INTERNATIONAL PHYTOBIOMES CONFERENCE 2018

4-6 DECEMBER

LE CORUM
MONTPELLIER
FRANCE

International Phytobiomes Conference 2018
Le Corum, Montpellier, France
4-6 December

Welcome

Dear colleagues,

It is with great pleasure that we welcome you to Montpellier for the International Phytobiomes Conference 2018.

Over the next three days, public and private scientists from all over the world, agronomists, plant pathologists, geneticists, microbiologist, soil scientists, data scientists, biostatisticians, plant physiologists, nutrient management experts, weather/climate scientists – to name only a few disciplines – will present their research, discuss, and share their expertise to advance knowledge on how phytobiome components interact and affect each other.

Plants grow in association and interaction with complex communities of organisms, environmental conditions, and management practices. The term “Phytobiomes” encompasses all of this complexity. A phytobiome includes the plant itself, all micro- and macro-organisms living in, on, or around the plant – such as microbes, animals, insects and other plants – and the environment, including soil, air, water, weather, and climate.

The Conference scientific program covers a wide range of topics related to phytobiomes, from the study of the interactions between microbial communities and associated plants, efforts to improve nutrient management and uptake, to the development of databases and modeling tools for next generation agriculture and the transformation of Phytobiome discoveries into products.

We hope that the conference will generate stimulating discussions and initiate collaborations within and across disciplines for the advancement of phytobiomes research to increase the production of a sufficient supply of safe and nutritious food, feed, and fiber. Translation of phytobiomes knowledge will be critical to ensuring sustainable global food security in the next decades in the context of population growth, climate change, and the necessity to preserve biodiversity and natural resources.

We would like to thank the conference partners for their financial support: the International Phytobiomes Alliance, Montpellier University of Excellence, Bayer Crop Science, the French National Research Institute for Sustainable Development (IRD), The American Phytopathological Society, NewLeaf Symbiotics and Noble Research Institute.

We also would like to thank the French National Institute for Agricultural Research (INRA) for providing support to eight early career scientists to attend the Conference.

We wish you an excellent conference, stimulating interactions with colleagues, and a great time in the beautiful city of Montpellier.

The Scientific Committee

Acknowledgements

The International Phytobiomes Conference 2018 is organized by

- the International Phytobiomes Alliance
- the French National Institute for Agricultural Research (Institut National de la Recherche Agronomique – INRA)
- the French National Research Institute for Sustainable Development (Institut de Recherche pour le Développement – IRD).

The **International Phytobiomes Alliance** is an international, nonprofit alliance of industry, academic, and governmental partners. The mission of Alliance is to establish a science and technology foundation for site-specific, phytobiome-based enhancement of sustainable food, feed and fiber production. The Alliance goals are to identify research gaps and help coordinate projects to address those gaps and to establish national, international, and multi-national public-private projects and networks. The Alliance is a 501(c)(3) nonprofit organization registered in the United States.

INRA is Europe's top agricultural research institute and the world's number two centre for the agricultural sciences. Its scientists are working towards solutions for society's major challenges. Specializing in food, nutrition, agriculture and the environment they focus on competitiveness, regional land use, health, sustainable development and bioeconomy.

The **IRD** is a French research organism, original and unique on the European development research scene. Emphasizing interdisciplinarity, the IRD has focused its research for over 75 years on the relationship between man and its environment, in Africa, Mediterranean, Latin America, Asia and the French tropical overseas territories

Scientific Committee

- Kellye Eversole, International Phytobiomes Alliance, US
- Corrine Vacher, INRA, FR
- Valérie Verdier, IRD, FR
- Matthieu Barret, INRA, FR
- Gwyn Beattie, Iowa State University, US
- Gilles Béna, IRD, FR
- Natalie Breakfield, NewLeaf Symbiotics, US
- Magalie Guilhabert, Bayer Crop Science, US
- Jan Leach, Colorado State University, US
- Christophe Mougel, INRA, FR
- Matthew Ryan, CABI, UK
- Angela Sessitsch, AIT Austrian Institute of Technology, AT

Local Organizing Committee

- Gilles Béna, IRD, FR
- Yann Moreau, IRD, FR
- Valérie Verdier, IRD, FR

Conference Office - Eversole Associates

- Mollie Hogan (Coordination)
- Isabelle Caugant (Communication)
- Lori Leach (Finance)

INTERNATIONAL ALLIANCE FOR PHYTOBIOMES RESEARCH

An international nonprofit industry, academic, and governmental agency consortium

Vision

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

Mission

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

Goals

Identify research gaps and help coordinate projects to address those gaps

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

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Kellye Eversole
Executive Director
+1 301-618-9543
eversole@eversoleassociates.com

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Phytobiomes consist of plants, their environment, and their associated communities of organisms.

- Interactions within phytobiomes have profound effects on soil, plant and agroecosystem health, which in turn impacts soil fertility, crop yields, and food quality and safety.
- Knowledge of the phytobiomes network can be translated into new tools for agroecosystem management.
- A systems-level understanding of phytobiomes will enable us to sustainably and profitably produce sufficient crops to meet global demands while minimizing negative impacts on the environment.

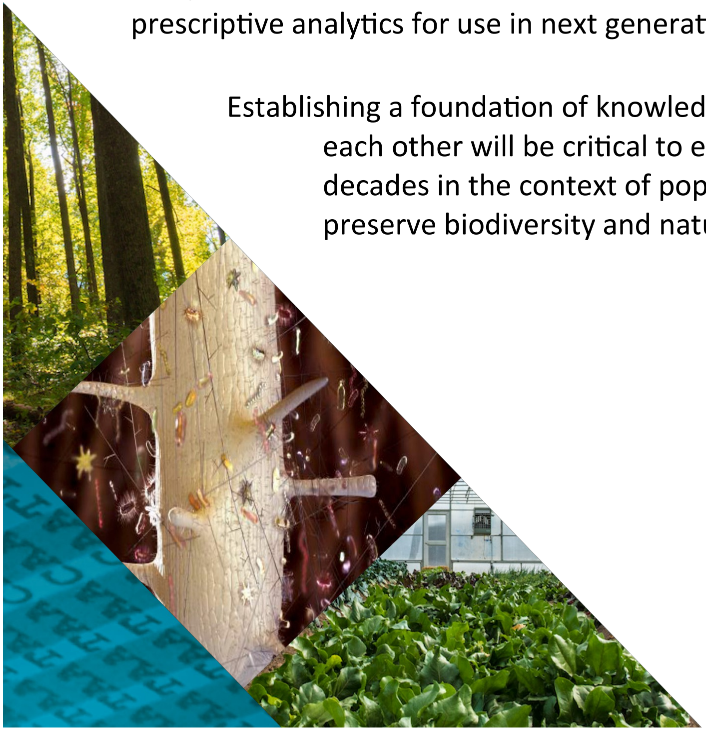
Studies of phytobiomes relate to the entire system of factors that affect or are affected by plants, including:

- microbial communities (microbiomes) of the plants, soils, and animals
- insects, nematodes, and other animals
- plants
- soils
- environment

Plants grow in association and interaction with complex communities of organisms, environmental conditions, and management practices. The term “Phytobiomes” encompasses all of this complexity. A phytobiomes is a plant (“phyto”) in a distinct geographical unit (“biome”) – a field, grassland, greenhouse, garden, or forest. A phytobiome includes the plant itself, all micro- and macro-organisms living in, on, or around the plant – such as microbes, animals, insects and other plants – and the environment, including soil, air, water, weather, and climate.

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

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



International Phytobiomes Conference Program

Tuesday 4 December

11:00-13:00	Registration and Packet pick up: Space Joffre (Level 1)

Auditorium Einstein (Level 0)

13:00-13:20	Welcome and Opening- **Kellye Eversole, International Phytobiomes Alliance, US**
13:20- 14:05	Keynote Address - **Gary Felton, Pennsylvania State University, US** *The role of microbes in mediating plant-insect interactions – Benefit or betrayal?*
14:05-14:10	Welcome from iSITE MUSE
14:10-14:20	INRA Early Career Award Announcements

Session One: Exploring Interactions within Phytobiomes

Chair: Corinne Vacher, INRA, FR

14:20-14:45	Opening speaker - **Eoin Brodie, University of California, Berkeley, US** *Deciphering the signatures of niche adaptation in soil microbial communities*

Topic 1: Climate and the environment: Predicting impacts

14:45-15:10	**Lisa Wingate, INRA, FR** *From enzyme to Earth system: linking soil community function and composition to constrain the magnitude of the terrestrial biosphere CO2 sink*
15:10-15:30	**Short talk - Isai Salas-Gonzalez, University of North Carolina, US** *Bacterial community maintenance of plant root development*
15:30-15:55	**Shiji Hou, Max Planck Institute for Plant Breeding Research, DE** *The root microbiota coordinates trade-offs between shade and immune responses in Arabidopsis*
15:55-16:30	Refreshments and networking: Space Joffre (Level 1)

Auditorium Einstein (Level 0)

Topic 2: Soil, plant and insect microbiomes: Discoveries and technological advances

Chair: Matthew Ryan, CABI, UK

16:30-16:55	**Paolina Garbeva, Netherlands Institute of Ecology, NL** *Deciphering belowground microbe-microbe and plant microbe chemical communication*
16:55-17:15	**Short talk - Stephanie Kivlin, The University of Tennessee, Knoxville, US** *Climate change may differentially disrupt leaf and root phytobiomes*
17:15-17:35	**Short talk - Charlotte Tollenaere, IRD, FR** *Multiple infections in rice from West Africa: mechanisms, epidemiological and evolutionary implications*
17:35-18:00	**Terrence Bell, Pennsylvania State University, US,** *Microbial colonization of soils: implications for agriculture and experimental systems*
18:00-19:30	Welcome Cocktails, Poster Viewing, and Exhibitors: Space Joffre (Level 1)
18:30-20:30	Analysis of Microbiomes Community Data in R Workshop: Auditorium Einstein (Level 0) *pre-registration required*
19:30	Adjourn for the day

Wednesday 5 December

Auditorium Einstein (Level 0)

8:30-8:40	Welcome for the day - **Valérie Verdier, IRD, FR**

Session One Continued: Exploring Interactions within Phytobiomes

Topic 3: Exploring microbiomes in natural habitats to better understand their functions and assembly process

Chair: Valérie Verdier, IRD, FR

8:40-9:05	**Jonathan Adams, Cranfield University, UK** *Soil fungal diversity in grasslands of the Tibetan Plateau: Is it Driven by plant Diversity and Productivity?*
9:05-9:30	**Morgane Ourry, INRA, FR** *Deciphering Brassica napus-microbiome associations in interaction with root herbivorous insect Delia radicum: a feedback loop in the rhizosphere*
9:30-9:50	**Short talk - Emily Luna (presented by Jan Leach), Colorado State University, US** *Insect Bacteria-Plant Interactions: Microbiomes of Russian Wheat Aphid (Diuraphis noxia) Contain Bacteria that Increase Virulence to Wheat*

Topic 4: Exploring plant responses to other organisms

9:50-10:15	**Lionel Moulin, IRD, FR** *Comparative transcriptomics of the wheat response towards diverse partners of its microbiome*
10:15-10:40	**Jean-Benoit Morel, CIRAD, FR** *Plant-plant interactions modify disease susceptibility*
10:40-11:10	Refreshments and Networking: Space Joffre (Level 1)

Session Two: Integrating Phytobiome Systems-based Knowledge

Auditorium Einstein (Level 0)

Chair: Jan Leach, Colorado State University, US

11:10-11:35	Opening speaker - **Sally Flis, The Fertilizer Institute, US** *Using 4R Nutrient Stewardship to Optimize Soil and Plant Health*

Topic 1: Optimizing soil and ecosystem health through nutrient management and nutrient use efficiency

11:35-11:55	**Short talk - Joelle Sasse Schlaepfer, Lawrence Berkeley National Laboratory, US** *How plants shape the rhizosphere: physiological adaptations, exudation, and metabolite uptake*
11:55-12:20	**Larry Halverson, Iowa State University, US** *Can diversified cropping systems shape maize rhizosphere microbiomes towards more robust, interconnected communities?*
12:20-12:40	**Short talk - Tania Galindo-Castañeda , Pennsylvania State University, US** *Rhizosphere microbiome of field-grown maize as influenced by root cortical aerenchyma*
12:40-13:40	Buffet lunch and networking: Space Joffre (Level 1)

Auditorium Einstein (Level 0)

Topic 2: Exploiting interactions within phytobiomes to optimize plant health, fitness, and production

Session Chair: Gwyn Beattie, Iowa State University, US

13:40-14:05	**Tim Mauchline, Rothamsted Research, UK** *Rooting around the wheat microbiome*

Wednesday 5 December

14:05-14:25	**Short talk - Lilach Iasur Kruh, ORT Braude College, IL** *The phytobiome of a unique ecological system: parasitic weed and its host plant*
14:25-14:50	**Jay-Ram Lamichhane, INRA, FR** *A conceptual framework to better understand interactions between seedbed abiotic and biotic factors under the influence of cropping systems and their overall impact on field crop establishment*
14:50-15:15	Refreshments: Space Joffre (Level 1)

Session Three: Phytobiome Engineering

Auditorium Einstein (Level 0)

Topic: Engineering plant, insect and microbial communities to promote agroecosystem health and productivity

Chair: Natalie Breakfield, NewLeaf Symbiotics, US

15:15-15:40	**Angela Sessitsch, AIT Austrian Institute of Technology, AT** *The plant microbiome from lab to field*
15:40-16:00	**Short talk - Aude Rochefort, INRA, FR** *Influence of environment and host plant genotype on the structure and diversity of the Brassica napus seed microbiota*
16:00-16:20	**Short talk - Leo van Overbeek, Wageningen University, NL** *Human pathogens in plant microbiomes*
16:20-16:45	**Gwendolin Wehner, Julius Kuhn-Institut, DE** *Breeding for priming triggered leaf rust resistance in barley*

Session Four: Applying Phytobiome-based Solutions for NexGen Agriculture

Topic 1: Advances in precision agriculture, modeling, and large-scale data collection

Chair: Gilles Béna, IRD, FR

16:45-17:10	**Stéphane Dupas, IRD, FR** *Bayesian learning for decision support in the Internet of phytosystems things*
17:10-17:30	**Short talk - Andreas Makiola, INRA, FR** *Characterising plant pathogen communities and their environmental drivers at a national scale*
17:30-17:50	**Short talk - Surya Saha, Boyce Thompson Institute, US** *AgriVectors: a portal for plant diseases transmitted by insect vectors*
17:50-18:30	Poster Viewing: Space Joffre (Level 1)
18:30	Adjourn for the day
18:45-19:00	Busses leave for Gala Dinner (**Allée de la Citadelle - Level 0)**
19:30-23:00	Gala Dinner - Chateau Puech Haut (tickets purchased ahead of time)

Thursday 6 December

Auditorium Einstein (Level 0)

8:30-8:40	Welcome for the day - **Corinne Vacher, INRA, FR**

Session 4 Continued: Applying Phytobiome-based Solutions for NexGen Agriculture

Topic 2: Applying big-data analytics to understand phytobiomes

Session Chair: Matthieu Barret, INRA, FR

8:40-9:05	**Daniel Jacobson, Oak Ridge National Laboratory, US** *Systems Biology Models of the Interactions Between Host, Phytobiome and Environment*

Topic 3: Diversifying our approach to crop production: urban and indoor agriculture

9:05-9:30	**Trevor Charles, University of Waterloo, CA** *Microbiome dynamics during enrichment culture on ACC as nitrogen source: relevance to controlled environment agriculture*

Session Five: Transforming Phytobiome Discoveries into Products

Chair: Angela Sessitsch, AIT Austrian Institute of Technology, AT

9:30-9:55	Opening Speaker - **Natalie Breakfield, NewLeaf Symbiotics, US** *M-trophs for sustainable agriculture*

Topic: Translating complexity into products: biologicals for agriculture

9:55-10:20	**Richard Broglie, Pivot Bio, US** *Reimagining Crop Nutrition*
10:20-10:45	**Steven Vandenabeele, ApheaBio, BE** *An integrated technology pipeline for the development of superior agricultural biologicals*
10:45-11:15	Refreshments and Networking: Space Joffre (Level 1)

Auditorium Einstein (Level 0)

11:15-11:35	**Short talk - David Hallahan, Corteva Agriscience , US** *From the field to the lab and back again – delivery of an entomopathogenic fungus for corn rootworm control*
11:35-11:55	**Short talk - Andrea Marino, Advanced Biological Marketing, US** *RNA-Seq: A tool for investigating the influence of biological seed treatment on crop performance during periods of osmotic stress*
11:55-12:20	**Claudia Preininger, AIT Austrian Institute of Technology, AT** *Formulation of microbial bioeffectors - a materials perspective*
12:20-12:45	**Andrea Molt, BASF, DE** *BASF – A chemical company mastering the challenges of biologicals*
12:45-13:00	Closing Remarks and Conference Adjournment – **Kellye Eversole, International Phytobiomes Alliance, US**

Conference Partners

The International Phytobiomes Conference 2018 is made possible through the generosity and dedication to the mission of collaborative science of our Conference Partners. Thank you to all our Conference Partners for supporting this meeting.

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This event has received financial support of the French I-SITE MUSE Investment for the Future ANR grant, referenced n° ANR-16-IDEX-0006ANR

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INRA Early Career Award Winners

The INRA PhytoMic network, supported by the Microbial Ecosystems and Meta-omics Metaprogram, funded eight awards of 500 € each to encourage the participation of early career scientists to the International Phytobiomes Conference 2018.

Congratulations to the Award Winners

- Pascal Alonso - CIRAD, FR
- Tania Fort - INRA, FR
- Tania Galindo-Casteñada - Pennsylvania State University, US
- Charles Mason - Pennsylvania State University, US
- Morgane Ourry - INRA, FR
- Charlie Pauvert - INRA, FR
- Alberto Prado-Faris and Gloria Torres-Cortes - INRA, FR
- Aude Rochefort - INRA, FR

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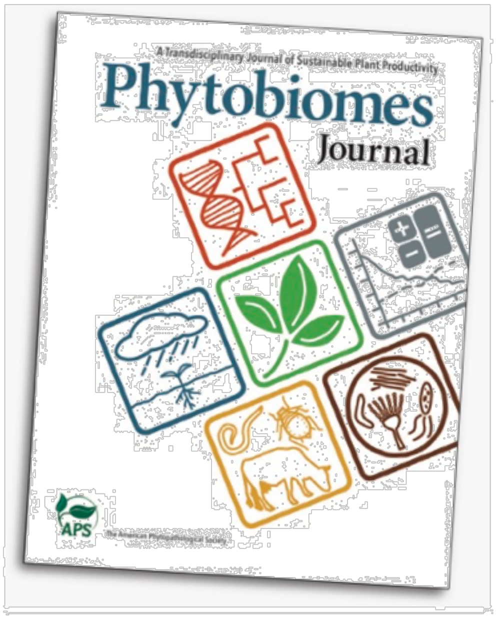

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* *$1,100 for up to 9 pages; and $150 per page after that, capped at $1,550. To qualify for the reduced rate, you must have attended the* 2018 International Phytobiomes Conference *and be the first or corresponding author on the paper. When you submit your paper, please include in your cover letter that you were an attendee.*

Speaker Profiles

Keynote Speaker - Gary Felton

Pennsylvania State University, US

Gary W. Felton is Professor and Head of the Department of Entomology at Pennsylvania State University, USA. He is a graduate of the University of California, Irvine (BS), University of Kentucky (MS) and the University of California, Davis (PhD). Felton's research focuses on mechanisms of plant defense and the adaptations that herbivorous insects use to avoid them. This research has uncovered unique ways in which insect herbivores use salivary secretions and microbes to suppress the induced responses of their host plants and has been published in journals such as Nature and the Proceedings of the National Academy of Science. He has published more than 130 refereed papers, including numerous review articles for book chapters and journals such as Plant Physiology, Annual Review of Phytopathology, Current Opinion in Plant Biology, and Annual Plant Reviews. He was elected a Fellow of the Entomological Society of America in 2014 and currently serves as Editor-in-Chief for the Journal of Chemical Ecology.

Jonathan Adams

Cranfield University, UK

Jonathan Adams is Professor of Soil Biology at Cranfield University, UK. He has a BA in Botany from Oxford University, and a PhD in Quaternary Geology from Universite de Aix-Marseille II. He held academic positions at Rutgers University and at Seoul National University before joining Cranfield in 2017. He has authored around 130 published papers (including papers in Nature and ISME) and two books. After working on the global carbon cycle and paleoenvironments, he now focuses on environmental DNA and its potential for understanding ecological processes.

