and *Metarhizium* were the most prominent genera in forest ecosystems. In conclusion, our study showed that litter properties consistently responded to a chronosequence of forest restoration development. Litter is easily measurable and should never be neglected in restoration assessments.

POSTER ABSTRACT

P-31

Influence of Microgeo use on chemical and biological attributes of the soil

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Key words: Soil microbiome, sustainable, Organic Matter

The objective of this work was to evaluate the biological and chemical indicators of the soil in areas with 4 and 11 years of continuous use of Microgeo®. Soil bioanalyses in an area with 4 years, 11 years and a control area showed an increase in Organic Matter (M.O.) and 24 (control) to 36 (4 years) and 52 g dm-3 (11 years). An increase in the remaining P was also observed, going from 11.37 (control) to 22.16 (4 years) and 21.27 mg dm-3 (11 years), which means that microorganisms improve P solubility and increase from M.O. reduced the P fixation capacity in the soil. The Betaglucosidase and Arylsulfatase values were

increased, going from High to Very High for Betaglucosity and for Arylsulfatase from Low to High in the control area for those with 4 and 11 years of use of Microgeo®. Soil microbiology is responsible for the decomposition of organic materials, the cycling of nutrients and the flow of energy, influencing both the transformation of M.O. and in the stock of carbon and nutrients in the soil. The results show that there is no lack of organic matter, but microorganisms that make systems more sustainable.

POSTER ABSTRACT

P-33

Biological fertilizer applied in depth in soil cultivated with sugarcane

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Key words: Quality of soil, sugar cane, biological fertilizer

The objective of applying Microgeo at a depth of 50 to 60 cm in the planting furrow of sugar cane would contribute to improving the biological, chemical, and physical quality of the soil at this depth level. Aiming at improving the physical and chemical qualities of this localized furrow, where an organomineral fertilizer source is also applied in depth, Microgeo was added in different dosages in several treatments, to study what would be its effect on the balance and sustainability of this soil profile. These data were proven in chemical, physical and more elaborate analyzes such as enzymatic and molecular analyses. Evaluating all the results obtained in this field experiment, I am convinced that the objective of introducing a biological source such as Microgeo in depth in the localized furrows of the sugar cane culture reached the expectation of improving all the indicators of this soil, when compared to the control where the same physical and chemical operations were performed. Based on this field experiment and proven the effect of Microgeo in these conditions, the possibility of using it in commercial conditions opens, always seeking to improve the physical, chemical and biological conditions of these soils, their agronomic and commercial sustainability

POSTER ABSTRACT

P-34

Unravelling the mycobiome of the genus Scalesia, the 'Darwin's finches of the plant world' from the Galapagos Islands

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Keywords: Scalesia, Mycobiome, Galápagos islands, fungal metataxonomy, *Phaeosphaeria scalesiae*

In the diverse and harsh ecosystems of the Galápagos archipelago, certain plants have exhibited a remarkable adaptability. This Scalesia genus has rapidly radiated into 15 different species which are called Giant Daisies as they resemble the daisies, which thrive on various islands under different environmental conditions. Surprisingly, very little is known to date on the taxonomic and functional diversity of the microbiomes associated with endemic plant species on Galápagos, and how members of these plant-associated microbiomes contribute to the growth and survival of Scalesia species. Our study focused on the characterization of the rhizosphere and the phyllosphere fungal communities. Samples were collected from Isabela, Santa Cruz, and San Cristóbal islands. Using the molecular marker, ITS, we analyzed the mycobiome of several Scalesia species inhabiting the islands and revealed that the genera Fusarium (Hypocreales) and Aspergillus (Eurotiales) dominated the rhizosphere of S. cordata and S. affinis, encompassing species known for their mostly phytopathogenic properties. In Santa Cruz, the mycobiome primarily consisted of species belonging to the Cladosporium genus (Capnodiales), which includes beneficial strains promoting plant resistance to biotic and abiotic factors. Comparing Alpha diversity values between the islands, indicated that Santa Cruz hosted the most diverse fungal mycobiome, followed by San Cristóbal, and Isabela. Interestingly, Isabela contained the most enriched sequences, followed by San Cristóbal, and Santa Cruz. Additionally, we present to the world a new fungal species, Phaeosphaeria scalesiae Crous, sp. nov., which has been cultured and characterized from stem tissue and represents a novelty for its association with Scalesia as its host. This study provides valuable insights into the fungal mycobiome associated with various Scalesia species in the Galápagos archipelago, highlighting distinct fungal community compositions between the three islands, including the discovery of a new fungi. We will obtain insights into the diversity of microorganisms associated with the Galápagos endemic Scalesia and how speciation of this plant genus affects root and leaf microbiome assembly, and we hope to uncover the factors that facilitated their evolutionary success.