Natalie Breakfield

NewLeaf Symbiotics, US

Natalie Breakfield is the Molecular Biology Director at NewLeaf Symbiotics in Saint Louis, Missouri, USA. In this role, she is responsible for isolations, sequencing, and initial phenotyping of new *Methylobacterium* spp. (M-troph) isolates. She works closely with other teams to ensure that the most promising candidates are advanced through NewLeaf's product pipeline. NewLeaf is focused on discovering how M-trophs benefit plants across a large variety of field conditions, and currently has two bio-complement products on the market: Terrasym401 for soy and Terrasym402 for peanut. Dr. Breakfield obtained her Ph.D. from Duke University and was a postdoctoral fellow at the University of North Carolina at Chapel Hill.

Eoin Brodie

University of California, Berkeley, US

Eoin Brodie obtained his Ph.D. from University College Dublin in Ireland and joined Berkeley Lab following postdoctoral research at the University of California, Berkeley. At Berkeley Lab he is Deputy Director of the Climate and Ecosystem Sciences Division. His research focuses on the feedbacks between microorganisms and their natural environments, with a primary focus on soil and subsurface systems, scaling from microbial mechanisms to ecosystem scale processes.

Richard Broglie

Pivot Bio, US

Richard Broglie is Chief Technology Officer at Pivot Bio, an innovative agriculture technology company that identifies and fine-tunes microbes with the ability to fix atmospheric nitrogen for use by cereal crops. Prior to joining Pivot Bio, he held the position of Research Director for microbiome discovery in the Agriculture Division of DowDuPont. In his more than 30-year career at DuPont, Rich has led various discovery programs that resulted in soybean and canola crops with healthier and more stable seed oil compositions, and traits for disease and pest resistance in soybean, corn, wheat, rice, and sugarcane. He also served as Vice President of Research and member of the Board of Directors of InterMountain Canola, a joint venture between DuPont and DNA Plant Technology. The author of more than 30 scientific publications and an inventor on several important patents, Rich received his graduate training in microbiology at Rutgers University and his postdoctoral training in plant molecular biology at The Rockefeller University, where he also served as Assistant Professor in the Laboratory of Plant Molecular Biology.

Trevor Charles

University of Waterloo, CA

Trevor Charles is a bacterial geneticist with a research program in plant-microbe interactions, functional meta-genomics, and bacterial genome engineering for bioproducts. Following B.Sc. Microbiology at University of British Columbia, he obtained his Ph.D. in Turlough Finan's lab at McMaster University (symbiotic nitrogen fixation) and did postdoctoral work in Gene Nester's lab at University of Washington (*Agrobacterium*). He held a faculty position at McGill University before moving to his current position at University of Waterloo in 1998, where he is director of Waterloo Centre for Microbial Research. He is co-founder and CSO of the company Metagenom Bio Inc., which applies metagenomic and microbial community analysis to challenges in the agriculture and mining sectors.

Sally Flis

The Fertilizer Institute, US

Sally Flis is the Director of Agronomy at The Fertilizer Institute (TFI) in Washington D.C., USA. In her role at TFI, Sally works with the 4R Nutrient Stewardship programs to help increase the science base and understanding of on-farm practice implementation. Sally is also involved in providing science support for state and national nutrient policy issues. Before joining TFI, Sally worked with famers in the Northeastern U.S. to implement and develop nutrient management plans. Dr. Flis received her Ph.D. in Plant and Soil Science from the University of Vermont, her M.S. Dairy Science and B.S. in Dairy Science and Agronomy from the University of Wisconsin-Madison.

Paolina Gerbeva

Netherlands Institute of Ecolog, NL

Paolina Garbeva is a senior scientist and a research group leader at the Department of Microbial Ecology, at the Netherlands Institute of Ecology (NIOO-KNAW). She is a microbiologist by training with a strong affinity for Microbial Chemical Ecology and Plant-Microbe Interactions. She obtained her PhD from Leiden University, the Netherlands in 2005.The focus of her current research is to understand the fundamental mechanisms of microbial chemical interactions and communication. Secondary metabolites (both volatile and water-soluble) play an important role in microbial interactions, e.g. as signaling compounds for communication or as suppressive agents in interference competition. Using omics-based tools, advanced analytical chemistry and novel imaging techniques, her research aims to decipher, explore and exploit the so far unknown belowground microbe-microbe and plant-microbe chemical interactions and communication.

Speaker Profiles

Larry Halverson

Iowa State University, US

Larry J. Halverson is an Associate Professor in the Department of Plant Pathology and Microbiology at Iowa State University, USA. He is a graduate of Luther College (BA), University of Tennessee-Knoxville (MS) and the University of Wisconsin-Madison (PhD). He conducted postdoctoral research at the University of California, Berkeley. His research focuses on physiological and ecological mechanisms contributing to cell-cell, bacteria-alga, and microbe-plant interactions. He is particularly interested in how the interactions between microbes influence fitness and evolutionary trajectories, particularly in soil and the rhizosphere.

Jay-Ram Lamichhane

INRA, FR

Jay-Ram Lamichhane is a research scientist at the French National Institute for Agricultural Research. He is an agronomist by training and previously he worked on plant pathogenic bacteria, their disease epidemiology and integrated management. His current research focuses on the effect of abiotic and biotic factors as well as cropping systems on seed germination and seedling emergence of field crops. In particular, he is interested in understanding how agroecological cropping practices influence biotic and abiotic factors and their interactions and how this finally affect field crop establishment. Jay-Ram has authored or co-authored over 50 publications in peer-reviewed international journals.

Tim Mauchline

Rothamsted Research, UK

Tim Mauchline is based at Rothamsted Research in the UK where he leads the plant microbiome research group. He is interested in understanding the role of the plant microbiome in promoting plant growth as well as plant protection. He has spent his entire research career studying microbial interactions in the plant root environment. He is interested in the ecology of microbial communities in cropping systems, especially the process of microbial niche occupation in plants (including the rhizosphere and endosphere), from the seed as well as the bulk soil microbial reservoir. The aim is to understand the function and potential of plant-associated microbes for nutrient cycling, plant stress tolerance and disease suppression. His ultimate goal is to maximise the contribution of microbes for the development of sustainable agricultural systems.

Andrea Molt

BASF, DE

Andrea Molt is a molecular biologist who obtained her Ph.D. from Heidelberg University, Germany. Following post doctoral research at Chalmers University of Technology in Gothenburg, Sweden, she joined BASF's White Biotechnology department in Ludwigshafen, Germany, in 2011. Andrea is a research scientist working as a lab team leader within the Microbiology group. In her role she is responsible for isolation, identification and characterization of bacterial isolates potentially increasing abiotic stress resilience of certain crops. Currently, BASF's business unit Agricultural Solutions has various biological products on the market including bio-pesticides as well as bio-fertilizers. The biologicals can also be applied in combination with chemistry-based crop protection products.

Claudia Preininger

AIT Austrian Institute of Technology, AT

Claudia Preininger is a senior researcher at the AIT Austrian Institute of Technology, Tulln, Austria. She is responsible for formulation development including microbial seed coatings, foliar spray and soil amendment in the field of plant growth promotion and biocontrol. She has over 20 years experience in immobilization of enzymes, proteins and microbes. Current research includes the development and characterization of microbial micro- and nanocomposite seed coatings, granules and powders, the fabrication of microbial beads and core-shell capsules with distinct function and properties and microbial spray formulations for maize. She is a chemist and actually coordinates two m-era.net projects on microbial seed coatings with main focus on material – microbe interaction.

Angela Sessitsch

AIT Austrian Institute of Technology, AT

Angela Sessitsch heads the Bioresources Unit of the AIT Austrian Institute of Technology. She studied biochemistry at the University of Technology in Graz, holds a PhD in Microbiology from the Wageningen University, the Netherlands, and is habilitated at the Vienna University of Natural Resources and Life Sciences. She has pioneered plant-associated microbiomes, particularly in the endosphere, and she is interested in understanding the interactions between plants, microbiomes and the environment as well as to develop applications. Her group explores the diversity and functioning of plant microbiota by applying a range of molecular approaches, interaction modes between plants and model bacteria, colonization behaviour of endophytes as well as various application technologies for biocontrol and crop enhancement applications. Together with her group, Dr. Sessitsch published more than 160 peer-reviewed publications.

Steven Vandenabeele

Alphea Bio, BE

Steven Vandenabeele holds a PhD in biotechnology (University of Ghent) and has 20 years of experience in plant biotech (VIB Department of Plant Systems Biology, Rockefeller University, BASF Plant Science). Steven has worked in the ag-biotech industry for more than 10 years: he worked at BASF Plant Science as a group leader Technology Management, as the coordinator for the high-throughput plant phenotyping platform, and as research manager of the global rice yield project. Serving in these functions, he has gained strong experience in people, process and research project management. Three years ago, together with the VIB, he started building the business strategy to develop superior agricultural biologicals based on microbials. Aphea.Bio NV is currently operational for more than 1 year, backed by venture capital. Steven is Aphea.Bio's Chief Scientific Officer and heads a team of 18 expert scientists.

Lisa Wingate

INRA, FR

Lisa Wingate's undergraduate, postgraduate and postdoctoral research has a strong foundation in ecosystem physiology and the geosciences (The University of Edinburgh). She has worked alongside experimentalists and modellers to develop theoretical understanding of stable isotope fractionation in a range of ecological systems in order to interpret the responses of ecosystem components to climate, holding positions at the University of Cambridge before joining the Institut National de la Recherche Agronomique (INRA Bordeaux) in 2012 and building the ECOFUN team with colleagues. Her current research lies at the interface between geochemistry, physics, biology and ecology, and aims to describe the regulation of atmospheric CO2 and COS concentrations at scales spanning the enzyme to the globe.

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Speaker Abstracts - Tuesday 4 December

Felton – Keynote Speaker

The role of microbes in mediating plant-insect interactions – Benefit or betrayal?

Gary Felton
Professor and Head of the Department of Entomology at Pennsylvania State University, US

All plant-herbivore interactions occur in a microbial context. Herbivore-associated microbes may benefit herbivores through supplementing herbivore nutrition, assisting in digestion, aiding in detoxification of plant defenses, and/or priming their immune systems. One aspect of microbial mediation of plant-herbivore interactions that has been overlooked is the ability of microbes to alter the perception of herbivores by their host plants. Plants recognize herbivore feeding cues found in their saliva and oral secretions and use these cues to mount defensive responses against herbivores. We will present evidence that an array of microbes associated with herbivores (bacteria, fungi, baculoviruses, and polydnaviruses) can alter the recognition of these cues in ways that may benefit or betray the herbivore. Ultimately these microbes mediate both herbivore and plant immunity

Brodie

Deciphering the signatures of niche adaptation in soil microbial communities

Eoin Brodie
Deputy Director of the Climate and Ecosystem Sciences Division, UC Berkley, US

Soil is perhaps the most complex biological ecosystem, where physical and chemical heterogeneity results in abundant and distinct metabolic and physiological niches for soil microorganisms to survive and thrive. This complexity is apparent in genetic observations of soil microbiomes, however a number of observations suggest that consistent rules of rhizosphere assembly might play out in disparate ecosystems and that generalizable principles might be within reach. Deriving these principles and approaches to evaluate them is a necessary step towards building predictive models of soil microbiome activity and response to manipulation. In this presentation I will discuss several advances in illuminating microbial functional traits in soil and a framework to incorporate this new knowledge into mechanistic models of soil biogeochemistry.

Wingate

From enzyme to Earth system: linking soil community function and composition to constrain the magnitude of the terrestrial biosphere CO2 sink

Lisa Wingate
Institut National de la Recherche Agronomique (INRA Bordeaux)

When microscopic organisms such as bacteria, fungi and unicellular algae are assembled into communities they can exert a profound effect on the chemical composition of the atmosphere and modify climate at the Earth’s surface. This is because microbial processes drive global photosynthesis, organic matter decomposition and nutrient cycling. However, modelling and scaling microbial physiology at the global scale and predicting the function of microbial communities to global change is an enormous scientific challenge. Here I present some ideas about how a multi-functional enzyme-based approach could help us constrain estimates of the CO2 sink strength of the terrestrial biosphere. I also discuss how this approach could lead to new insights into the spatial regulation of microbial community function and diversity as soil and plant properties vary.

Salas-Gonzalez

Bacterial community maintenance of plant root development

Isai Salas-Gonzalez[1,2,3]*, Omri M. Finkel[1,2], Gabriel Castrillo[1,2,7], Theresa F. Law[1,2] and Jeff Dangl[1,2,3,4,5,6]
[1]Department of Biology, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[2]Howard Hughes Medical Institute, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[3]Curriculum in Bioinformatics and Computational Biology, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[4]Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[5]Curriculum in Genetics and Molecular Biology, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[6]Department of Microbiology and Immunology, University of North Carolina, Chapel Hill, NC 27599-3280, USA
[7]Present Address: Centre for Plant Integrative Biology, School

Plants intimately associate with microbial communities collectively known as the plant microbiome. The microbiome contributes to plant processes such as development, nutrient acquisition and pathogen protection. The establishment of community assembly rules and community-host feedback patterns has been limited due to the complexity of natural microbial communities. Here, we applied a synthetic ecology approach to an amenable plant-microbiome mesocosm to unravel novel community-host and microbe-microbe interactions.

A. thaliana plants were inoculated across a gradient of phosphate, salinity, pH and temperature conditions with a genome-sequenced bacterial inoculum composed of 185 phylogenetically diverse isolates (SynCom). Colonization patterns across the fractions and conditions sampled were quantified using 16s amplicon sequencing. We used the correlation of these abundance profiles among all members of the community to split the SynCom into four modules which exhibited a characteristic colonization pattern and high phylogenetic coherence.

Subsequently, we measured plant molecular and morphological phenotypes when inoculated with each of these modules independently and in combination. Plant phenotypes induced by some modules were attenuated when co-inoculating with other modules exhibiting ecological epistasis between guilds in the community. Following our top-down approach, we identified a single genus that was responsible for dampening the effects that all other members of the community exerted over the root morphology of the plant.

This demonstrates that in the context of a complex community there are multiple interactions that strongly influence plant development and that a balanced microbiome is required to equilibrate these interactions and prevent host dysbiosis.

Hou

The root microbiota coordinates trade-offs between shade and immune responses in Arabidopsis

Shiji Hou*, Thorsten Thiergart and Stéphane Hacquard

Light is one of the fundamental environmental factors underlying plant growth and development, and can also influence plant immune responses. Besides the impact of abiotic factors, plant growth in nature is also regulated by diverse microbial assemblages collectively called the plant microbiota. The microbiota is thought to help plants overcome specific environmental constraints, likely promoting plant adaptation in their natural habitats. However, the role of the root microbiota in plant growth and plant immune responses under shade stress remains unclear.
We used synthetic microbial culture collections (bacteria, fungi, and oomycetes) and gnotobiotic plant systems to reconstitute the root microbiota under strictly controlled laboratory conditions. Together with amplicon-based high-throughput microbial profiling, these experiments indicated that the root microbiota augments host shade tolerance and revealed shade-dependent microbial community shifts in Arabidopsis roots. Moreover, RNAseq data identified microbiota-dependent shade-responsive genes in both roots and shoots, indicating a functional link between the microbiota and shade responses in Arabidopsis. Notably, immune responses in roots and systemic defense responses in shoots are induced in the presence of the root microbiota under normal light conditions but are largely shut down under shade, implying that the induction of plant defense by the root microbiota is light-dependent. Ongoing analysis of Arabidopsis mutants impaired in immunity and light signaling pathways will shed new light onto the underlying mechanisms coordinating microbiota-dependent trade-offs between growth and defense under shade. These findings may facilitate efforts to define and deploy useful microbes that enhance plant performance under suboptimal light conditions.

Garbeva

Deciphering belowground microbe-microbe and plant-microbe chemical communication

Paolina Garbeva
Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands

Research on soil and plant microbiomes has increased exponentially over the last ten years, revealing the tremendous diversity of microbial communities. At the same time, our knowledge concerning the chemical interactions in the soil, between microbes and between microbes and plants is still rudimentary. Plant and microbe derived compounds play an important role in belowground interactions, e.g. in signalling and interference competition. Both plants and microorganisms produce and secrete a wide variety of primary and secondary metabolites including volatile organic compounds (VOCs) and non-volatile exudates. In my talk, I will present our recent discovery of the ecological role of VOCs in the long-distance belowground microbe-microbe and microbe-plant interactions. Furthermore, in this presentation I will reveal the importance of microbial VOCs in soil fungistasis and disease suppressiveness.

Kivlin

Climate change may differentially disrupt leaf and root phytobiomes

Stephanie N. Kivlin[1,2]*, Michael Mann[2,3], Melanie R. Kazenel[2,3], Joshua S. Lynn[2,3], and Jennifer A. Rudgers[2,3]
[1]University of Tennessee, Knoxville, TN
[2]Rocky Mountain Biological Laboratory, Gothic, CO
[3]University of New Mexico, Albuquerque, NM

While the direct effects of climate change on plants are now readily apparent, determining how climate change affects the interactions between plants and their associated microbiomes is still not resolved. For example, fungal symbionts may not be able to track shifting plant distributions and phenology under future climates. Plants may therefore leave behind their original fungal symbiont communities and encounter novel fungal symbionts as their temporal and spatial distributions shift. Here we characterized how dispersal limitation, environmental factors (climate, soil nutrients), and plant hosts affected the abundance and composition of horizontally transmitted leaf and root fungal endophytes and arbuscular mycorrhizal (AM) fungi along steep elevational gradients in the Colorado Rocky Mountains and used these community assembly rules to predict how plant-fungal symbioses may be disrupted with climate change.

Plant hosts were the main factor affecting the composition of all three fungal phytobiome groups. However, leaf endophytes were more sensitive to elevation and associated differences in climate than belowground fungal symbionts. Yet, in samples of airborne fungi collected to characterize dispersal potential, leaf endophytes were more abundant than root endophytes, and AM fungi were totally absent. Thus, leaf endophyte communities were structured by plant host and environmental filtering and not dispersal limitation per se. In contrast, root endophytes were structured by dispersal limitation and plant hosts. Taken together, these data suggest that as plants move to higher elevations with climate change, leaf endophytes will be able to co-disperse but root endophytes will not, resulting in belowground phytobiome disruption in future climates.

Tollenaere **Poster 166**

Multiple infections in rice from West Africa: mechanisms, epidemiological and evolutionary implications

Charlotte TOLLENAERE[1, 3]*, Issa WONNI[1,2] , Drissa SEREME[1,2], Mariam BARRO[1,2], Severine LACOMBE[1,3], Sebastien CUNNAC[3], Eugénie HEBRARD[3], Martine BANGRATZ[1,3], Christophe BRUGIDOU[1,3]

[1] Laboratoire Mixte International Patho-Bios IRD-INERA ; Observatoire des Agents Phytopathogènes en Afrique de l'Ouest

[2] Institut National de l'Environnement et Recherches Agronomiques (INERA), Bobo-Dioulasso, Burkina Faso

[3] Institut de Recherche pour le Développements (IRD), UMR IPME, Interactions Plantes-Microorganismes-Environnement, Montpellier, France

Plant pathologists have long focused on the tight interaction between a pair of species 'one plant / one pathogen'. However, the recent concept of the 'pathobiome' proposes to define pathogenesis beyond a one-to-one interaction and instead integrating the pathogen within the whole biotic community of the host, including other pathogen species (i.e. co-infection or multiple infections) as well as non-pathogenic microbial species. This paradigm shift considers the effect of the within-host biotic community on infection outcome, epidemiology and evolutionary trajectories of plant pathogen populations. We apply the 'pathobiome' concept to the pathogen species causing major rice diseases in West Africa, in particular the Rice yellow mottle virus (RYMV) and bacterial leaf streak (BLS) due to the bacterium Xanthomonas oryzae oryzicola (Xoc). We showed that yellow mottle disease and BLS are frequently found in the same fields and co-infect naturally the same rice plants. Our experiments reveal that rice co-infected by RYMV and Xoc present more severe bacterial symptoms, while viral accumulation is reduced, compared to the mono-infected mock treatment. Our analyses finally suggest that RNA silencing mechanisms would likely be involved in such RYMV-Xoc within-plant interactions. We then extend our focus to other major rice diseases, with intensive pluri-annual field work and multi-pathogen detection. Associations between microbes (either positive or negative) in the field may be due to within-host interactions but this requires confirmation through experimental work. We believe the pathobiome approach applied to crop diseases will ultimately provide a wealth of new high-impact insight concerning plant diseases, providing valuable knowledge to allow for an eco-friendly increase of agricultural production.

Bell

Microbial colonization of soils: implications for agriculture and experimental systems

Terrence Bell[1]*, Laura Kaminsky[1], Idalys Bonet[1], Ryan Trexler[1]
[1]Department of Plant Pathology and Environmental Microbiology, The Pennsylvania State University

The ability microorganisms to establish and proliferate in soils is broadly relevant to the biogeography of plant-associated microorganisms. These traits are also of applied importance for phytobiome management, particularly as they impact microbial inoculant survival/activity, and the recolonization of agricultural soils that are cleared to control pests (e.g. through soil disinfestation, fungicide applications). Despite numerous studies on the relationship between abiotic soil parameters and microbiome composition, we know little about soil microbial colonization. I will present data from our lab that shows the impact of modifying soil resources and disturbances on soil microbial colonization. I will also show the impact of microbial source (i.e. forest vs. agricultural soil) on the composition and carbon preferences of early-colonizing microorganisms.

In addition, we are determining how soil microbial colonization can be applied to establish replicable microbiome systems, which allow probing of plant-microbe interactions through time and across labs. In particular, our goals are to A) avoid excluding yet-to-be-cultivated microbes, B) limit the transfer of compounds from parent soils, and C) preserve interactions that have developed over time between microorganisms from a particular soil environment. We have reintroduced microbiomes from a bank of cryopreserved soils into different sterile soil environments, and show how the relationship between microbiome composition in parent soils and recipient soils is impacted by the abiotic parameters of each. Ultimately, we aim to understand how colonization impacts management of agriculturally-relevant microorganisms, and to develop realistic soil microbiome models to enhance investigations of the phytobiome in controlled lab and greenhouse settings.

Adams

Soil fungal diversity in grasslands of the Tibetan Plateau: Is it Driven by Plant Diversity and Productivity?

Jonathan Adams
Professor of Soil Biology at Cranfield University, UK

It is unclear whether soil fungal diversity correlates with the diversity and productivity of plant communities. Previous studies have revealed inconsistent correlations between fungal diversity and plant diversity from local to global scales, and there is a lack of information about the diversity-diversity and productivity-diversity relationships for fungi in alpine regions. We investigated the relationships between soil fungal diversity, plant diversity and productivity across 60 grassland sites on the Tibetan Plateau, using metagenetics for fungal identification. Fungal alpha and beta diversities were best explained by plant alpha and beta diversities, respectively, when accounting for environmental drivers and geographic distance. Our study points to a predominant effect of plant diversity, along with other factors such as carbon : nitrogen (C : N) ratio, soil phosphorus and dissolved organic carbon, on soil fungal richness.

Ourry

INRA Early Career Award Winner

Poster 165

Deciphering Brassica napus-microbiome associations in interaction with root herbivorous insect Delia radicum: a feedback loop in the rhizosphere

Ourry M.[1]*, Lebreton L.[1], Chaminade V.[2], Guillerm-Erckelboudt A.Y.[1], Hervé M.[2], Linglin J.[1], Marnet N.[1,3], Ourry A.[4], Paty C.[2], Poinsot D.[2], Cortesero A.M.[2], Mougel C.[1]
[1] IGEPP, INRA, Agrocampus Ouest, Université de Rennes 1, Le Rheu, France
[2] IGEPP, INRA, Agrocampus Ouest, Université de Rennes 1, Rennes, France
[3] BIA, Team "Polyphenols, Reactivity & Processes", Le Rheu, France
[4] Normandie Université, UNICAEN, INRA, UMR 950 Ecophysiologie Végétale, Agronomie et nutritions N, C, S, Esplanade de la Paix, Caen, France

Plants are known to be major biological hubs, which above- and belowground organs interact with either beneficial or detrimental macro- and microorganisms. Even though plant-microorganism interactions are better understood, tripartite interactions involving herbivorous insects remain more complex.
We studied the feedback loop of the tripartite interaction between soil microorganisms, oilseed rape (*Brassica napus*) and a specialist belowground herbivore, the cabbage root fly (*Delia radicum*). Our aims were i) to determine the effects of herbivory on the plant root chemistry and on the root and rhizosphere microbiota and ii) to assess in return the effects of selected soil microorganisms on the herbivore development. To tackle this question, we focused on the plant root primary and secondary metabolites and chemical elements, and analyzed both bacterial and fungal communities assemblages.
In this study, herbivory influenced the temporal dynamics of root metabolites by decreasing most metabolites but increasing trehalose, indolyl glucosinolate and sulfur contents. These changes modified the dynamics of root and rhizosphere microbial communities, such as enhancing the abundance of *γ-Proteobacteria* and *Firmicutes*. Among these bacterial phyla, four genera (*Bacillus*, *Paenibacillus*, *Pseudomonas*, and *Stenotrophomonas*) had a higher abundance following herbivory, which was associated to modifications of root chemical compounds. Also, plants associated to different levels of soil microbial diversity marginally influenced root metabolite profiles but contributed to a modification of the fly emergence rate.
Further research would help to identify the biological function of plant, microbiome and insect and the potential implications of microbiome in plant defenses.

Luna

Insect-Bacteria-Plant Interactions: Microbiomes of Russian Wheat Aphid (*Diuraphis noxia*) Contain Bacteria that Increase Virulence to Wheat

Emily Luna[1], Christine Chang[2], Jennifer Shipp[1], Jessica Metcalf[3], Janet Ziegle[3], and Jan E. Leach[1]*
[1]Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO 80523-1177
[2]Pacific Biosciences, Menlo Park, CA 94025
[3]Department of Animal Sciences, Colorado State University, Colorado State University, Fort Collins, CO 80523-1177

Phenotypic responses to biotic stresses are often studied as the interactions between two species; however, in the phytobiome, these responses frequently result from complex interactions involving several organisms. We previously demonstrated that variation in chlorosis caused by feeding of Russian wheat aphid (RWA, *Diuraphis noxia*), a major pest of wheat world-wide, is determined, in part, by aphid-associated bacteria. The saliva of the aphid contains proteins mainly from bacteria in the families *Enterobacteriacae* and *Erwiniacae*. As a first step in determining which bacteria are necessary for the increased virulence of aphids, we characterized the microbiome of artificial diets fed upon by either control aphids or aphids reared with reduced bacterial populations using 16S sequencing and whole genome sequencing with Pacbio SMRT sequencing. Additionally, we characterized the microbiome of wheat leaves fed upon by either control aphids or aphids with reduced bacterial populations. This data revealed that the microbiomes of artificial diets fed upon by RWA, like the RWA saliva, are comprised mainly of bacteria from families *Enterobacteriacae* and *Erwiniacae.* Genome annotation of relatively abundant bacteria suggest a repertoire of virulence factors such as: type III and type VI secretion systems as well as antibiotic resistance genes. Bacteria in communities from wheat leaves infested by RWA were similar to those from artificial diets fed upon by RWA, suggesting bacteria were delivered to leaves by RWA.

Moulin

Comparative transcriptomics of the wheat response towards diverse partners of its microbiome

Daniel Garçia-Seco[1], Valentina Fiorilli[2], Claudia Vannini[3], Alexis Dereeper[1], Marco Chiapello[3], Marcella Bracale[3], Pierre Czernic[1], Paolo Bagnaresi[4], Valeria Terzi[4], Florence Wisniewsky-Dyé[5], Paola Bonfante[2], Lionel Moulin[1]*
[1] Interactions Plant-Microbes-Environment (IPME), IRD, Cirad, University Montpellier, France
[2] Department of Life Sciences and Systems Biology, University degli Studi di Torino, Italy
[3] Dipartimento di Biotecnologie e Scienze della Vita, University degli Studi dell'Insubria, Italy.
[4] CREA-GB, Research Centre for Genomics and Bioinformatics, Fiorenzuola d'Arda, Italy.
[5] Ecologie Microbienne, CNRS, INRA, University Lyon 1, France.

Plants constantly live with a variety of microorganisms that can be beneficial or pathogenic. Although host-pathogen interactions are relatively well described at present in several models, those concerning the response of plants to beneficial and multiple interactions, remain poorly studied. In the MIC-CERES project (funded by Agropolis and Cariplo fondations), we analyzed the composition of the wheat microbiomes, and also the physiological and transcriptomic response of tender wheat (Triticum aestivum cv Chinese Spring) during its interaction with different actors of its phytobiome: two PGPR bacteria (one rhizospheric, Azospirillum brasilense; one endophyte, Paraburkholderia graminis), one mycorrhizal fungi (Funneliformis mossae), and a wheat pathogen, Xanthomonas translucens (Xt). In order to decipher the different responses of wheat to these microbes, we produced RNAseq data from wheat roots and leaves 50 days after inoculation (except Xt which was monitored at 1 dpi), in the same growth system for all interactions. The responses were analyzed at a global level, revealing clear difference between organs and types of interactions, and at gene-level, revealing specific gene networks linked to observed phenotype (Plant-growth promotion for bacteria, defense against Xt, plant biocontrol mechanisms induced by mycorrhiza against Xt).

Morel

Plant-plant interactions modify disease susceptibility

Aurélie DUCASSE[1], Coline TEMPLE[1], Elsa BALLINI[1], Jean-Benoit MOREL[1]*
[1] BGPI, INRA, CIRAD, SupAgro, Univ. Montpellier
Campus International de Baillarguet TA A-54 / K 34398 Montpellier cedex 5

Many reports indicate that crop mixtures (either inter or intra-specific), reduce the incidence of microbial diseases. Besides mechanisms operating at the field level like inoculum dilution, there is recent evidence that plant-centered mechanisms with identified plant molecules and pathways are also involved. For instance, molecules produced by one plant, either above or below ground, can directly inhibit pathogens or indirectly trigger resistance through the induction of the plant immune system in neighboring plants. Alternatively, competition for resources like light or nutrients may indirectly modify the expression of the plant immune system (Morel and Zhu, 2018). We evaluated under controlled conditions and in the field if such plant-centered mechanisms were operating, using inter-specific (rice and maize, wheat and pea) and intra-specific mixtures (rice and rice, wheat and wheat). Our result show that the physiology (as measured by gene expression analysis) of a given plant can be modified by the identity of the neighboring plants. This modification can lead to measurable changes in disease susceptibility. We have evidence that several mechanisms are operating: some involve molecules produced by roots exudates while in other cases the trade-off between growth and defense may be involved. We further explored these plant-plant interactions in intra-specific mixtures. We could identify good neighbors that hold new promises for crop protection in intra-specific mixtures.
Zhu S, Morel JB (2018) doi: 10.1094/MPMI-03-18-0058-CR

Flis

Using 4R Nutrient Stewardship to Optimize Soil and Plant Health

Sally Flis
Director of Agronomy at The Fertilizer Institute (TFI) Washington D.C., USA

The 4R Nutrient Stewardship Framework helps farmers achieve cropping system goals such as increased production, increased farmer profitability, enhanced environmental protection and improved sustainability, through consideration of the right source of fertilizer applied at the right rate, at the right time and in the right place. Making the most effective and efficient 4R decisions requires the farmer and their trusted consultants to examine soil physical, chemical, and biological characteristics, site characteristics like waterways and slope of a field, crop system goals and practices, and weather. Understanding how 4R decisions fit in a whole crop production system will optimize the economic, environmental, and social outcomes for a farmer.

Sasse-Schlaepfer

How plants shape the rhizosphere: physiological adaptations, exudation, and metabolite uptake

Joelle Sasse Schlaepfer[1,2]*, Josefine Kant[3], Benjamin J. Cole[1,2], Andrew P. Klein[4], Borjana Arsova[3], Pascal Schlaepfer[5], Jian Gao[1,2], Kyle Lewald[1,2], Kateryna Zhalnina[1,2], Suzanne Kosina[1,2], Benjamin P. Bowen[1,2], Daniel Treen[1,2], John Vogel[1,2], Axel Visel[1,2,6], Michelle Watt[3], Jeffery L. Dangl[4] & Trent R. Northen[1,2]
[1]Environmental Genomics and Systems Biology, Lawrence Berkeley National Laboratory, USA
[2]Joint Genome Institute, USA
[3]Institut für Bio-& Geowissenschaften, Forschungszentrum Jülich, Germany
[4]Howard Hughes Medical Institute and Dept. of Biology, University of North Carolina Chapel Hill, USA
[5]Institute of Molecular Plant Biology, ETH Zürich, Switzerland
[6]School of Natural Sciences, University of California, Merced, USA

Plant roots not only associate with a core microbiome, but also with specific microbes defined by the host genotype. The plant traits leading to associations with microbes are still mostly enigmatic, but likely, root morphology and plant-derived metabolites are important, as they define the physical and chemical environment of the root. Importantly, plant morphology and metabolism are also influenced by microbes, and by soil properties.
Here, we investigated how the model grass Brachypodium distachyon shapes and is shaped by various environments by growing it in phosphate-sufficient or phosphate-deficient mineral media, or a sterile soil extract in a model growth system, the EcoFAB. We also assessed the reproducibility of the physiological and metabolic responses across four laboratories. Excitingly, all traits investigated were distinct between experimental conditions, and consistent across laboratories. For plants grown in soil extract, we also made a number of interesting findings: these plants exhibited elongated root hairs, a specific metabolic profile, and they depleted 50% of the investigated metabolites from the substrate. This suggests that plants not only release, but likely also take up a wide variety of compounds from their environment, significantly changing the metabolite availability for other organisms present. Our study highlights the importance of studying plants not only in standard laboratory, but also in more natural environments, and is a first step towards understanding how plants shape their interaction with microbes in the rhizosphere.

Halverson

Can diversified cropping systems shape maize rhizosphere microbiomes towards more robust, interconnected communities?

Larry Halverson
Iowa State University, US

We have little insight into whether differences in agricultural management and the forms of fertilization affect the recruitment and metabolic activities of the root-associated microbiome over the course of plant development.
We investigated these questions in two contrasting cropping systems; a conventional (two-year rotation, inorganic fertilization) and a diversified (four-year rotation, manure amendments) system. Despite large differences in management, diversified cropping systems can be as productive as conventional systems, reduce N losses to groundwater, and promote retention of C and N. These documented ecosystem services allow us to explore how agricultural management affects the coupling between microbial communities and plant roots, and how this interaction may factor into increased nitrogen use efficiency. In this study, we examined prokaryotic and fungal communities of the maize root-associated microbiome at various maize developmental stages with varying predicted N demand in the field and laboratory. We show that root-associated prokaryotic and fungal community composition shifts significantly over the course of plant development in a cropping-system specific manner. Moreover, total resident (DNA-based) and metabolically active (rRNA-based) community profiling indicates prokaryotic species richness and the number of differentially abundant taxa is greater in diversified systems, but in a manner influenced by proximity to the root. Co-occurrence analysis suggest diversified cropping system prokaryotic communities exhibit more robust and efficient networks as they generally have more nodes with greater connectivity (links). It is unclear whether the similarity between rhizosphere and bulk soil prokaryotic communities and greater interconnectedness contributes to the crop yield benefit and reduced N losses in the diversified system.

Galindo-Castañeda

INRA Early Career Award Winner

Poster 163

Rhizosphere microbiome of field-grown maize as influenced by root cortical aerenchyma

Tania Galindo-Castañeda[1]*; Claudia Rojas-Alvarado[2]; Ulas Karaöz[3]; Eoin L. Brodie[3]; Kathleen M. Brown[1]; Jonathan P. Lynch[1]
[1]Department of Plant Science, The Pennsylvania State University, University Park, PA. 16802, USA
[2]Universidad de O'Higgins, Rancagua, Chile
[3]Ecology Department, Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, Berkeley CA 94720, USA.

Root cortical aerenchyma (RCA) is a selection target for maize breeding programs because it decreases the cost of soil exploration of roots and improves plant growth under drought and low-nutrient stress. RCA may modify the microenvironment of rhizosphere microorganisms by transporting oxygen to the soil or changing carbon rhizode position around the root. We tested the hypothesis that plants with contrasting levels of RCA will have different rhizosphere bacterial communities. The rhizospheres of maize inbreds with contrasting RCA levels and growing under low and high nitrogen conditions in Limpopo Province, South Africa and Pennsylvania, USA were studied for bacterial composition using metabarcoding of the 16s rRNA genes. Other anatomical and architectural root traits were studied as covariables in addition to RCA. The most important factor driving the rhizosphere bacterial composition was geographic location. In both sites, root phenotype, RCA included, grouped the diversity of bacterial communities better than genotype. RCA was among the significantly explanatory variables for the composition of the bacterial communities at the South African site and was neutral at the site in Pennsylvania. High-RCA rhizospheres harboured significantly enriched and depleted bacterial species compared to low-RCA plants at the two sites. Potential metabolisms related to N-cycling in soils were related to a positive effect of RCA on oxygen and a negative effect of RCA on carbon rhizodeposition in the rhizosphere. These results pave the way to further study the root phenotypes as drivers of rhizosphere microbial communities.

Mauchline

Rooting around the wheat microbiome

Tim Mauchline
Rothamsted Reasearch, UK

The root microbiome is recruited by plants and influences plant growth, health and resource use efficiency. These microorganisms can benefit crop plants in several ways including improved plant nutritional status as well as protection against biotic and abiotic stresses. There are various factors which determine the crop microbiome community structure and understanding how agricultural practices influence the microbiome structure is imperative for the development of sustainable agricultural systems. This talk explores our work into the relative importance of several factors that shape the wheat root microbiome namely: land use conversion at the Rothamsted Highfield experiment, wheat genotype in reference to contrasting plant height, fertilisation regime at the Rothamsted Broadbalk experiment as well as the interaction of seed microbial load and land use in determining microbiome structure.

Kruh

The phytobiome of a unique ecological system: parasitic weed and its host plant

Lilach Iasur Kruh[1]*, Jacline Abu-Nassar[2], Shiri Freilich[3] and Radi Aly[2]
[1]Department of Biotechnology engineering, ORT Braude College, Israel
[2]Department of Weed Science, Newe Ya'ar Research Center, Agricultural Research Organization, Israel
[3]The Institute of Plant Sciences, Newe Ya'ar Research Center, Agricultural Research Organization, Israel

Phelipanche and Orobanche species (broomrapes) are holoparasitic plants that connect to the vascular systems of their hosts, allowing the transfer of various substances including a possible exchange of endophytic bacteria that inhabit the internal tissues of both plants. To shed light on the microbial aspects of the parasitic interaction between Phelipanche aegyptiaca and its host, tomato, we characterized the endophytic composition in both plants before and after attachment using mass sequencing analysis. Endophyte communities of the parasitic weed were significantly different from that of the nonparasitized tomato root but no significant differences were observed between the parasite and its host, parasitized tomato root, suggesting bacterial exchange between these two plants. In addition to molecular analysis, isolation of endophytic bacteria from the parasitic weed- host plant system enabled to examine whether these isolates can affect the dynamics of host – parasite interaction. Endophytic bacteria isolates were examined for their ability to secrete substances that may affect the dynamics of this system, and indeed, a few isolates inhibit the growth of the parasitic weed. The current study focuses on the bacterial aspect of host – parasite interaction and highlights the potential of exploiting alternative environmentally friendly approaches for parasitic weed control.

Lamichhane

A conceptual framework to better understand interactions between seedbed abiotic and biotic factors under the influence of cropping systems and their overall impact on field crop establishment

Jay-Ram Lamichhane* and Jean-Noël Aubertot
INRA, UMR AGIR, CS52627, F-31326 Castanet-Tolosan Cedex, France

Seed germination and seedling emergence are the very beginning phase of a crop cycle and thus determine success or failure of any crop establishment. This early phase is affected by five major groups of drivers namely seed and seedling characteristics, seedbed physical components, seedbed chemical components, seedbed biological components, and cropping systems. While several studies have been carried out on these drivers, they mainly focused on only one or a few factors without taking into account their overall interactions and impact on seed germination and seedling emergence. Therefore, there is a need to adopt a systems-level approach for a better understanding of these interactions and their overall effect on the quality of crop establishment. In particular, a focus is needed on the impact of cropping systems on the functioning of plant- and soil-associated organisms. It is important to combine experimental approaches, regional agronomic diagnoses and simulation modeling in order to tackle the question. Such a holistic approach will allow designing of more resilient and environment-friendly agricultural systems less reliant on synthetic inputs. Such agroecological systems are the only alternative to feed the increasing global population, on one hand, and to minimize negative impacts on the human health and biodiversity, on the other.