POSTER ABSTRACT

P-35

Ultra-high resolution amplicon sequencing reveals cross-kingdom antagonists and synergists driving fungal infections in the wheat phyllosphere

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Keywords: *Pseudomonas*, *Zymoseptoria tritici*, PacBio, wheat, biocontrol

Plant-associated microbiomes promote plant health in natural environments and can confer resistance to pathogens. Within these microbial networks, plant-beneficial and plant pathogenic strains are often closely related. Hence, monitoring pathogenic and plant beneficial microbes at the strain level is critical for our understanding of microbiome functions. However, high-resolution strain level monitoring is hindered by the available barcoding loci. Here, we introduce multiple 3-kb highly polymorphic bacterial and fungal amplicons to be sequenced in 10,000-multiplex pools on the PacBio Sequel II system. We analyzed large sets of high-quality genomes covering the phylogenetic breadth of *Pseudomonas* bacteria and the major fungal wheat pathogen *Zymoseptoria tritici* to define highly robust amplicon sets. Pseudomonads include synergistic and antagonistic species of *Z. tritici* in the wheat phyllosphere. We complemented the sequencing with the full-length 16S and fungal ITS loci to generate deep insights into crop microbiomes. We apply our set of amplicons to a hierarchical set of 500 wheat samples spanning the growing season, different plant genotypes, as well as replicated leaf and root compartments. The deep sequencing revealed highly granular structures of both the focal pathogen and the co-existing *Pseudomonas* diversity. We used evidence for co-occurrence and exclusion of individual genotypes to investigate synergistic and antagonistic microbiome interactions. A comprehensive strain collection from the same field allowed us to validate the predicted interaction network under controlled conditions. We build a model of biotic and abiotic factors determining the ecological niche of the crop pathogen and reveal broad principles of competitive exclusion and persistence. Overall, our work introduces a powerful new approach for ultra-deep amplicon analyses to interrogate plant microbiome interactions.

POSTER ABSTRACT

P-37

Aphid infestation changes metabolic activity and composition of bacterial communities in the wheat rhizosphere

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Keywords: Plant defence, plant volatiles, community-level metabolism

Plant-microbe interactions are fundamental to plant defence against herbivores, which cause significant losses in food production worldwide. This project aims to study the effect of aphid feeding on the plant system and its effect on bacterial communities in the wheat rhizosphere. In the first part of this project, we designed a microcosm experiment consisting of two treatments (wheat plants with and without aphid infestation). Rhizosphere samples were taken before infestation and two weeks post-infestation. We analysed bacterial community profiles at taxonomical (16S rRNA gene sequencing) and physiological levels (Ecoplates, Biolog). Moreover, aboveground volatiles were collected to characterise their chemical composition. After two weeks of infestation, bacterial diversity was reduced in the rhizosphere of aphid-infested plants in comparison with the non-infested, but a higher abundance of Actinobacteria and Firmicutes was observed. The physiological profiling showed a higher microbial metabolic activity in the rhizosphere of aphid-infested plants, particularly in response to D-Xylose, N-acetyl D-glucosamine, and some amino acids ($p < 0.05$). Unsurprisingly, we detected aboveground volatiles involved in herbivory response (e.g., limonene, α-cubebene, β-Ocimene) in aphid-infested plants, which validated that plant chemistry changed under aphid feeding. Following these results, we are currently conducting another experiment to characterise changes in soil microbial communities (taxonomical and physiological) associated with two cultivars from the ancestral wheat Triticum monococcum under aphid herbivory. These cultivars have been previously identified as resistant (MDR049) and susceptible (MDR037) to aphid feeding. We hope that the results of this experiment will increase our understanding of the role of soil microbial communities in the plant response to herbivory and will help design future strategies to increase plant resistance to pests that threaten food security.

POSTER ABSTRACT

P-38

Molecular validation of *Rhynchophorus palmarum* as the main vector of the red ring disease in Colombian coconut cultivation.

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Key words: nematode; palm*; Bursaphelenchus cocophilus*; LSU; DNA extraction.

The coconut is a crop of the tropical regions around the world and represents an economic importance for the agricultural sector. Colombia has potential to be a huge exporter of coconut, regard climatic conditions, variety of soils and its high productivity per palm. However, there are phytosanitary problems, that limit its productivity which leaves Colombia without the capacity to meet its own demand. Thus, the red ring, a disease caused for the nematode *Bursaphelenchus cocophilus* (vectored by the insect *Rhynchophorus palmarum*), has been reported as a threat for *Cocos nucifera* L in Colombia. However, in Antioquia state (Urabá region) this disease has not had an accurate diagnostic. Thus, the aim of this research is to validate molecularly the presence of *B. cocophilus* in *R. palmarum*, collected from molasses traps of coconut crops. Then, the DNA extraction of the nematode was stablished trough a modified methodology, in conjunction with the DNA extraction of the insect. Nematodes were extracted and put under de light microscope at 10X objective, in this way, the nematodes were taken using the 10uL micropipette and put in an 0.6 mL tube, conforming samples with a variable number, in order to test the optimal for DNA extraction. Once the extraction was done, it was possible to amplify the nuclear Large subunit of 28S (LSU) gene of the D2-D3 region, and Sanger sequenced. As a result, the amplification was successful for samples containing from one to eight nematodes. However, samples containing from two to four showed clarity in the electropherogram patterns, suggesting a same haplotype by sample. However, the BLAST hits shown an identity of 92% with *Caenorhabditis sp.*