Sessitsch

The plant microbiome from lab to field

Angela Sessitsch*, Günter Brader, Friederike Trognitz, Stéphane Compant, Birgit Mitter
AIT Austrian Institute of Technology GmbH, Center for Health & Bioresources, Bioresources Unit, 3430 Konrad-Lorenz-Straße 34, 3430 Tulln, Austria

The plant microbiome is considered as an accessory genome for plant providing complementary functions to their host such as nutrient mobilization and acquisition or functions to better cope with biotic and abiotic stresses. A number of microorganisms has been identified and selected for application as biofertilizer, plant strengthener or biopesticide and benefits seen in lab and greenhouse trials are highly promising. Nevertheless, field application remains a challenge. Reasons for this include the extreme complexity of plant-associated microbiota with which an inoculant strain has to compete or the poor availability of suitable delivery approaches for microbial inoculants. Furthermore, still mechanistic understanding on plant-microbe interactions or on holobiont interactions is missing. Ecological understanding, science-drive product development and smart delivery approaches are likely to improve plant microbiome applications and will pave the way to the integration of microbiome functions in smart agricultural systems. In this talk different aspects on microbiome understanding and the use of seed-based application approaches will be presented.

Rochefort

INRA Early Career Award Winner

Influence of environment and host plant genotype on the structure and diversity of the Brassica napus seed microbiota

Aude ROCHEFORT[1]*, Martial BRIAND[2], Coralie MARAIS[2], Anne LAPERCHE[1], Matthieu BARRET[2], Alain SARNIGUET[1]
[1]INRA, Université de Rennes 1, Agrocampus-Ouest, UMR 1349 IGEPP (Institute of Genetics, Environment and Plant Protection) – Le Rheu, France
[2]INRA, Université d'Angers, Agrocampus-Ouest, UMR 1345 IRHS (Research Institute on Horticulture and Seeds) – Beaucouzé, France

Seeds are involved in the vertical transmission of microorganisms from one plant generation to another and consequently act as reservoirs for the plant microbiota. Exploring the ecological processes involved in the assembly of the seed microbiota is therefore of interest for selecting in the future microbial communities that could promote plant-growth and plant-heath. In this work, the relative contribution of host- and environmental-filtering on the assembly of the seed microbiota of Brassica napus was investigated. The taxonomic structure of seed microbiota was estimated with two molecular markers, gyrB and ITS1, on a range of B. napus genotypes, representative of winter oilseed rape diversity, cultivated for two successive years in self-fertilization. Our results highlighted a significant influence of the harvesting year and the host genotype on the structure of the seed microbiota. Investigation of the core seed microbiota of B. napus highlighted 20 fungal taxa shared between all the genotypes, while there was no bacterial taxa conserved across all genotypes, underlying the specific influence of host genotype on the structure of the seed microbiota. This latter aspect was confirmed by community-based collection of more than 2,000 seed-associated bacterial isolates. The opportunity to change seed microbiota composition through environmental and genotype selection provides an interesting starting point for investigating its consequences on B. napus growth and health.

van Overbeek

Human pathogens in plant microbiomes

Leo van Overbeek[1]*
[1]Wageningen University and Research

Food-borne disease outbreaks resulting from consumption of plant-derived fresh produce have been reported world-wide such as from spinach in the USA, from mung bean sprouts in Japan and most recently also in Europe from fenugreek sprouts (Hamburg, 2011). It is clear that particular groups of human pathogenic micro-organisms (HPMO) can be found in plant microbiomes. Basic resources for agro-production, such as soil, water and fertilizers can play a role in contamination of plants. Contamination routes of HPMO to plants are poorly understood, and further it is not always easy to make a distinction between microbial contaminants (i.e. HPMO invading plants from other environments) and HPMO that are indigenously present in plant microbiomes. Because many taxonomic groups of HPMO are ecologically competent in plants, these groups must therefore be considered as integral components of the plant microbiome. Potential human pathogens typically associated with plants are species belonging to the genera of Fusarium, Aspergillus, Pseudomonas, Serratia, Enterobacter, Bacillus, Burkholderia and Stenotrophomonas. Recently we gained circumstantial evidence that even particular strains of Escherichia coli may be indigenous to plant microbiomes. Many microbial species supportive to plant growth are taxonomically related to potential human pathogenic groups. For biological control purposes it is relevant to make better distinction between potential pathogenic and plant-beneficial groups. It is the intention of the new EU COST Action HUPLANTcontrol (16110) to coordinate research on potential negative aspects of plant microbiomes on human health and to integrate novel scientific insight into sanitary measures and agricultural management practices.

Wehner

Breeding for priming triggered leaf rust resistance in barley

Gwendolin Wehner[1]*, Karolin Pohl[2], Nina Bziuk[2], Adam Schikora[2], Kornelia Smalla[2] and Frank Ordon[1]
[1] Julius Kühn-Institut (JKI), Institute for Resistance Research and Stress Tolerance, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany
[2] Julius Kühn-Institut (JKI), Institute for Epidemiology and Pathogen Diagnostics, Messeweg 11/12, 38104 Braunschweig, Germany

Leaf rust (*Puccinia hordei*) is one of the most important diseases of barley (*Hordeum vulgare* L.) leading to yield losses up to 60%. Resistance genes *Rph1-Rph25* are known in barley but most of these have been overcome meanwhile.
But, priming of barley may offer an opportunity to enhance resistance to *P. hordei*. By quorum sensing of bacterial communities N-acyl homoserine-lacton (AHL) is produced, which is known to induce systemic resistance. The present study therefore aims at the detection of genomic regions involved in priming capacity of barley which is one of the most important cereal crops, worldwide.
A diverse set of 200 spring barley accessions were treated with bacteria, i.e. repaired *Ensifer meliloti* natural mutant *expR+ch* overexpressing AHL and transformed *E. meliloti* carrying the lactonase gene *attM* from *Agrobacterium tumefaciens* which inhibits AHL production. After three bacterial inoculations, plants were infected with *P. hordei* strain I-80 at the three leaves stage. 12 days after infection scoring of the leaf area diseased and the infection type was conducted. Results of two experimental replications revealed significant effects ($p<0.001$) of the bacterial treatment indicating a positive effect of priming on *P. hordei* resistance. Based on the observed phenotypic differences and 23,417 filtered SNPs derived from the Illumina 9k iSelect chip and genotyping by sequencing, 21 quantitative trait loci (QTL) involved in priming-efficiency were identified by genome wide association studies**.** Experiments will be repeated once to validate QTL regions and develop molecular markers facilitating marker assisted selection of priming efficient accessions in barley breeding.

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Dupas

Bayesian learing for decision support in the Internet of phytosystems things

Stéphane Dupas*[1,2], Diego Clavijo[3], Camilo Pattaroyo[1,2], Laura Gonzalez[3],, Gastón Lyons[3], Carlos Carpío[4], Alvaro Barragán[5], Silvia Restrepo[1].
[1] Laboratoire Evolution, Génome, Comportement et Ecologie, Univ Paris-Sud, CNRS, IRD 247, 1 Avenue de la Terrasse, 91198 Gif-sur-Yvette Cedex, France
[2] Departamento de Ciencias Biológicas, Universidad de Los Andes, Bogotá, Colombia
[3] Direccion de Servicios de Información y Tecnología, Universidad de Los Andes, Bogotá, Colombia
[4] Facultad de Recursos Naturales de la Escuela Superior Politécnica de Chimborazo (ESPOCH)
[5] Departamento de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador, Quito, Ecuador

The international laboratory Bio_inca “Biodiversity of natural and cultivated tropical andean phytosystems” groups researchers from IRD France, Uniandes Colombia, and PUCE Ecuador in the areas of genetic, ecology, ecosystem services and modelling. We present here a development from this laboratory consisting on a generic algorithm to learn decision support model on phytosystem dynamics from real-time series data. The approach consists on building the model based on the relevant field data we do have : usually incomplete and multiple source, including epidemiological, genetic, ecological and socio-economical. Scientific hypotheses, models and experiments are used as prior in a Bayesian scheme that combines likelihood and simulations. We present the general algorithm and its declination to potato epidemiological modelling.

With this approach we aim to structure an Internet of phytosystems that connect real-time series with ecological models. Sampling devices can now be connected in real-time to the cloud from almost everywhere at low velocity and low cost. They can include in-farm biophysical sensors, remote imagery, and participative science smart-phones application or text telephones. Such devices can send data and/or receive decision support. They have to be designed based on social evaluation of small farm-holders attempts and relationships to technologies of information and communication.

We are finally making a call on phytosystem community to build an open-source global real-time social ecological database on phytosystems. The purpose is to develop decision tools that facilitate inputs cost reduction (pesticides fertilizers), ecological intensification, and land use, market, and value chain optimization, at the different scales.

Makiola

Characterising plant pathogen communities and their environmental drivers at a national scale

A Makiola[1,2], IA Dickie[3], RJ Holdaway[4], JR Wood[4], KH Orwin[4], TR Glare[2], CK Lee[5]
[1] Agroécologie, AgroSup Dijon, INRA, Univ. Bourgogne, Univ. Bourgogne Franche-Comté, F-21000 Dijon, France
[2] Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand
[3] Bio-Protection Research Centre, School of Biological Sciences, University of Canterbury, New Zealand
[4] Manaaki Whenua – Landcare Research, Lincoln, New Zealand
[5] Waikato DNA Sequencing Facility, School of Science, University of Waikato, Hamilton, New Zealand

Understanding what drives the dynamics of plant pathogens at the largest scales is crucial for the maintenance of global food security, conservation of natural ecosystems and future resilience and sustainability of ecosystem services in general. Although interactions between plant pathogens, the environment, land use and plants have been described many times, the contribution of these different parameters remain largely unknown. Recent advances in next-generation sequencing (NGS) methods and extended DNA barcode libraries are allowing, for the first time, surveys and the study of entire plant pathogen communities and their interactions across diverse landscapes at national scales. The inference of functional traits from metabarcoding data, such as those associated with plant pathogen status, presents a range of interesting scientific challenges. Here I present what we have learnt from doing this in New Zealand: (1) the advantages and pitfalls of NGS metabarcoding of plant pathogens; (2) the first biomonitoring of fungi, oomycete and bacteria plant pathogens at the national scale of New Zealand; and, (3) the relative importance of environmental factors for plant pathogens and what this likely means for us in face of ever increasing changes in climate and land use.

Saha

AgriVectors: a portal for plant diseases transmitted by insect vectors

Surya Saha*, The AgriVectors Consortium, Wayne Hunter and Lukas Mueller
Boyce Thompson Institute, US

Plant-feeding hemipteran pests are global threats to food security and production. Agricultural disease vector systems are an under-served area of research despite being one of the fundamental challenges for increasing food consumption. We propose to build an open and comprehensive resource for plant disease systems where the pathogen is transmitted by an insect vector. The portal will connect to established public repositories such as NCBI and EMBL together with pathosystem-specific repositories like citrusgreening.org. Furthermore, topical resources such as RNAi, CRISPR, insect feeding assays like EPG, etc. will also be included and leveraged to create a knowledgebase for plant diseases and vector biology. This system will also support privileged access for databases with private and unpublished data. We have created the citrusgreening.org portal as a model for a tritrophic disease system with genomics and bioinformatics resources for the vector Asian citrus psyllid (ACP, Diaphorina citri), the host citrus (C. clementina and C. sinensis) and multiple pathogens including Ca. Liberibacter asiaticus (CLas) for the citrus greening disease. We have used Biocyc Pathway Tools databases to model biochemical pathways within each organism that can be used to explore the entire disease complex. Psyllid Expression Network (PEN) is an expression atlas with proteomics and RNAseq data for ACP from adult and nymph life stages, various conditions and multiple hosts. The citrusgreening.org model will be extended beyond gene-centric omics data to pathosystem-wide data including integrated pest management data, behavioral and climate data in addition to phenotyping information from disease trials to create the AgriVectors portal.

Jacobson

Systems Biology Models of the Interactions Between Host, Phytobiome and Environment

Daniel Jacobson*, Piet Jones, Ben Garcia, David Kainer, Jared Streich, Gerald Tuskan, Wellington Muchero, Timothy Tschaplinski, Jessy Labbe, Ben Brown, Jay Chen, Anna Furches, Ashley Cliff, Jonathon Romero, Debbie Weighill

We have created Parakraken, a parallelized kmer profile-based taxa identification approach that uses full kmer profiles from every publicly available genome sequence (including bacteria, archae, fungi, viruses, nematodes, insects, protists, etc.). This allows us to detect the cryptic phytobiome in the DNA or RNA sequence of any host tissue. We are using Parakraken as well as OTU-based amplicons to identify taxa in different host tissues across a genome wide association study (GWAS) population of Populus trichocarpa. We also have other independent layers of data across this population, including metabolomics, transcriptomics, phenology, pyMBMS and many climactic phenotypes measured across the original locations of the genotypes in the population. In addition, we have developed new methods for GWAS that allow us to achieve considerable sensitivity and use rare alleles found in the population. Furthermore, we have developed explainable-AI approaches to find complex epistatic architectures responsible for the host's ability to detect and modulate its microbiome and other phenotypes. The result is a comprehensive systems biology model of a plant and its regulation of its microbiome, its adaptation to its climactic environment and the metabolic intermediaries involved therein. We believe that many of the genes responsible for host-phytobiome association have orthologs across the plant kingdom. Thus, we combine the results of these approaches in Populus with many orthogonal layers of information in order to score each hypothesis supported by multiple lines of evidence in order to prioritize specific mechanisms for cross species experimental validation.

Charles

Microbiome dynamics during enrichment culture on ACC as nitrogen source: relevance to controlled environment agriculture

Aashi Saraf, Michael Lynch, Elena Zaikova, Jiujun Cheng, John Heil, Trevor C. Charles*

Controlled environment agriculture systems, such as hydroponic greenhouses and vertical farms, offer unprecedented opportunities for ensuring optimal microbiome composition for plant growth, product yield and quality, and resilience against disease-causing microbes. We have carried out microbiomic and metagenomic surveys of the fertigation systems of commercial vegetable greenhouses, and observe clear, crop-specific effects on microbial community structure. Rhizospheric conditions and characteristics are expected to result in enrichment effects. In this context, we are using macrobiotic analysis to investigating the enrichment of microbial communities by nutrients of importance in the plant-microbe interactions. The ability to degrade 1-aminocyclopropane-1-carboxylic acid (ACC), the immediate precursor to ethylene, is associated with many rhizospheric and endophytic bacteria that have plant beneficial effects. The key enzyme is ACC deaminase, which catalyzes the conversion of ACC to ammonia and α-ketobutyrate. As a result, ACC can serve as nitrogen and carbon source, and the resulting reduction of ACC levels reduces stress ethylene. Of interest is the role that ACC plays in shaping the phytobiome, and how this in turn influences crop health and productivity. As an initial step towards understanding this, we used 16S rRNA gene sequence analysis and meta-genomics to investigate the community dynamics of soil enrichment cultures with ACC as nitrogen source, compared to ammonia. We found that the community became much more constrained on ACC, consistent with ACC metabolism being more of a specialized trait. The ACC-enriched cultures were able to promote plant growth.

Breakfield

M-trophs for sustainable agriculture

Natalie Breakfield
NewLeaf Symbiotics

Pink-pigmented facultative methylotrophs in the genus *Methylobacterium* (M-trophs) are highly abundant members of the plant microbiome. NewLeaf Symbiotics is harnessing the power of these beneficial bacteria to improve yield and strengthen plants under field conditions. We are optimizing genotypic and phenotypic data in our Prescriptive Biologics Knowledgebase ^{TM} (PBK) to make predictions of which M-trophs will perform best for a given condition and crop. These predictions are tested in the field, and these data are used to improve our processes. This pipeline has led to the introduction of our first two products,
Terrasym 401 for soybean and Terrasym 402 for peanut.

Broglie

Reimagining Crop Nutrition

Richard Broglie
Chief Technology Officer at Pivot Bio

While synthetic fertilizers have accelerated crops yields worldwide, most of the synthetic nitrogen that farmers apply is never absorbed by the crops they produce; instead, the nitrogen evaporates into the atmosphere and is washed into nearby waterway that become polluted or becomes the greenhouse gas nitrous oxide, which is 300 times more potent than CO^2.
Biological nitrogen fixation (BNF) by plant-associated bacteria has the potential to provide a sustainable and efficient source of nitrogen to crop roots. However, the abundance of fertilizer and residual nitrogen in agricultural soils has repressed BNF in natural rhizosphere microbes. To address this problem, we have restored BNF in the rhizosphere of cereal crops by creating a platform to identify, characterize and fine-tune plant-associated microbes. Fine-tuning the genetic regulation of BNF resulted in strains able to fix nitrogen in fertilized conditions and release scaled amounts of nitrogen to cereal crop roots. As measured by ^{15}N abundance studies in field conditions, these microbes supply up to 25 kg N/ha directly to corn plants. These first-generation nitrogen-producing microbes are the first commercially-viable example of BNF as a nitrogen management solution.

Vandenabeele

An integrated technology pipeline for the development of superior agricultural biologicals

Steven Vandenabeele
Aphea Bio

Aphea.Bio, a Gent based R&D company, is developing sustainable and superior agricultural products based on natural microorganisms to increase crop yields (biostimulants) in cereals and to protect them against fungal diseases (biocontrol).
Aphea.Bio stands out by its unique technology pipeline. bio-informatics and metagenomics approaches are used to build microbiome maps for selection of the best candidate microorganisms and for building robust consortia that positively impact plant growth and health. Using a combination of proprietary microbial culturing technologies, a unique microbial collection is built up. Microbial strains are further tested for beneficial effects in planta in an automated high-throughput phenotyping platform under controlled growth conditions and eventually screened in field trials. In this presentation, an overview of Aphea.Bio's pipeline and the latest developments will be discussed.

Hallahan

From the field to the lab and back again – delivery of an entomopathogenic fungus for corn rootworm control

Hallahan, D*., Qi, S., Burns, R and Bruck, D.

Many plant-beneficial microbes are documented in the plant microbiome literature, but relatively few have made it into widespread use in agriculture. Most fall at one or other of the many hurdles between initial proof-of-concept and translation from lab to field. Technical failure modes include feasibility and cost of production and scaleup, formulation compatibility, and stability. Even if these obstacles are overcome, efficacy requires establishment in the environment or target site with appropriate timing and dose. Entomopathogenic fungi of the genus Metarhizium have well-characterized efficacy against a variety of insects. We describe progress in production, formulation and stability of this organism for the control of corn rootworm, Diabrotica spp., major pests of corn production in North America and Europe.

Marino

Poster 164

RNA-Seq: A tool for investigating the influence of biological seed treatment on crop performance during periods of osmotic stress

Andrea Marino*[1], Molly Cadle-Davidson[1], Bob Patrick[1], Brenden Otero[1], Wendy Amidon[1]
[1]Advanced Biological Marketing, Inc. Geneva, NY 14456 USA

While global usage of BCAs and biostimulants in maize continues to rise, the implications of these varied crop inputs are underappreciated. Among them is the potential for alteration of the maize phytobiome and how significantly that may influence crop performance. We have reported that application of a microbial or metabolite seed treatment correlates with differences in alpha diversity (16S, ITS) in the rhizosphere of Zea mays. Here we report on a parallel study from the same replicated trial, where gene expression in leaf tissue was analyzed by RNA-Seq. Following Illumina NGS, AgriGO's SEA tool was used to identify enriched GO terms. Later, we repeated the maize transcriptome study using similar treatments in a setting lacking the native soil microbiome. Instead, seedlings grown in sterile media were harvested within a week, with half exposed to pre-harvest osmotic stress. Analyses from the field trial revealed that genes involved in mitigating abiotic stress are upregulated in plants inoculated with the target biological seed treatments compared to controls. These findings, combined with phenotypic data and rhizosphere metagenomic a nalyses from the field, point to possible mechanisms for the resulting improved plant performance. The input could (1) directly influence the host transcriptome, or (2) act indirectly by recruiting and/or competing with native inhabitants to alter the phytobiome which subsequently triggers changes in host gene expression. Results highlight a need for further study of the consequences of an altered phytobiome on the maize transcriptome.