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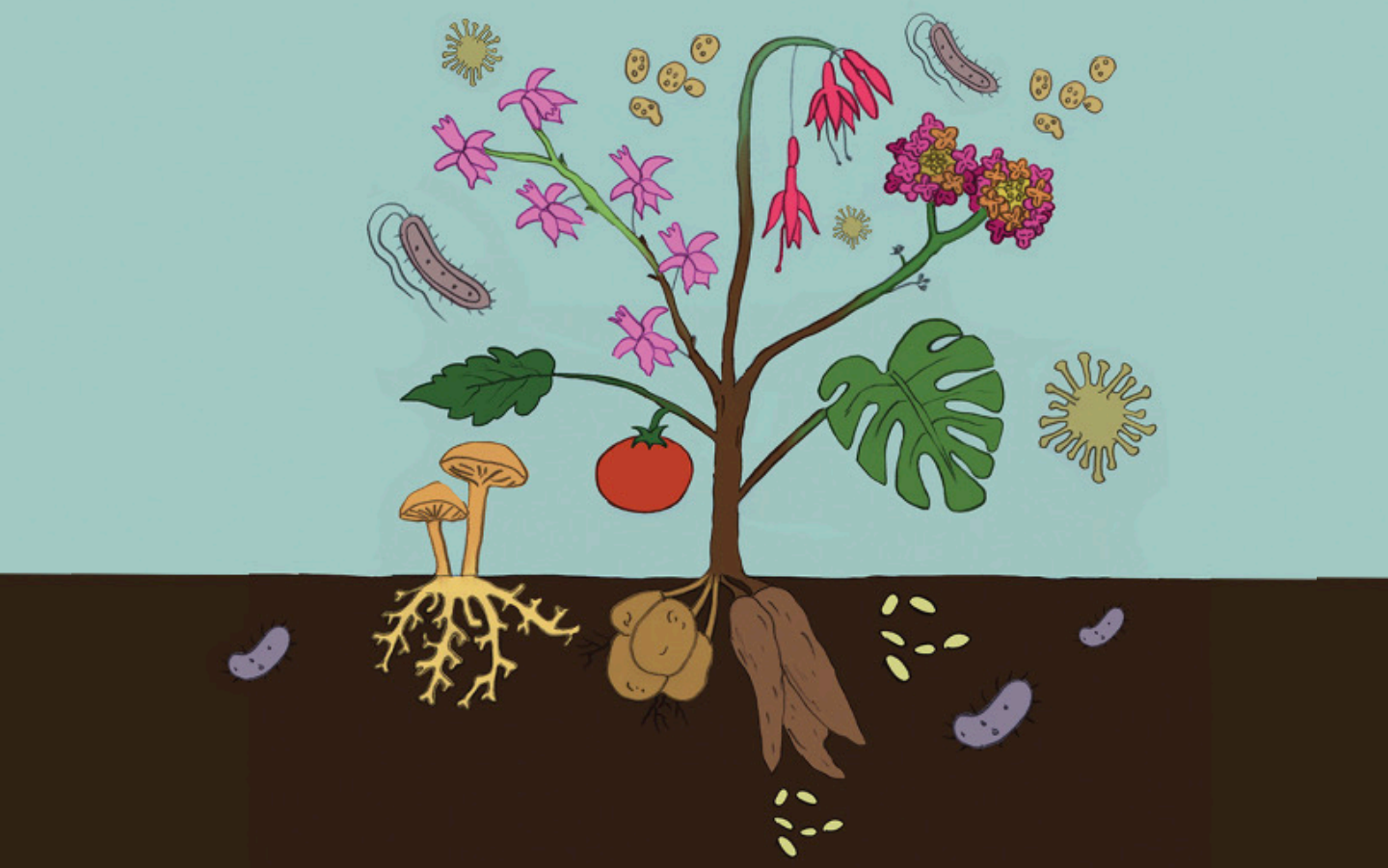

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Kula Bio

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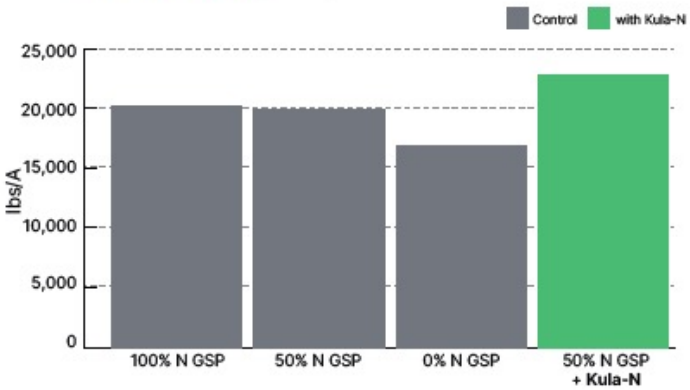

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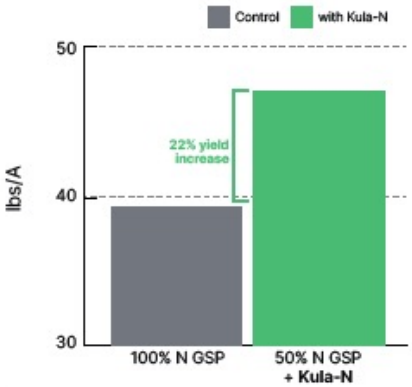

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