Preininger

Formulation of microbial bioeffectors - a materials perspective

Claudia Preininger
AIT Austrian Institute of Technology GmbH, Center for Health & Bioresources, Tulln, Austria

Microbial biofertilizers and biocontrol agents are promising alternatives to agrochemicals in sustainable agriculture; however the lack of effective formulations is a major limitation for their successful application in the field.
The scientific challenge is therefore to elucidate microbial responses to multiple factors including the properties of the used materials, the formulation process itself and the environmental conditions during processing and storage, and to estimate the driving factors that impact stability (viability, shelf life, metabolic activity), performance (germination, plant penetration) and function (release efficiency). Examples will be given for different types of bacteria and application (seed coatings, granules, capsules, foliar spray) highlighting the necessity of taking into account the interplay between materials and microbes to better understand the impact of materials and eventually optimize the formulation process.

Molt

BASF – a chemical company mastering the challenges of biologicals

Andrea Molt
BASF

115500 people are employed worldwide within the BASF group. BASF is investing more than any other chemical company into research - in 2017 BASF spent 23% of its EBIT for R&D.
Agricultural Solutions is one of five business segments of BASF. Agricultural Solutions provides innovative solutions in the areas of chemical and biological crop protection, seed treatment and water management as well as solutions for nutrient supply and plant stress.
27% of the company’s research investment was allocated to Agricultural Solutions in 2017. Through innovation Agricultural Solutions intends to expand its portfolio in and beyond crop protection, such as biological solutions. Currently, the portfolio of biologicals comprises various products including bio-pesticides as well as bio fertilizers. In addition to the acquired biologicals, Agricultural Solutions also has proprietary discovery pipelines for biologicals. In order to meet all the challenges when working with biologicals, BASF being a multidisciplinary company - is well positioned.

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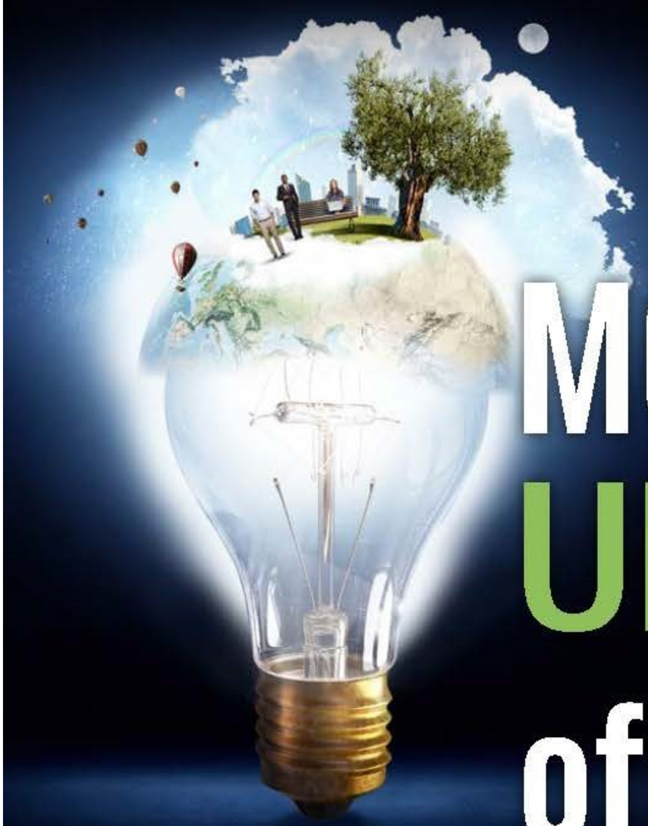

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Abhishek 101

Genetic differences in barley govern the receptiveness to priming agent

Abhishek Shrestha[1]*, Ahmed Elhady[1], Shimaa Adss[1], Gwendolin Wehner[2], Christoph Böttcher[3], Holger Heuer[1], Frank Ordon[2] and Adam Schikora[1]
[1]Julius Kühn-Institut, Federal Research Centre for Cultivated Plants (JKI), Institute for Epidemiology and Pathogen Diagnostics, Messeweg 11/12, 38104 Braunschweig, Germany
[2]Julius Kühn-Institut, Federal Research Centre for Cultivated Plants (JKI), Institute for Resistance Research and Stress Tolerance, Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany
[3]Julius Kühn-Institut, Federal Research Centre for Cultivated Plants (JKI), Institute for Ecological Chemistry, Plant Analysis and Stored Product Protection, Königin-Luise-Straße 19, 14195 Berlin, Germany

Priming crop plants for enhanced resistance using biocontrol agents is an efficient disease management strategy, since it results in robust resistance and higher yield. The beneficial effects of the bacterial quorum sensing (QS) molecules e.g. N-acyl homoserine lactones (AHL) on resistance and plant growth have been shown in different plant species. Here, we present the effects of the AHL, oxo-C14-HSL, on the priming capacity of barley. We demonstrated that barley primed with Ensifer meliloti, expresses enhanced resistance against Blumeria graminis. We also showed that the capacity to induce priming varies among different barley genotypes. Among a set of barley genotypes, we identified "primable" genotypes that had better ability to enhance resistance and "non-primable" genotypes that were non-responsive to oxo-C14-HSL and therefore, did not have any ability to enhance resistance. This suggests that appropriate genetic component is required for AHL-induced priming. We further showed that priming for enhanced resistance in barley involves stronger activation of the barley ortholog of the MPK6, regulation of defense-related PR1 and PR17b genes and remodeling of the cell wall structure. Noticeable was the stronger accumulation of lignin upon priming after a chitin challenge. Interestingly, the global metabolomic changes in barley during priming are rather subtle and specific. Identification of these metabolites is important as it opens doors to study the mechanisms and understand the relation between the plant genomic background and the priming agent. This understanding would further increase the efficacy of priming approaches and lead to novel breeding strategies.

Acedo 102

Microbiome assembly in vineyard soils: understanding biodiversity through functional and pathogenic patterns and co-occurrences

Ignacio Belda[1], Rüdiger Ortiz-Álvarez[1], Héctor Ortega[1], Luis J. López-Iglesias[1], Nuria Gómez[2], Alberto Acedo[1,2,3]*
[1]Biome Makers Spain (WineSeq division), 47011-Valladolid, Spain
[2]AC-Gen Reading Life, 47009-Valladolid, Spain
[3]Biome Makers Inc (WineSeq division), 95605-West Sacramento, USA.

Understanding the biodiversity of agroecosystems is a major aim in a context of sustainable farming. Given the key role soil microorganisms play in crop health and yield, describing microbiome patterns of functional and pathogenic groups in vineyards represent a critical step for a future knowledge-based viticulture. Thus, it is necessary to understand individual and community roles of microorganisms, their relationship with vine health, and the impact of human practices on them.

This work arises with the establishment of a robust database of vineyard soils microbiomes. A total of 786 soil samples from 15 countries (Argentina, Australia, Chile, Croatia, Cyprus, Denmark, France, Germany, Hungary, Italy, Portugal, South Africa, Spain, India, and USA) has been analyzed by Next-Generation DNA Sequencing (WineSeq-technology). For microbiome definition, a 16S/ITS amplicon sequencing approach (Illumina-MiSeq) was applied for bacterial and fungal communities description, respectively. The main aim of this work was to establish microbiome patterns in vineyards, defining ranges and boundaries in taxonomical biodiversity, microbial drivers of biodiversity (core microbiomes), and taxonomic/functional/pathogen co-occurrences networks.

Ranges of relative abundance for fungal and bacterial pathogens, related with the main vine and grape diseases, have been calculated, also defining geographical-epidemiological patterns. Apart from that, an estimation of the presence and abundance of nutrition-related metabolic pathways (microbial-derived genes related with nutrients (C, N, P, K, S, Fe, etc) metabolism) was analyzed by genome matching through the Tax4Fun routine for the estimation of KEGG-based function predictions. Finally, boundaries of resistance/vulnerability levels of vineyard soil microbiomes have been calculated by a metacommunity definition.

Ali 103

Microbiome as a potential actuator of medicinally important cannabidiol in Cannabis sativa

Irum Iqrar, Zabta Khan Shinwari and Gul Shad Ali*
Mid-Florida Research and Education Center and Department of Plant Pathology, University of Florida/Institute of Food and Agricultural Sciences, 2725 Binion Rd, Apopka, FL 32703
Department of Biotechnology, Quaid-i-Azam University Islamabad, Pakistan

Plant microbiome plays an important role in plant health and plant-environment interactions. Several previous studies suggest that microbes play an important role in the modulation of medicinally important secondary metabolites in plants. In this study, endophytic bacteria were isolated from Cannabis sativa, and based on initial plant growth promoting and antimicrobial screening, several bacterial species, which were identified using 16S rRNA gene sequencing, were selected for further analyses. These bacteria displayed strong anti-Phytophthora activity. Diffusable and volatile organic compounds as well as ethyl acetate extracts of these bacteria displayed high potency against P. parasitica. Bioactivity-driven fractionation assays using High performance liquid chromatography combined with mass spectroscopy revealed several that bioactive compound(s) have different physicochemical properties. Preliminary data on the potential of these microbes in inducing cannbidiols (CBD) and other medicinally important componds in hemp and other medicinal plants will be discussed.

Alonso 104

INRA Early Career Award Winner

Impact on plant microbiota and plant health of a recent shift in rice genetic diversity in a sustainable and century-old Chinese rice agrosystem

Pascal Alonso[1]*, Laurence Blondin[1], Frédéric Mahé[2], Denis Filloux[1], Elisabeth Fournier[1], Pierre Gladieux[1], Aurélie Ducasse[1], Jean-Benoit Morel[1], Pierre Mournet[3], Huichuan Huang[4], Jin Bai hui[4], Xiahong He[4], Sajid Ali[5], Romain Ferdinand[1], Emmanuel Fernandez[1], Christian Verniere[1] and Philippe Roumagnac[1]
[1]BGPI, CIRAD, INRA, Montpellier SupAgro, Univ Montpellier, Montpellier
[2]LSTM, CIRAD, Montpellier, France
[3]AGAP, CIRAD, Montpellier, France
[4]The National Center for Agricultural Biodiversity, Yunnan Agricultural University, Kunming 650201, China
[5]Khyber Pakhtunkhwa Agricultural University, Peshawar, Pakistan

Plant microbial communities may moderate the plant responses to different abiotic or biotic stresses like pathogens. On the other hand, plant genotypes may influence the composition and structure of the plant microbiota. In the Chinese Yuanyang terraces (YYT), a sustainable rice disease control has been achieved for centuries using mixtures of traditional genetically diverse rice varieties harboring a wide panel of resistance genes. However, this centuries-old agrosystem is currently challenged by the introduction of several “modern” rice varieties. The potential simplification of the rice varietal landscape is likely to drive a modification of the rice microbiota, which may have an impact on the plant-pathogen dynamics, and further on the frequency, extent and impact of disease emergence events. We here investigated the microbial communities (bacteria, fungi and viruses) associated with roots and aerial organs from eleven and eight YYT fields cultivated with traditional and “modern” rice varieties, respectively. Besides using a genotyping-by-sequencing approach (GBS) to decipher the rice genetic diversity, microbial communities were characterized by metagenomics approaches. The GBS approach confirms a shift of the rice genetic diversity and split the varieties into three lineages (traditional varieties, “modern” introduced varieties and one Japonica traditional variety). Metagenomics approaches show that microbial communities from aerial organs are lineage-dependent and that microbial communities from the roots are more homogeneous and not different among rice lineages. Interestingly, our study reveals a high prevalence (15%) of Southern rice black-streaked dwarf virus in Yuanyang terraces, and that this virus is significantly more prevalent in traditional local varieties.

Araújo 105

Transcriptome profiling of the endophyte Methylobacterium mesophilicum during Citrus sinensis roots interaction

Aline Aparecida Camargo-Neves, Manuella Nóbrega Dourado, Almir José Ferreira, Jennifer Salguero, Welington Luiz Araujo*

Methylobacterium genus has been found in association with a range of plant species. In this work we focused on evaluating the initial step of M. mesophilicum colonization in Citrus sinensis roots, since in previous work we verified that this association improves Citrus development. Here using CG-MS we demonstrated that metabolic compounds from citrus root exudates are modified in presence of M. mesophilicum. Using global gene expression analysis, we identify key genes from M. mesophilicum regulated during two different steps of the colonization: i. Plant recognition and ii. Plant colonization. The present study shows that genes related to energy production, stress and amino acid transport were down regulated in both step evaluated, and genes related to peptidoglycan biosynthesis, plant interaction and thioreodoxin and specially sugar transporter were up regulated. The up regulation of sugar transporter together with the presence of sugar compounds (fructose, arabinose and maltose) produced by the host plant exclusively in the presence of the bacteria, strongly indicates that these sugars are key compounds in first steps of M. mesophilicum SR1.6/6 – citrus interaction. These results contribute to understand the first step of citrus-M. mesophilicum interaction.

Babińska 106

Biodiveristy of plant pathogenic bacteria from the genera Dickeya and Pectobacterium in surface waters

Weronika Babinska*, Agata Motyka-Pomagruk, Sabina Zoledowska, Wojciech Sledz, Ewa Lojkowska

Bacteria from the genera Pectobacterium and Dickeya belong to family Pectobacteriacae are capable of causing blackleg on potato and soft rot on various plant species, including vegetables, crops and ornamentals. Economic damage they trigger is increasing worldwide. Lack of control methods to eradicate these bacteria once they have infected the plant, underlines importance of conducting the monitoring procedures. This research evaluates biodiversity of Dickeya and Pectobacterium spp. strains isolated from different depths of 9 Pomeranian lakes. Secondary goal was to check whether these reservoirs are important sources of disease-causing agents spread. During 14 months of study, water samples have been collected monthly from every 5 m depth within 10 lakes by a qualified scuba-diver. 15 strains of pectinolytic bacteria were isolated from 2 lakes. 9 isolates identified as Dickeya chrysanthemi, 1 as Dickeya spp., 3 as Pectobacterium atrosepticum and 2 isolates as Pectobacterium spp. where one of it was Pectobacterium carotovorum subsp. brasiliense. Notably, this is the first report on the occurrence of Pectobacterium carotovorum subsp. brasiliense in Polish waterways. Characterisation of Pectobacterium carotovorum subsp. brasiliense strain was based on phenotypic features such as pectinase, cellulose, protease activities, motility, siderophore and virulence on potato. It is worth to notice that, the Pectobacterium and Dickeya spp. isolates were solely isolated from 0 m nearby the shore. Therefore, usage of irrigation water originating from depths instead of the surface water, might contribute to limitation of the spread of the Pectobacteriaceae.

Barrio Duque 107

Bacterial helpers interact positively with the fungus Serendipita indica and enhance plant resistance against pathogens

Alejandro del Barrio Duque*, Livio Antonielli, Angela Sessitsch, Ole Nybroe, Stéphane Compant

Some bacterial endophytes are known to increase plant growth and enhance tolerance to biotic and abiotic stresses. Similarly, the root-colonizing fungus Serendipita indica (syn. Piriformospora indica) boosts plant vigor and confers resistance against plant pathogens. This fungus is further known as having a bacterial endosymbiont living inside its hyphae. We aimed to boost effects of the fungus and its bacterial symbiont on plants by combining the fungus and its symbiont with some new bacterial helpers. More than 600 endophytic bacteria from potato and tomato roots were isolated, identified and combined with the beneficial fungus Serendipita indica in order to study the type of interaction. Several bacteria completely inhibit the growth of the fungus. However, some endophytes can stimulate Serendipita growth under axenic conditions. Some of these bacteria can further help to reduce tomato disease caused by Fusarium oxysporum and Rhizoctonia solani while others do not. Genomes of selected isolates have been sequenced and annotated to understand more the genomic contents of the bacterial helpers. Certain gene clusters have been identified and hypothesized to be responsible for the stimulation of fungal growth, such as those involved in vitamin secretion, hormone synthesis, or biofilm formation. The future transcriptomics will unravel the mechanisms behind these interactions during the interplay as well as the ways of hyphae and plant colonization.

Beattie 108

Spatial and temporal mapping of soybean root microbiomes to leverage root traits and associated microbial consortia for plant breeding

Amy Welty-Bernard[1], Sarah Honken[1], and Gwyn Beattie[1]*
[1]Dept of Plant Pathology & Microbiology, Iowa State University, Ames, IA, USA

The plant-soil microbiome plays a pivotal role in plant fitness, fine-tuning the expression of host genes. This interaction effectively expands the plant functional genome and the host's capacity to respond to stress. Current crop breeding programs have yet to leverage optimal plant-microbiome phenotypes, as both core and functional microbiomes are still poorly understood. A previous study in our lab captured distinct community signatures for the microbiomes tied to water-use efficiency for drought-tolerant soybean lines subjected to extremes in water availability. We have initiated a follow-up study to evaluate these signatures in the context of the core microbiome recruited under non-stress conditions by a drought-tolerant and a drought-susceptible soybean line. These two cultivars represent extremes in root system architecture, a high-yielding elite genotype with high water-use efficiency characterized by deep roots, and a cultivar from Jilin, China characterized by shallow, lateral roots. To track the spatial and temporal patterns underlying recruitment and microbiome assembly, we intensified sampling across the root network and over time, sampling up to six discrete root regions from emergence to pod set. We are evaluating whether the microbiome varies among discrete root regions, the extent to which the microbiome changes with time in each region, and whether the changes reflect three physiological phases: germination and early root growth, initial nodulation during vegetative growth, and increased root growth and N demand upon onset of reproductive growth. These studies are aimed at generating insights into the interactions between root traits and root-associated communities, thus potentially highlighting key transitions belowground.

Bedini 109

Acclimatisation of arbuscular mycorrhizal inocula as a tool to overcome phosphate inhibition in practical condition

Bedini, A[1,2] Mercy, L[1] Schneider, C[1] Franken, P[2,3] Lucic-Mercy, E[1]
[1] INOQ GmbH, 29465 Schnega, Germany
[2] Humboldt Universität zu Berlin, 10099 Berlin, Germany
[3] Leibniz-Institut für Gemüse- und Zierpflanzenbau, Großbeeren, Germany

Arbuscular mycorrhizal (AM) fungi establish a symbiosis with the roots of the majority of land plants. For their capacity to support plant nutrition and increase stress tolerance, AM fungi have the potential to reduce the "chemical dependency" of modern agriculture. Despite the promising potential and the numerous successful applications of AM fungi in controlled environments, contrasting results are often reported under practical conditions. The well-known inhibition of the symbiosis by phosphate, occurring in fertilized crop soils, is indeed considered as the main factor limiting AM fungal use in agriculture.

AM fungi can be acclimatized to abiotic stress conditions by propagating them in presence of the stressor. The acclimatisation process is associated with increased root colonization and improved plant performance after inoculation with the acclimatised fungal strain. In the current project, we tested whether it was possible to acclimatise AM fungi to high phosphate concentrations. In vivo and in vitro acclimatisation were performed and acclimatized fungi were tested as inoculum in greenhouse and field conditions. Acclimatisation resulted in higher colonization plants rate in greenhouse and field conditions and improved plant growth in greenhouse.

First evidences suggest that acclimatisation during inoculum production can promote AM fungal development at high phosphate concentrations. This possibly represents a breakthrough in mycorrhizal technology, allowing the large-scale use of these microorganisms under conditions of conventional fertilisation practice. Moreover, the acclimatisation to high phosphate concentrations would permit the investigation of the effects of the symbiosis under a condition that has been so far never investigated.

Beirinckx 110

The endosphere is a key compartment for selecting bacteria that promote maize growth under cold temperature conditions.

Stien Beirinckx[1,2,3]*, Tom Viaene [1], Caroline De Tender[2,4], Jane Debode[2], Sofie Goormachtig[1,3]
[1]Center for Plant Systems Biology, VIB, Ghent, Belgium
[2]Plant Sciences Unit, Flanders Research Institute for Agriculture, Fisheries and Food (ILVO), Merelbeke, Belgium
[3]Department of Plant Biotechnology and Bioinformatics, Ghent University, 9052, Ghent, Belgium.
[4]Department of Applied Mathematics, Computer Science and Statistics, Ghent University, Ghent, Belgium.

Using 16S rRNA next generation sequencing, we undertook an approach in which hybrid maize seeds were grown in parallel in vitro and in pots with field soil in a controlled environment to determine the contribution of seed endophytes and soil microbiota to the microbial colonization of the maize root endosphere. Through in depth determining of the microbial traffic into the root endosphere of this maize hybrid line, we could recurrently show the maize endosphere microbiome and assess the contribution of the seed-inherited root microbiome to the endomicrobiome of maize roots.

A bacterial collection of 300 bacterial strains was generated from the maize endosphere. Families enriched within the endosphere were selected for screening for their growth promoting effects on juvenile maize under cold stress conditions. From the collection, more than 40 strains were screened of which 10 give growth promoting effects. To test whether growth promotion and microbiome communities are linked, the endosphere of maize is analysed again in two different temperature conditons, cold and control temperatures. The enrichment and depletion of endosphere families is analysed. We figured out that the enrichment in the cold is not necessary for its growth promoting effect under cold stress conditions.

Berard 111

Effects of maize inoculation with the PGPR A. Lipoferum CRT1 on rhizospheric microbial communities and their stability towards a heat-drought disturbance

Bérard A.[1]*, Ruy S. [1], Capowiez L. [1], Czarnes S. [2], Legendre L. [2], Florio A. [2], Le Roux X. [2], Doussan C. [1]
[1] INRA, Université d'Avignon UMR1114 EMMAH, Site Agroparc, 84914, Avignon, France.
[2] Laboratoire d'Ecologie Microbienne LEM, INRA UMR 1418, CNRS UMR 5557, Université Lyon1, Université de Lyon, F-69622, Villeurbanne Cedex, France.

Climatic Changes will include shifts in the frequency and intensity of droughts and heat waves. These extreme events directly affect plants but can also act indirectly through their impacts on soil microbial functions, particularly in the rhizospheric soil.

Rhizosphere has particular biophysical characteristics related to water, which depend on roots, production of exopolysaccharides (EPS) in connection with the development and physiology of plants, themselves influenced by microbial communities, including plant growth-promoting rhizobacteria (PGPR). The objective of this study was to evaluate the effects of maize inoculation with the PGPR A. lipoferum CRT1 on rhizospheric microbial communities and their stability with respect to heat-drought. The biomass and catabolic profiles (CLPPs) of microbial communities, and their respiration stability to a heat-drought disturbance were measured in the rhizosphere of inoculated and non-inoculated maize plants twice per year over three consecutive years. Rhizospheric EPS and soil water retention capacity were also measured.

The effect of inoculation led to an increase in catabolism of soil nitrogen likely through a "priming effect". The water holding capacity of the top-soil from inoculated maize plots increased during experiment as well as rhizospheric EPS content. Stability of microbial communities facing heat-drought increased in response to inoculation. The positive effect of the inoculation on the microbial parameters decreased with the maize crop ageing in parallel with the decrease of A. lipoferum CRT1 survival at the root surface. It is hypothesized that A. lipoferum CRT1 inoculation induced a favourable environment for the development of rhizospheric biofilms protective from water disturbances.

Blondin 112

Characterization of the rice microbiota: development and contribution of the 'culturomics' approach

Laurence Blondin*, Pascal Alonso, Isabelle Pierreti, Sylvain Godreuil, Philippe Roumagnac, and Christian Verniere

Plant microbiota that colonize different compartments of the host plant plays a key-role in nutrient availability, growth promotion and plant health. Understanding and managing plant microbiota could allow promoting beneficial microbial communities and reducing the impacts of detrimental microbes. While metabarcoding analyses targeting different regions of the 16S rRNA have recently gained popularity to describe large microbial communities of different ecosystems, these culture-independent surveys may have presented a depth bias and fail in detecting microbial populations with low concentrations. The diversification of culture conditions together with a high throughput identification by mass spectrometry system (MALDI-TOF), i.e. a culturomics approach, can greatly increase and complement the number of detected species. Using rice as a plant model we aimed at describing the spatio-temporal dynamics of rice endophyte microbiota along the 2017 rice life-cycle (5 sampling points from May to October) of two fields production of the Rhône delta region of France. Our objectives were to (i) establish a collection of rice-associated cultivable bacteria, (ii) develop a MALDI-TOF database for routine identification of bacterial isolates and (iii) compare Sanger sequencing of the 16S rRNA gene and the culturomics approach in terms of identification and characterization of microbial community diversity. We isolated more than 2000 bacterial colonies from superficially disinfected tissues. The score identification of both approaches will be compared to evaluate the power of identification of the MALDI-TOF database. We will further compare the community diversity estimated from results obtained using both 16S rRNA metabarcoding and culturomics approaches.

Boivin 113

The competitiveness to form nodules shape the ability of Rhizobium communities to promote efficient symbiosis with compatible legumes.

Stéphane Boivin*; Nassima Ait Lahmidi; Doriane Dijon; Karine Heulin-Gotty; Antoine Le-Queré ; Marjorie Pervent; Mathilde Tancelin ; Marc Tauzin ; Frédéric Mahé ; Stefano Colella; Brigitte Brunel; John Peter Young; Marc Lepetit

Legumes form root nodules resulting from interaction with Rhizobia. The major emerging property of this symbiosis is the ability to escape mineral nitrogen limitation by fixing gaseous nitrogen. However, in soil these bacteria form communities of members able to associate alone with their host but displaying wide range of competitiveness to form nodule (CFN) with a specific host in mixture. Because CFN of a Rhizobium and its capacity to fix nitrogen are genetically independent, CFN may limit the effectiveness of symbiotic services. Little is known about genetic determinants of CFN. In this work, we present a strategy to identify genes controlling this trait in Rhizobium leguminosarum sv. viciae (Rlv) associated with cultivated viciae legumes (pea, fababean). A worldwide collection of 240 Rlv isolates has been obtained by aggregating bacteria described in Genbank to new isolates obtained by pea and fababean root nodule trapping. Genomes were sequenced. Rlv is formed by 13 species but evidence that variability of CFN is mainly related to symbiotic plasmid has been obtained. By characterizing symbiotic traits of these bacteria, we identified phylogenetic clades of Rlv displaying contrasted levels of CFN upon pea and fababean opening the way of comparative genomic approaches. A symbiotic barcode was designed to discriminate and quantify intraspecific variability of Rlv and estimate CFN in symbiotic pea, fababean or lentil associations with multiple Rlv partners. Large mixtures of Rlv are co-inoculated to diverse plant hosts to identify bacterial and plant genetic determinants potentially associated to CFN. Recent finding will be discussed.

Dangles 114

Sowing the seeds for interdisciplinary research on phytobiomes in the tropical Andes

Olivier Dangles[1,2]*, Silvia Restrepo[3] and Rommel Montúfar[4]
[1]Centre d'Ecologie Fonctionnelle et Evolutive, UMR 5175, CNRS, Université de Montpellier, Université Paul Valéry Montpellier, EPHE, IRD, Montpellier, France
[2]Cornell University, Department of Ecology and Evolutionary Biology, Ithaca, NY, USA
[3]Universidad Los Andes, Departamento de Ciencias Biológicas, Bogotá, Colombia
[4]Pontificia Universidad Católica del Ecuador, Facultad de Ciencias Exactas y Naturales, Quito, Ecuador

The tropical Andes harbour an outstanding diversity and endemism of wild and domesticated plant species and ecosystems. While plant diversity in the region is relatively well studied, the diversity of their phytobiomes (bacteria, viruses, fungi and invertebrates interacting with plants and their environment) in both natural and cropped systems is mostly unknown. Nevertheless, phytobiome diversity and function are essential to provide food security and ecosystem services to local populations. In this poster, we advocate the need for and present the creation of an operational international joint laboratory (BIO_INCA), specialized in integrative studies, from genomes to ecosystem services, of phytobiomes in natural and cultivated ecosystems in Colombia and Ecuador. This interdisciplinary platform merges ecological, agronomical, social, and economical expertises and promotes the development of new technologies in bioinformatics, robotics, image analysis and modelling. A key aspiration of the platform is to capitalize on plant community interactions and functions to provide novel ways to increase and ensure resource-efficient use and conservation of cultivated and natural ecosystems.

Daval 115

The soil microbiota diversity influences clubroot disease by modulation of Brassica napus and Plasmodiophora brassicae transcriptomes

Daval S.*, Gazengel K., Belcour A., Linglin J., Guillerm-Erckelboudt A.Y., Lebreton L., Mougel C.
IGEPP, INRA, Agrocampus Ouest, Université de Rennes 1, Le Rheu, France.

The contribution of surrounding plant microbiota to disease development has led to the postulation of the “pathobiome” concept, which represents the interaction between the pathogen, the host-plant, and the associated biotic microbial community, resulting or not in plant disease. The structure, composition and assembly of different plant-associated microbial communities (soil, rhizosphere, leaf, root) are more and more described, both in healthy and infected plants. A major goal is now to shift from descriptive to functional studies of the interaction, in order to gain a mechanistic understanding of how microbes act on plant growth and defense, and/or on pathogen development and pathogenicity.

The aim herein is to understand how the soil microbial environment may influence the functions of a pathogen and its pathogenesis, as well as the molecular response of the plant to the infection, with a dual-RNAseq transcriptomics approach. We address this question using Brassica napus (Bn) and Plasmodiophora brassicae (Pb), the pathogen responsible for clubroot. A time-course experiment was conducted to study interactions between Pb, two Bn genotypes, and three soils harboring High, Medium or Low microbiota diversities. These soils, characterized with bacterial 16S and fungal 18S markers, displayed different levels of richness and diversity, particularly between High and Low soils. The soil microbial diversity levels had an impact on disease development (symptom levels and pathogen quantity). Finally, the Pb and Bn transcriptional patterns were modulated by these microbial diversities, leading to the identification of pathogen and plant-host functions potentially involved in the change of plant disease level.

Effa Effa 116

Research of genetic determinants and physiological mechanisms involved in rice drought tolerance under endomycorrhizal symbiosis

Effa Effa B[3,6], Moukouanga Daniel[3], Mbodj D[1,2], Kane A[2,4,5], Laplaze L[2,3,5], Gantet P[3], Manneh B[1,2], Diedhiou AG[2,4,5], R. Arocad and Grondin A[3]
[1]Africa Rice Center (AfricaRice), Saint-Louis, Sénégal;
[2]Laboratoire Mixte International Adaptation des Plantes et microorganismes associés aux Stress Environnementaux, Centre de Recherche de Bel Air, Dakar, Sénégal;
[3]Institut de Recherche pour le Développement, Université de Montpellier, Montpellier, France; [4]Université Cheikh Anta Diop (UCAD), Faculté des Sciences et Techniques, Département de Biologie Végétale, Dakar-Fann, Sénégal;
[5]Laboratoire Commun de Microbiologie IRD/ISRA/UCAD, Centre de Recherche de Bel Air, Dakar, Sénégal; dEstacion Experimental del Zaidin, CSIC, Granada, Spain ;
[6]Institut de Recherches Agronomiques et Forestières (IRAF), Libreville, Gabon.

Future climate models are suggesting a significant decrease of rainfalls in West Africa towards 2100. Therefore, it is necessary to improve the resilience of rice varieties that are grown in this area. Establishment of arbuscular mycorrhizal (AM) symbiosis in rice roots can lead to better growth under drought stress (Ruíz-Sánchez et al, 2011) but the mechanisms involved are not well understood and the beneficial effects of such interactions are strongly rice variety-dependent (Miransari, 2014; Diedhiou et al, 2016). We propose to uncover the genetic determinants and the physiological mechanisms involved in drought-resistance improvement by AM infection in a panel of 165 African rice (Oryza glaberrima) varieties. For that, the panel will be phenotyped for shoot growth and water use efficiency after infection by Rhizophagus irregularis and induction of a drought stress. A GWAS will be conducted to identify QTLs associated with beneficial drought-associated traits upon root AM infection. A subpanel of rice varieties showing contrasting responses (beneficial, neutral or detrimental AM interaction for drought-resistance) will be selected for detailed physiological characterization including root water fluxes, root system architecture (RSA), and shoot gas exchange. In this poster, we present preliminary work on defining growth conditions favoring rice growth and root infection suitable for large scale phenotyping of AM symbiotic effects.

Finkel 117

Pi status-dependent modulation of the plant microbiome

Omri M. Finkel*, Isai Salas-Gonzalez, Gabriel Castrillo, Theresa F. Law, Jeff Dangl

Soil Pi concentration can dictate the nature of plant-microbe interactions. PHR, a master transcriptional regulator of phosphate starvation response (PSR) negatively regulates certain components of the plant's immune system, which can lead to enhanced pathogen susceptibility but also to the alteration of the plant's microbiome. Arabidopsis microbiomes are altered in phr1 mutants, as well as in mutants in the PHF1 gene, which is required for Pi transport, suggesting that PSR-induced physiological changes to plant immunity and exudation can alter the microbiome. One problem with studying the PSR-microbiome interaction is that microbiomes are exposed to the same abiotic stresses endured by their plant hosts. This confounds our ability to infer whether observed shifts are due to the abiotic component – the difference in Pi content – or due to the biotic component – PSR-induced changes in the plant immune system or exudation profile. We aimed to tease these two components apart, by comparing PSR mutants to wild type Arabidopsis along a Pi fertilization gradient, which allowed us to examine whether the effect of PSR on the microbiome is Pi-status dependent.

In order to study how these PSR-dependent plant-microbe interactions influence the plant, we inoculated gnotobiotic Arabidopsis with a synthetic community (SynCom) composed of 185 genome-sequenced isolates. This model system allows measurement of abiotic interactions by manipulating the chemical composition of growth media and of biotic interactions by editing the SynCom. We measured the response of this community to a wide Pi gradient, identifying strains that are recruited by the plant under Pi stress.

Fort

INRA Early Career Award Winner

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Vertical transmission of microbiota is influenced by maternal and environmental effects in sessile oak (Quercus petraea)

Tania Fort[1]*, Charlie Pauvert[1], Thomas Caignard[1], Sylvain Delzon[1], Matthieu Barret[2], Stéphane Compant[3], Amy E. Zanne[4]* & Corinne Vacher[1]
[1]BIOGECO, INRA, Univ. Bordeaux, 33615 Pessac, France
[2]IRHS, Agrocampus-Ouest, INRA, Université d'Angers, SFR4207 QuaSaV, 49071 Beaucouzé, France.
[3]AIT Austrian Institute of Technology GmbH, Center for Health and Bioresources, Bioresources Unit, Tulln, Austria
[4]George Washington University, Biological Sciences Department, 2023 G Street NW, Washington DC 20052, USA;
*co-last authors

Plant-associated microorganisms can be transmitted from one generation to the next through seeds. These vertically-transmitted microorganisms can have beneficial, neutral or detrimental effects on plant fitness. Conversely, the dynamics and evolution of seed-borne microorganisms depend on seed dispersal and survival and on seedling growth. These ecological and evolutionary relationships between the host plant and seed-associated microbiota have been overlooked so far. To better understand the processes shaping seed microbiota, we analyzed the microbial turnover in seeds of a forest tree species (Quercus petraea), using a hierarchical sampling design including three spatial scales (seed microhabitat, maternal tree and forest site). We focused on the fungal component of the microbial community as Q. petraea often hosts seed-borne fungal pathogens (Ciboria sp.). We combined a metabarcoding a pproach with quantitative PCR to characterize the richness, composition and abundance of the fungal community and further visualized fungi within the seed by advanced microscopy techniques. Our results revealed significant effects of the maternal tree and forest site on the fungal community of the acorns that are in the canopy. Interestingly, the maternal effects disappear when acorns fall on the ground as seed-borne fungal taxa are largely replaced by soil-borne taxa. Future analyses using Hierarchical Modeling of Species Communities (HMSC) will enable us to highlight the associations between seed-borne pathogens and other microorganisms. The currents results will be discussed in light of local adaptation processes.

Foster

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The effects of cultivar, production system, and nursery on the composition of the rhizosphere microbiome of cultivated rhododendrons in Oregon

Zachary S. L. Foster[1, 2]*, Jerry E. Weiland[2], Carolyn F. Scagel[2], Nilkaus J. Grunwald[2]
[1]Oregon State University, Department of Botany and Plant Pathology, Corvallis, Oregon, United States.
[2]United States Department of Agriculture, Agricultural Research Service, Horticultural Crops Research Laboratory, Corvallis, Oregon, United States.

The composition of plant microbiomes influences processes important to agriculture such as nutrient absorption and defense against pathogens. Plant genotype and environment affect the microbiome, so understanding their relative importance and interactions could be helpful in optimizing crop productivity. We evaluated the effect of host genotype, nursery, and production system (potted versus in-ground planting) on the composition of the fungal and oomycete rhizosphere microbiome of rhododendrons in Oregon nurseries. Rhizosphere and roots were sampled from randomly selected, potted and in-ground plants of 3 host cultivars at 4 nurseries. ITS1 amplicons were sequenced using the Illumina MiSeq. Sequences were clustered and assigned to taxa using vsearch. Organism trophic mode was inferred using the FUNGuild database. Diversity statistics, ordination plots, and heat trees were calculated in R with vegan and metacoder. There was little difference in alpha diversity between potted and in-ground plants, but nurseries that grew plants with both production systems had higher diversity overall. Cultivar did not account for observed differences in community composition; however, nursery and production system had a significant effect. Ordination suggests that production system had the dominant effect on microbiome composition, followed by a moderate effect from nursery, and no effect from cultivar. Most fungal species were predicted to be saprotrophs (50%), followed by pathogens (12%) and symbionts (6%).

Froussart 120

The use of Plant Growth Promoting Rhizobacteria (PGPR) to alleviate drought stress in wheat (Triticum aestivum)

Emilie Froussart, Kelly Hamonts, Jeroen Raes, Tom Viaene, Steven Vandenabeele, Sofie Goormachtig

Wheat is one of the most important agricultural crops globally. Today, it is grown on more land area than any other commercial crop and continues to be the most important food grain source for humans. Wheat yield increases have stagnated over the last decade and technological innovations such as GMO and hybrid line production has proven to be cumbersome.
One other opportunities is to use Plant Growth Promoting Rhizobacteria (PGPR) which promote plant growth and help the plant to overcome different biotic and abiotic stresses. Deep sequencing analysis revealed several bacteria that correlate with growth of wheat plants in drought conditions and that might help the plant to alleviate drought stress. We apply those bacteria and analyze whether the inoculated plants are more protected against drought than the uninoculated ones by phenotypic analysis. In addition, we perform a molecular characterization of the plant-microbe interaction in order to understand the mechanisms behind the growth promotion. As a result, we will identify bacterial strains that can be used to promote wheat development with a decrease of water availability.

Germida 121

Microbiome associated with the rhizosphere and root interior of field crops in Saskatchewan, Canada

J. Cordero[1], J.R. de Freitas[2] & J.J. Germida[3]*
[1]Department of Soil Science
[2]University of Saskatchewan,
[3]Saskatoon, SK, S7N 5A8, Canada.

Root associated bacteria are an important component of the plant-microbiome and influence growth and productivity of crops. Thus it is important to investigate their diversity and function in different plant species and how edaphic factors influence this relationship. This study assessed bacterial communities associated with the rhizosphere and root interior of canola (Brassica napus), wheat (Triticum aestivum), lentil (Lens culinaris) and field pea (Pisum sativum) grown at four agricultural fields in Saskatchewan. High throughput sequencing and DGGE analyses of 16S rRNA amplicons from bacterial communities suggested a selection of the root endophytic microbiome from the rhizosphere. Proteobacteria, Actinobacteria and Bacteroidetes were the dominant phyla in the root interior, whereas Gemmatimonadetes and Firmicutes were only present in rhizosphere soil. Pseudomonas and Stenotrophomonas were predominant genera in the rhizosphere and root interior of all crops, suggesting a generalist distribution of these bacteria. However, genera, such as Xanthomonas, Arthrobacter, Streptomyces, Acinetobacter, Variovorax and Rhizobium were dominant in the root interior of specific crops. Relative abundance of specific bacterial groups in the rhizosphere, as well as bacterial PLFA in the bulk soil, were significantly correlated with soil pH, silt and organic matter contents. There was, however, no correlation between soil properties and the most abundant endophytic bacterial genera, thus suggesting that soil characteristics may not influence bacterial communities within the plant roots.

Ghneim-Herrera 122

Demetorhizobium oryzae sp. nov., a novel species of endophytic bacteria isolated from Oryza glumaepatula endosphere, able to enhance growth and yield in cultivated rice (Oryza sativa L.).

Eliana Torres-Bedoya, Katherine Rivera, Luz Andrea Gómez, Thaura Ghneim-Herrera*.

A novel strain SOG26, able to fix atmospheric nitrogen, was isolated from the surface-sterilised seeds of Oryza sativa L. and Oryza glumaepatula Steud. (Poaceae). Phylogenetic analysis of 16S rRNA gene and multilocus sequence analysis based on partial sequences of atpD, gyrB, rpoB, revealed that strain SOG26 was closely related to Neorhizobium galegae HAMBI 540. However, the results from GenBank based-genome blast, average nucleotide identity, in silico DNA-DNA hybridisation and fatty acid analysis demonstrated that strain SOG26 represents a novel bacterial genus, for which we propose the name Demetorhizobium GEN. NOV. oryzae sp. nov. Confocal microscopy observation revealed that strain SOG26 efficiently colonises the roots of O. sativa, O. glumaepatula, Arabidopsis thaliana and several legumes species. SOG26 was able to promote the production of vegetative biomass and accelerated flowering in several rice genotypes but only enhanced grain yield in its native hosts. SOG26 growth- and yield promoting differential effects did not correlate with its colonisation density. Our findings represent the report of a new bacterial genus closely related to Neorhizobium, isolated from grasses and demonstrate that some beneficial effects of endophytic bacteria are dependent on plant genotype.

Grunwald 123

Metacoder and taxa: R packages for visualization and manipulation of community taxonomic diversity data

Zachary S. L. Foster[1, 2], Thomas J. Sharpton[3], Scott Chamberlain[4], Nilkaus J. Grunwald[2]*
[1]Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon, United States.
[2]Horticultural Crops Research Laboratory, United States Department of Agriculture, Agricultural Research Service, Corvallis, Oregon, United States of America.
[3]Department of Microbiology, Oregon State University, Corvallis, Oregon, United States of America; Department of Statistics, Oregon State University, Corvallis, Oregon, United States of America; Center for Genome Research and Biocomputing, Oregon State University, Corvallis, Oregon, United States of America
[4]rOpenSci, University of California, Berkeley, Berkeley, CA, USA

Metabarcoding is revolutionizing microbial ecology by circumventing the limits of traditional culture-based techniques, but the massive hierarchical (e.g. taxonomic) datasets produced are difficult to plot and manipulate using current tools. Hierarchical data are more challenging to subset and otherwise manipulate than typical tabular data. We have developed the “taxa” package to provide a standard for the storage and manipulation of any data associated with a taxonomy, modelled after the popular dplyr data-manipulation philosophy. In addition, we have developed “metacoder” for parsing, analyzing, and visualizing hierarchical data associated with metabarcoding research. The reliance on color to depict taxa in stacked bar charts and pie graphs limits the number of taxa displayed to the number of discernible colors. Metacoder implements a novel visualization called heat trees that use the color and size of nodes and edges on a taxonomic tree to quantitatively depict up to 4 statistics distributed over a hierarchy. This allows for rapid exploration of data and information-dense, publication-ready graphics. In addition, metacoder provides tools for reading common file formats and evaluating primers and barcode loci using simulated PCR. The metacoder and taxa packages are already being adopted by the community and have been applied to diverse projects including research on gut microbiota, soil microbiota, wastewater communities, and mycorrhizal associations.

Holden 124

Relating tillage management systems of barley to rhizosphere composition and fungal disease

Nicola Holden*, Jacqueline Marshall, Tracy Valentine, Adrian Newton
James Hutton Institute, DUNDEE, DD2 5DA, UK

Soil microbial communities are known to be diverse across different soil types and in different environmental contexts and can be classified according to their functional potential. Plants play a key role in selecting or enriching communities within the rhizosphere and endosphere, recruiting members from the surrounding soil microbiome. However, soil communities are also known to be prone to anthropogenic disturbance. Therefore, a key question is what is the impact that different agricultural practices have on soil microbial communities that in turn affect the rhizosphere communities and associated functional roles in plant health. We generated the hypothesis that arable plants grown under regimes that inflict the least amount of soil disturbance or perturbations are more diverse, which is reflected in the diversity of the rhizosphere microbiome and a positive impact associated plant health. To test this, we designed a field trial (Spring -Summer 2018) to characterise the barley rhizosphere bacterial and fungal taxonomic compositions from plants grown under a minimum tillage / sustainable regime compared to conventional management. In parallel, fungal disease assessments were made to allow a correlation analysis. Spring barley was selected as a common arable crop in Scotland, and a single field site was split into parallel plots of different tillage strategies. Disease assessment indicate that increased tillage has a negative impact on symptomatic fungal disease. The results of the taxonomic community analysis are expected Winter 2018.

Imperial 125

Widespread Occurrence of Non-Symbiotic Rhizobia in Agricultural Soils

Amalia Soenens[1], Beatriz Jorrín[1,2], and Juan Imperial[1,3]*
[1] Centro de Biotecnología y Genómica de Plantas (CBGP), Universidad Politécnica de Madrid – Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Spain
[2] Department of Plant Sciences, University of Oxford, United Kingdom
[3] Instituto de Ciencias Agrarias, Consejo Superior de Investigaciones Científicas, Spain

Alpha-Proteobacteria able to establish highly specific, nitrogen-fixing, root-nodule symbioses with legumes are collectively known as rhizobia. This symbiosis plays a key role in the biological N cycle and is at the basis of many of the ongoing approaches to improve agricultural sustainability. Rhizobia exist in soils in modest numbers that can, however, increase significantly upon cultivation of host legumes. Mounting evidence from chance isolations and, more recently, from plant microbiome data, suggest that a number of rhizobia lacking the ability to establish symbiosis exist as members of the microbiota of many different plants, where they could play a role in plant nutrition or health. Through a combination of semi-selective culture media and genus-specific gene markers we have been able to isolate and characterize a wide variety of non-symbiotic rhizobia from unrelated agricultural soils that represent a hitherto unexplored source of rhizobial diversity, including representatives of new genomic species from the genera Rhizobium, Ensifer, and Neorhizobium. The significance of these non-symbiotic rhizobia for the biology of rhizobia in particular, and for plant microbiomes in general, will be discussed.

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Jung 126

The stereoisomers of a bacterial volatile 2,3-butanediol differently elicit systemic defense responses of pepper against multiple viruses in the field

Jihye Jung, Hyun Gi Kong, Teak Soo Shin, Tae Hoon Kim, and Choong-Min Ryu*

The effects of a volatile compound 2,3-butanediol, which is produced by certain strains of root-associated bacteria, consists of three stereoisomers, on resistance induction against plant pathogenic fungi and bacteria have been investigated. However, little is known about its effects on induced resistance against plant virus. To investigate the effects of 2,3-butanediol on plant virus, we evaluated their disease control capacity in pepper plants. Specifically, at the first year, we investigated the optimal concentration of 2,3-butanediol to use for disease control against Cucumber mosaic virus (CMV) and Tobacco mosaic virus (TMV) in the greenhouse and examined the effects of drench application of these compounds in the field. 2,3-Butanediol including two enantiomers (2R,3R- and 2S,3S-) and one meso compound (2R,3S-). At the second year field trial, treatment with 2R,3R-butanediol and 2R,3S-butanediol significantly reduced the incidence of naturally occurring viruses compared with 2S,3S-butanediol and control treatments. In addition, 2R,3R-butanediol treatment induced the expression of plant defense marker genes in the salicylic acid, jasmonic acid, and ethylene signaling pathways to levels similar to those of the benzothiadiazole-treated positive control. Our study provides a new strategy to elicit induced resistance against diverse viral diseases in the 2,3-butanediol stereoisomer-dependent manner.

Kaminsky 127

Characterization of consistent early microbial colonizers of soils

Laura Kaminsky[1]*, Timothy Peoples[2], Terrence Bell[1]
[1] Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, USA
[2] Alcorn State University, USA

A fundamental issue in soil microbiome research is that our ability to sequence soil microorganisms has far outstripped our ability to describe their ecological niche. This is due to the resistance of most microorganisms to culturing. We have developed a soil mesocosm colonization approach to segregate microbes that are consistent early colonizers of sterile soils, thereby providing new ecological information about this subset without direct cultivation. Sterile recipient soil mesocosms were put in contact with unsterilized soil acting as a microbial source. Bacterial colonizers of the recipient soil were characterized at two and eight weeks. We describe the taxonomic and functional overlap of microbial colonizers from source soil microbiomes with different abiotic soils conditions (pH, nutrient profile) and land use histories (agricultural or forested). We also describe how recipient soil nutrient conditions and salinity shape the successful colonizer pool, indicating potential abiotic optima of different bacterial colonizers. This information is of practical use in understanding soil functional development following agricultural practices disrupting soil microbiomes (e.g. soil fumigation, anaerobic soil disinfestation).

Kankanala 128

Field microbiome studies identified shifts in the microbial populations during phymatotrichopsis root rot disease occurrence in alfalfa

Prasanna Kankanala*, Chakradhar Mattupalli, Raj Nandety, Venkatachalam Lakshmanan, Kelly D. Craven, Carolyn A. Young, Kirankumar S. Mysore

Phymatotrichopsis root rot (PRR), commonly known as cotton root rot, is a persistent disease that limits cotton and alfalfa production in Southwestern US. This disease is caused by the soil-borne ascomycete, Phymatotrichopsis omnivora and there are no effective genetic or chemical controls aganst this diseae in alfalfa. Enrichment of plant rhizosphere and endosphere microbiomes from bulk soil plays a critical role in diease management. To enhance our understanding of the spatial and temporal variations in microbial populations occurring in PRR infested alfalfa fields, we collected bulk soil, rhizosphere soil, and endosphere samples from three disease sites at different time intervals during 2016. We analyzed the microbiome changes in diseased, asymptomatic and survivor plants by sequencing bacterial 16S and fungal ITS amplicons on Illumina Miseq platform followed by bioinformatics and statistical analyses using QIIME 2 and R. The results indicated discrete groupings of microbial populations in the bulk, rhizosphere and endosphere zones. There was upto 16% variation in the phylogenetic diversities of bacterial populations during August and September when the disease was most prevalent. Similarly, 10% variation was observed in asymptomatic, diseased and survivor plants. While we did not see observe significant shifts in the temporal fungal populations, upto 11% variation was observed in the asymptomatic, diseased and survivor plants. The details of these microbial shifts and their correlation to disease will be discussed.

Keradraon 129

Dynamics of microbial community networks associated with the debris-borne wheat pathogen Zymoseptoria tritici

Lydie Kerdraon*, Marie-Hélène Balesdent, Matthieu Barret, Valérie Laval, Frédéric Suffert

Zymoseptoria tritici is one of the most damaging pathogens of wheat, causing yield losses of up to 40%. Like many other cereal foliar pathogens, it remains on crop residues during the intercropping season, where it reproduces sexually, with ascospores infecting seedlings at the beginning of subsequent seasons. Despite the importance of residues as source of inoculum, few studies have examined the impact of the whole microbial community of this particular ecosystem on the saprophyte/sexual stage of such kind of pathogens. Our study aims to characterize the interactions between Z. tritici and the micro-organisms present on residues and assess the impact of some factors (contact with soil, seasonality). To this end, residues of wheat plants preliminary infected with Z. tritici in greenhouse were left outdoor under different conditions, either with or without contact with soil. Non-infected residues were left in the same conditions, as control. Residue sampling was performed in July (zero-point, before contact with ground), in October, December and February. This has been done two successive years. The analysis of the communities was carried out by metabarcoding approach with ITS and 16S primers. In total, 420 residues samples were analyzed, with 15 replicates per condition. The effect of inoculation with Z. tritici was significant for both fungal and bacterial communities. The main determinants of diversity were year for fungal communities, and soil contact for bacterial communities. Co-occurrence network analyses (in progress) should help to identify micro-organisms that interact with Z. tritici, and some of which could even limit ascospores production.

Kim 130

A keystone species in the rhizosphere microbiome of tomato resistant to bacterial wilt

Jihyun F. Kim[1]*, Min-Jung Kwak[1], Jidam Lee[1], Pyeong An Lee[2], Soon-Kyeong Kwon[1], Kihyuck Choi[2], Ju Yeon Song[1], and Seon-Woo Lee[2]
[1]Department of Systems Biology and Division of Life Sciences, Yonsei University, 50 Yonsei-ro, Seodaemun-gu, Seoul 03722, Republic of Korea
[2]Department of Applied Biology, Dong-A University, Busan 49315, Korea

Bacterial wilt is a severe plant disease caused by the soil-borne bacterium Ralstonia solanacearum. Although plant disease resistance is known to be mediated by its own immune system, plant-associated microorganisms may play an important role. We initiated a whole metagenomic analysis of the rhizosphere communities of two tomato cultivars, Hawaii 7996 and Moneymaker, that are either resistant or susceptible to bacterial wilt, respectively. Taxonomic analysis of the 16S rDNA reads, which have been extracted from the whole metagenome data, revealed that the proportion of Flavobacteriia is higher in the rhizosphere of Hawaii 7996 than in the rhizosphere of Moneymaker, whereas the proportion of Betaproteobacteria is higher in Moneymaker than in Hawaii 7996. Through phylogenetic binning, we were able to reconstruct the genome of a novel uncultured Flavobacteriaceae bacterium, designated TRM1, from the metagenomic sequences of Hawaii 7996. Based on the genome information, we successfully isolated the corresponding bacterium that contributes to the disease resistance. Our study illuminates that microbiome structures of the rhizospheres are distinct between the two cultivars and underscores the pivotal role that the native microbiome plays in protecting plants from infection.

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Kudjordjie 131

Impact of selected microbiome treatment on healthy and Fusarium infested Arabidopsis thaliana rhizobiomes

Enoch Narh Kudjordjie[1], Meysam Bakhshi[2], Rumakanta Sapkota[1], Mogens Nicolaisen[1]
[1]Aarhus University, Faculty of Science and Technology, Department of Agroecology Forsøgsvej 1, DK4200, Slagelse Denmark.
[2]Department of Plant Pathology, Tarbiat Modares University, Tehran, Iran.

Plants in their natural environment employ several mechanisms to survive harsh conditions imposed by both biotic and abiotic factors. Key among these survival strategies is their strict association with a plethora of microorganisms that confer beneficial traits to enable them counter stress. Rhizosphere engineering approaches targets the utilization of whole or sub microbial communities in order to cultivate a more diversified, resilient and thus an optimized functional rhizobiomes. In this work, our aim was to study the effect of bacterial microbes transferred from previous plant generations on healthy and Fusarium oxysporum f.sp. matthioli (FOM) infested Arabidopsis thaliana rhizosphere microbiomes. We grew three A. thaliana genotypes Col-0, Ler-0 and a glucosinolate double mutant B2B3 over four generations in three different setups comprised of microbiome treated-FOM infested, a non-treated-FOM infested and a non-FOM infested-treated control. Preliminary results shows that microbiome treatment significantly influenced bacterial communities with the highest effect on non-infested and treated control setup. Genotypic effect was strongest in FOM-infested setups while no significant genotype effect was found in the non-infested and treated control setup. A. thaliana glucosinolates mutant B2B3 has strongest effect on FOM infested setups.

Lebreton 132

Do soil biodiversity modulate Brassica napus x bioagressor interactions?

Lebreton L.[1]*, Bousset L.[1], Chaminade V.[2], Cortesero A.M.[2], Ermel M.[1], Fournet S.[1], Gazengel K.[1], Guillerm-Erckelboudt A.Y.[1], Linglin J.[1], Luquet M. [1], Manzanares-Dauleux M.[1], Montarry J.[1], Paty C.[2], Poinsot D.[2], Porte C.[1], Simon J.C.[1], Mougel .C[1]
[1]IGEPP, INRA, Agrocampus Ouest, Université de Rennes 1, Le Rheu, France
[2]IGEPP, INRA, Agrocampus Ouest, Université de Rennes 1, Rennes, France

One of the major challenges faced by 21st century agriculture is to achieve food security under changing climatic conditions while mitigating adverse environmental effects in a sustainable way. Plant associated microbiomes have a tremendous and so far untapped potential to improve plant resilience to abiotic and biotic stresses and, ultimately, crop yield. . Akin to the role played by the gut microbiota in human health, belowground biodiversity can be considered as a reservoir of ”plant probiotic” microorganims deployable to enhance and secure crop yields.

We investigate the consequence of different soil communities assemblage on Brassica napus interaction with different bioagressors. Soil microbial diversity was manipulated through a dilution to extinction experiment and evaluated using high-throughput sequencing. Brassica napus were cultivated in these soils and confronted to five different bioagressors: three belowground with the protist Plasmodiophora brassicae, the nematode Heterodera schachtii and the cabbage root fly Delia radicum and two aboveground with the fungi Leptosphaeria maculans and the cabbage aphid Brevicoryne brassicae. The effect of soil microbial communities on each bioagressor was evaluated by measuring different life history traits of each bioagressors which are a reliable estimate of bioagressor feeding success and/or fitness. The result obtained showed modulation on disease index or bioagressors fitness only for belowground bioagressors. These results were discussed in regard of plant immune system, community ecology and potential applications for sustainable agriculture.

Lee 133

Aboveground whitefly infestation influence bacterial community dynamics in the pepper

Soohyun Lee*, Hyun Gi Kong, Byung Kwon Kim, Geun Cheol Song, and Choong-Min Ryu

Plants respond to various types of herbivore and pathogen attack using well-developed defensive machinery designed for self-protection. Infestation from phloem-sucking insects such as whitefly and aphid on plant leaves was previously shown to influence both the saprophytic and pathogenic bacterial community in the plant rhizosphere. However, the modulation of the root microbial community by plants following insect infestation has been largely unexplored. Only limited studies of culture-dependent bacterial diversity caused by whitefly and aphid have been conducted. In this study, to obtain a complete picture of the belowground microbiome community, we performed high-speed and high-throughput next-generation sequencing (V1-V3 region). Our analysis revealed that whitefly infestation reshaped the overall microbiota structure compared to that of the control rhizosphere, even after 1 week of infestation. Examination of the relative abundance distributions of microbes demonstrated that whitefly infestation shifted the proteobacterial groups at week 2. Intriguingly, the population of Pseudomonadales of the class Gammaproteobacteria significantly increased after 2 weeks of whitefly infestation, and the fluorescent Pseudomonas spp. recruited to the rhizosphere were confirmed to exhibit insect-killing capacity. Additionally, three taxa, including Caulobacteraceae, Enterobacteriaceae, and Flavobacteriaceae, and three genera, including Achromobacter, Janthinobacterium, and Stenotrophomonas, were the most abundant bacterial groups in the whitefly infested plant rhizosphere. Our results indicate that whitefly infestation leads to the recruitment of specific groups of rhizosphere bacteria by the plant, which confer beneficial traits to the host plant. This study provides a new framework for investigating how aboveground insect feeding modulates the belowground microbiome.

Ma

134

Comparison of double-stranded RNA (dsRNA) and Virion-associated nucleic acids (VANA) targets for high-throughput sequencing analysis of phytoviral metagenomes

Yuxin Ma*, Armelle Marais, Marie Lefebvre, Sébastien Theil, Laurence Svanella-Dumas, Chantal Faure,Thierry Candresse

High-throughput sequencing (HTS) has opened a new era of unbiased discovery and genomic characterization of viruses in environmental samples. However, the study of phytoviromes is still very recent and a number of methodological questions are yet unexplored. One such aspect concerns the choice of the target nucleic acid population to be submitted to HTS. We have compared the use of highly purified double stranded RNAs (dsRNAs) and of purified virion-associated nucleic acids (VANA) to evaluate the genetic diversity of plant viruses in 6 different agro-ecosystems or natural ecosystems in France. The complex pools thus analyzed comprise a total of 1200 individual uncultivated plants representing 112 plant species (200 plants per ecosystem). Viral diversity was estimated by counting viral Operational taxonomic units (OTUs) defined by clustering conserved RNA-dependent RNA polymerase signatures at a 10% threshold. A total of 239 viral OTUs were thus identified. As in previous phytoviral metagenome studies, the proportion of OTUs corresponding to novel agents are significantly different between ssRNA (55%) and dsRNA (99%) viruses.

Following a normalization of all samples to the same sequencing depth, the viral diversity observed with the dsRNA targets was systematically broader than that revealed using the VANA targets. As expected, only the VANA approach allowed the significant detection of DNA viruses. These were however rather infrequent as compared to RNA viruses. The influence of factors possibly underlying these differences between the two target nucleic acids populations will be discussed, together with a comparison in species richness between agroecosystems and less anthropic environments.

Mason

INRA Early Career Award Winner

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The leaky gut syndrome: plant defenses interact with caterpillar enteric bacteria to exacerbate consequences to the larval host.

Charles Mason*, Kelli Hoover, Gary Felton

Insects possess a diverse microbiome that can mediate several interactions with plants. Caterpillars (Lepidoptera) possess bacteria that are partially influenced by the interaction with plant dietary substrates. In our study, we utilized the fall armyworm and two maize lines, Mp708 and Tx601, which are resistant and susceptible to fall armyworm, respectively. Our objectives were to evaluate: 1. how a gut-deteriorating protease influences the growth of germ-free and gnotobiotic fall armyworm; 2. if bacteria “leak” from the gut into the hemolymph and induce immune responses; and 3. if the isolates we utilized have direct pathogenicity. We produced germ-free fall armyworm, and introduced isolates of Enterococcus, Klebsiella, and Enterobacter. We conducted bioassays evaluating the aforementioned objectives using gamma-irradiated maize under sterile conditions. We observed a negative effect of bacteria on the growth of fall armyworm for both resistant and susceptible maize. However, Enterobacter had significantly greater impacts on larval growth and mortality compared to the other isolates. Enterobacter–inoculated larvae consuming Mp708 had bacteria present in the hemolymph and elevated immune responses. Enterobacter injected into fall armyworm hemolymph caused reduced growth, but did not cause mortality. Our results strongly suggest that plant defenses not only act directly upon the insect, but can also weaponize the attacker’s microbiome. These results have major implications in how we evaluate and interpret plant-insect-microbiome interactions.

Masson 136

Shift of microbial diversity in rice roots following Root Knot Nematode infection

Anne-Sophie Masson[1], Hai Ho Bich[2], Stéphane Bellafiore[1], Huế Nguyễn Thị[3], Lionel Moulin[1]
[1] Interactions Plant-Microbes-Environment (IPME), IRD, Cirad, University Montpellier, France
[2] IOIT/USTH, VAST and UMMISCO, IRD, 18 Hoang Quoc Viet, Hanoi, Vietnam
[3] IRD, LMI RICE, University of Science and Technology of Hanoi, Agricultural Genetics Institute, Hanoi, Viet Nam

Microbial communities present in soils are key determinants of plant health. Beneficial or pathogenic, they can also indirectly play a role in the pathogenicity of pests such as the Root-Knot Nematodes (RKN; Meloidogyne spp.). For instance, it was demonstrated that certain bacteria directly parasite nematodes or compromise their mobility while other promote root penetration making the plant more susceptible to nematode infection. In order to support sustainable agriculture, the chemical pesticides used to control RKN are being progressively banned in all countries. As a consequence, RKN has become an emerging and uncontrolled pathogen that could compromise plant production. In this context, the use of bacteria for bio control strategies is a promising approach.

The presence of RKN induces a modification of the root structure with the formation of root galls characterized by giant feeding cells with active metabolism due to the presence of nematode. In natural infested rice fields in Vietnam, root plants were extracted and infected vs. non-infected roots collected independently. Using a metabarcoding approach, we analyzed the core microbiome modification of rice roots due to nematode infection. OTUs highlighted by the metabarcoding analysis were compared in order to reveal the microbiome of the “Gallosphere”. The identified bacteria and their enrichment in healthy roots or in the Gallosphere are discussed in regards to their known function in parasitism.

Mechan Llontop 137

The rain microbiome: A source of the plant leaf microbiome?

Marco E. Mechan Llontop[1]*, Long Tian[1,2], and Boris A. Vinatzer[1]
[1] School of Plant and Environmental Sciences
[2] Program of Genetics, Bioinformatics and Computational Biology, Virginia Tech, Blacksburg-VA, 24061

Plants live in association with a large diversity of microbial communities known as the plant microbiome. Root-associated bacteria have been found to be recruited from the surrounding soil; however, the source of the leaf microbiome has not been determined with confidence. Here we test the hypothesis that rain is a contributor to the plant leaf microbiome. We used 16S rRNA sequencing to characterize bacterial communities associated with rainfall and, subsequently, used rain-isolated bacterial communities to inoculate lab-grown tomato plants. We then compared the microbiome composition of tomatoes inoculated with (1) bacteria isolated from rain, (2) filter-sterilized rain, and (3) sterile water. Two time points were taken: (1) as soon as plants were dry after inoculation and (2) seven days later. Our analysis revealed a high relative abundance of Proteobacteria on tomato seven days after treatment with rain whereas Actinobacteria and Firmicutes were reduced significantly. At the family level, Pseudomonadaceae, Enterobacteriaceae, Burkholderiaceae and Oxalobacteriaceae present in rain increased the most in relative abundance while Streptomycetaceae, Xanthomonadaceae and Sphingomonadaceae decreased in abundance. We further performed metagenomic sequencing of rain samples and tomatoes treated with rain on day zero and day seven to start identifying bacteria in rain that efficiently colonize tomato at the strain level. This study provides preliminary evidence that some bacterial taxa present in rain efficiently colonize plant leaves. The question of the relative importance of rain compared to soil as source of the leaf microbiome cannot be answered yet and will be discussed in the context of existing literature.

Millican 138

Increasing Agrostis stolonifera nitrogen fertilization reduces Clarireedia jacksonii symptom development and selects for a persistent disease suppressive microbial community

Michael D. Millican* and Paul L. Koch

Maintaining turfgrass requires repeated applications of fertilizers and pesticides that are beneficial for a turf stand but have broader ecological costs. Dollar spot, a foliar fungal disease caused by Clarireedia jacksonii, is the most economically important disease in golf course turf and is endemic in temperate climates. Dollar spot management relies heavily on fungicides with limited cultural practices available, leading to financial strain and non-target environmental impacts. Increasing nitrogen fertilization to 29.29 kg N/ha reduces dollar spot in line with fungicide treatment and disease suppression persisted 1 year after treatments ended unlike fungicide-treated turf. Understanding how this maintenance regime impacts the turf phytobiome and leads to disease suppression is critical to reducing fungicide reliance. Nitrogen was applied to creeping bentgrass at 0, 9.76, and 29.29 kg N/ha bimonthly and soil cores were removed every four weeks. Bacterial and fungal composition and diversity were assessed using the 16S rRNA and ITS-2 DNA regions, respectively. Increasing nitrogen input to 29.29 kg N/ha results in bacterial communities distinct from 0 and 9.76 kg N/ha treated turf. Fungal communities were largely unchanged, while members of Actinobacteria and Proteobacteria increased in abundance. Increasing nitrogen input selects for a persistent and distinct bacterial community, suppressing dollar spot development. These results deepen our knowledge of how management practices affect the turf phytobiome and help create sustainable management strategies moving forward.

Motyka-Pomagruk 139

Insight into the pangenome of phytopathogenic bacterium Dickeya solani

Agata Motyka-Pomagruk[1]*, Sabina Zoledowska[1], Agnieszka Misztak[1], Wojciech Sledz[1], Alessio Mengoni[2], Ewa Lojkowska[1]
[1]Department of Biotechnology, Intercollegiate Faculty of Biotechnology University of Gdansk and Medical University of Gdansk, Poland
[2]Department of Biology, University of Florence, Italy

Dickeya solani is a pectinolytic plant pathogenic bacterium classified to the Pectobacteriaceae family that appeared in Europe in 2005 and have been continuously spreading since then. As one of the causative agents of soft rot and blackleg, this microorganism affects numerous plant species. Therefore, significant economic losses follow, amounting even 25% of the total crop yield. Former studies revealed notable phenotypic diversity between D. solani isolates, in contrast to the extremely low genomic variability as analyzed by DNA sequence variation in the housekeeping genes or REP, BOX and ERIC genomic patterns. The aim of this research was to investigate the pangenome of D. solani (basing on 22 whole genome sequences) in order to elucidate genetic foundations of virulence-related strain variation. D. solani species exhibits vast core (3726 genes), rather minor accessory (113-271 genes) and small unique (0-286 genes) pangenome fractions. Then function-based classification of the genes to the Clusters of Orthologous Groups was carried out. Notably, the highest percentage of unique Clusters of Orthologous Groups (after these of general function and function unknown) was attributed to transcription-related ones. Thus, a hypothesis may be put forward that diverse virulence of D. solani isolates is a result of variation in the regulation of transcription. Also by addition of the newly sequenced and de novo assembled genomes, closure ($b \approx 0.026$) of the D. solani pangenome according to Bacterial Pangenome Analysis software was achieved.

Mülner 140

The Sclerotia-associated Microbiome: Insights in the Microbiota of Persistent Survival Structures

Pascal Mülner*, Philipp Wagner, Alessandro Bergna, Dženana Sarajlić, Barbara Gstöttenmayr, Kristin Dietel, Rita Grosch, Tomislav Cernava, and Gabriele Berg

The soil-borne pathogens Sclerotinia sclerotiorum and Rhizoctonia solani are causing extensive crop damage across the globe. Both fungi can produce sclerotia to persist severe environmental conditions and are thus highly resistant to conventional pathogen treatments. We explored sclerotia-associated, microbiota on potato tubers by cultivation-dependent and –independent methods to screen for novel biocontrol agents and obtain deeper insights into their microbiome. The sclerotiome of R. solani AG-8 was shown to be highly similar to the microbiome of surrounding soil, while microbial communities of the unaffected potato peel displayed significant differences. Distinctive bacterial lineages were associated with healthy and sclerotia-affected tuber surfaces. Flavobacteriaceae and Caulobacteraceae were primarily found in unaffected areas, while Phyllobacteriaceae and Bradyrhizobiaceae were associated with the presence of sclerotia. In addition to volatile compounds from different Bacillus species, bioactive substances emitted by isolates assigned to the genera Enterobacter, Pseudomonas, and Buttiauxella exhibited high antagonistic activity. Differential imaging showed that volatiles emitted by the antagonists altered the morphology of sclerotia and increased the layer of non-viable hyphae. Distinct combinations of antagonists increased the pathogen inhibition up to 59.7% in comparison to single isolates. The integrative sclerotiome assessment showed that fungal survival structures are associated with a specific microbiome, which is also a reservoir for new biocontrol agents.

Ndour 141

Microbial diversity and soil activity in rhizosphere of different pearl millet lines: relation with their root-adhering soil fraction

Ndour Papa Mamadou Sitor[1,2]*, Barry Cheikh Mbacké[1,2], Tine Diamé[1,2], Gueye Mariama[1], Barakat Mohamed[3], Ortet Philippe[3], Achouak Wafa[3], Ndoye Ibrahima[2], Laplaze Laurent[4], Heulin Thierry[3] and Cournac Laurent[1].
[1] IRD, UMR Eco&Sols, LMI IESOL, BP1386, Dakar CP18524, Sénégal
[2] UCAD, Département de Biologie Végétale, BP 5005, Dakar, Sénégal
[3] LEMIRE, UMR 7265 BIAM, AMU, CEA, CNRS, Saint-Paul-lez-Durance, France
[4] IRD, LMI LAPSE, Dakar, Sénégal

In West Africa, farmers used pearl millet diversity to cope with climate change impact on rainfall distribution and water scarcity. However, in this selection-based adaptation, the interactions between the plant roots and rhizo-microbial communities were not taken in account. Indeed, these interactions that involve carbon root exudation in the rhizosphere could impact soil aggregation, nutrients cycling and consequently water and nutrients availability. Thus plant breeding to promote soil aggregating communities, with potential long-term benefits on yield sustainability, could be possible if genetic variability exists for this trait.

Here, we used 16S and ITS sequencing to compare microbial diversity in the root-adhering soil fraction (RAS) of inbred pearl-millet lines with contrasted RAS:roots ratios, grown in field conditions. We further analyzed some extracellular enzymatic activities involved on the recycling of main nutrient in soil in the same samples. Bacterial beta-diversity of dominant communities showed only weak differences between pearl millet lines whereas rare taxa were differently distributed. Fungal alpha-diversity showed significant differences between lines. Indeed, negative correlation was noticed between fungal alpha-diversity and rhizosphere soil aggregation whereas beta-diversity was not significantly different. Interestingly, chitinase, acid phosphatase and FDA enzymatic activities showed significant differences between lines and were positively correlated with RAS:roots ratios of pearl millet lines.

This study demonstrated that genetically governed rhizosphere soil aggregation, soil nutrient dynamics and microbial diversity were related in pearl millet. However, it appears that other factors are involved in this aggregation process, and the relative importance of soil microbial communities or phyla remains unknown.

Pauvert 142

INRA Early Career Award Winner

ITS all fun guys: a comparison of bioinformatic pipelines for metabarcoding plant and soil fungal communities

Charlie Pauvert[1]*, Marc Buée[2], Valérie Laval[3], Véronique Edel-Hermann[4], Laure Fauchery[2], Angélique Gautier[3], Isabelle Lesur[1,5], Jessica Vallance[6], Corinne Vacher[1]
[1]BIOGECO, INRA, Univ. Bordeaux, 33615 Pessac, France
[2]INRA, Université de Lorraine, UMR IAM 1136, Laboratoire d’Excellence ARBRE, Centre INRA-Lorraine, 54280 Champenoux, France
[3]BIOGER, INRA, 78850 Thiverval Grignon, France
[4]Agroécologie, AgroSup Dijon, CNRS, INRA, Univ. Bourgogne Franche-Comté, 21000 Dijon, France
[5]HelixVenture, 33700 Mérignac, France
[6]SAVE, Bordeaux Sciences Agro, INRA, ISVV, Univ. Bordeaux, 33882 Villenave d’Ornon, France

Fungal communities associated with plants and soil influence plant fitness and ecosystem functioning. They are classically studied by metabarcoding approaches targeting the ribosomal internal transcribed spacer (ITS), but there is no consensus concerning the most appropriate bioinformatic pipeline for the analysis of these data. We sequenced an artificial fungal community composed of 189 strains covering a wide range of Ascomycota and Basidiomycota, to compare the performance of 288 software and parameter combinations. The most sensitive pipelines, based on the USEARCH and VSEARCH clustering algorithms, detected almost all fungal strains but greatly overestimated the total number of strains. By contrast, pipelines using DADA2 to detect amplicon sequence variants were the most effective for recovering the richness and composition of the fungal community. Our results suggest that analyzing single forward (R1) sequences with DADA2 and no filter other than the removal of low-quality and chimeric sequences is a good option for fungal community characterization.

Persyn 143

The use of root endophytic bacteria to boost lettuce growth at low temperature conditions

Antoine Persyn*, Sofie Goormachtig
Systems Biology of Yield, University of Ghent

In flanders, lettuce farmers create a yearly turnover of 37 million euro, making it the regions second most grown vegetable. Lettuce growth is optimal at temperatures ranging between 20°C and 25°C, making it possible for farmers to grow it up to a consumable size in six weeks during spring and summer. During the winter time on the other hand, this process takes up to four months. A promising discipline to promote plant growth under stress conditions is the use of plant growth promoting rhizobacteria (PGPR). Through 16S amplicon sequencing, we aim at comparing the rhizo and endomicrobiome of different lettuce cultivars grown at low temperature conditions compared to control conditions to detect the enriched rhizosphere and endophytic bacterial genera in the cold. In addition we will isolate these PGPR out of the lettuce root and evaluate them for their plant growth promoting potential by adding and overdose of them to the plants. Subsequently, we want to know which plant associated molecular pathways are triggered by these bacteria to promote the plant's growth. The above mentioned experiments will provide us with insights into which bacteria live inside lettuce roots, which of these bacteria can promote lettuce growth and how they influence the plant's molecular pathways to do so. This project will significantly aid lettuce farmers living in temperate climate areas by increasing the crop's turnover rate during the cold season.

Pieretti 144

Development of a multigenic metabarcoding protocol for deciphering the diversity of <i>Archaea</i>

Isabelle Pieretti* [1,2], Frédéric Mahé [3], Pascal Alonso [1,2], Laurence Blondin [1,2], Philippe Roumagnac[1,2] and Christian Vernière [1,2]
[1] CIRAD, UMR BGPI, 34398 Montpellier Cedex 5, France.
[2] BGPI, INRA, CIRAD, SupAgro, Univ. Montpellier, Montpellier, France.
[3] CIRAD, UMR LSTM, 34398 Montpellier Cedex 5, France.

Soil and plant microbiota are playing an eminent role in shaping both natural ecosystems and agricultural production systems. It is now widely admitted that bacterial communities show a great diversity in both the plant rhizosphere and the plant endosphere. These microbial communities affect the fitness of the hosts and further play important roles in C and N cycles. While bacterial communities have been widely studied, much less is known about archaeal communities and the role they play within the rhizosphere and the endosphere. The objective of our study was to develop a multigenic metabarcoding approach to accurately describe the diversity of archaeal communities interacting with rice paddies in the Rhône delta region. This pilot agro-ecosystem was selected because it is annually subjected to several abiotic stresses (water stress associated to rice paddies flooding, soil salinity, high production of methane, etc.) that are likely to enhance archaeal growth. We used archaeal specific primers within the universal 16S rRNA gene and the mcrA gene (encoding the methyl-coenzyme M reductase subunit A of methanogens). An evaluation of the efficiency of the primers was carried out on mock cultures and plant samples. Two rice-compartments during both rice paddies flooding and drying periods were collected and analyzed. This study is likely to be a first step towards better describing rice-associated archaeal communities and understanding the dynamics of these communities in relation with abiotic constraints of rice paddies in Camargue.

Poulicard 145

Exploring within-host diversity of plant viruses in rice agrosystems using two high-throughput sequencing strategies

Nils POULICARD[1]*, Alexis DEREEPER[1], Agnès PINEL-GALZI[1], Emmanuel FERNANDEZ[2], Charlotte JULIAN[2], Judith HUBERT[3], Denis FILLOUX[2], Denis FARGETTE[1], Philippe ROUMAGNAC[2], Eugénie HEBRARD[1]
[1]UMR IPME, IRD, Cirad, Université Montpellier, France
[2]UMR BGPI, Cirad, INRA, Montpellier SupAgro, France
[3]AfricaRice, Tanzania

The virome is an essential component of the phytobiome as viruses correspond to the most abundant and diverse biological entity in Nature and interact with all living organisms. The recent advances in high-throughput sequencing (HTS) has proven efficient for characterizing within-host diversity of several viruses, which has shed light on the influence of this diversity on the global fitness and virulence of viruses. We here aimed at evaluating the impact of rice management on the within-host diversity of Rice yellow mottle virus (RYMV) in order to optimize the cultural practices and to limit the burden of Rice yellow mottle disease in Africa.

We worked on rice plants collected from traditional and intensive rice fields in East Africa, which is the center of origin of Rice yellow mottle virus. Interestingly, several strains with contrasted pathogenic and epidemiological parameters co-exist in this region and recombination between strains were identified recently. We selected twelve RYMV symptomatic samples from fields managed under different types of practices that were analyzed using two HTS strategies: a metagenomics-based approach and a RYMV specific sequencing approach.

Combining both strategies, we tested if the RYMV was associated with other viral species in rice, and if some cases of co-infections between RYMV strains occurred. Both approaches indicate a significant within-host RYMV diversity, which allows us to perceive the diversification processes of RYMV strains at the field scale. The detection of recombinants and the comparison of the within-host genetic diversity depending on the cultivation practices are underway.

Poulin 146

The biological cycle of the root parasitic plant Phelipanche ramosa can be altered by a bacterial activity

Lucie Poulin[1]*, Jean-Bernard Pouvreau[1], Philippe Delavault[1], Philippe Simier[1]
[1] Université de Nantes, Laboratoire de Biologie et Pathologie Végétales, UFR Sciences et Techniques, 44322 Nantes, France

Root parasitic plants of the Orobanchacae family are ones of the many agricultural threats in the regions whith intensive crop cultivation. Among them, Phelipanche ramosa is one of the most harmfull parasitic plants. It has a wide host range: oilseed rape, tobacco, hemp, tomato, melon, and other crops, and it remains viable for many years. These non-photosynthetic and obligate parasitic plants possess a sophisticated mechanism to detect the presence of potential hosts in the soil. They can perceive molecules that are exuded by their host roots and thus initiate their biological cycle. Considering that the rhizophere, where the parasitic interaction takes place, is a complex, rich and heterogeneous niche, the microbiota may have a significant role in the interaction. Therefore we tested and validated in the lab a significant bacterial role in the early molecular interaction.

Prado 147

INRA Early Career Award Winner

Bee pollination affects seed microbiota

Alberto Prado*, Gloria Torres-Cortes, Cédric Alaux, Bernard Vaissiere & Matthieu Barret

Flowers are known to be a hub for microbial transmission between plants and insects. This floral-insect exchange opens the possibility for insect-transmitted bacteria to colonize the ovule and subsequently the seed, and to pass then into the next plant generation. In this study, we applied metagenomics to evaluate the contribution of insect pollination to the seed microbiome. Brassica napus flowers were subjected to bee pollination or allowed to self-pollinate. Microbial communities of seeds coming from bee vs self-pollination were compared using a 16S rRNA library. Our results show that bee pollination participates in the microbial assembly of the seed. We find some bee-associated genera in higher abundances in bee pollinated vs self-pollinated seeds. Insect pollination is therefore an ecological process involved in the transmission of bacteria from flower to seeds.

Roach 148

Complex microbial community assembly and plant growth under phosphorus-limiting conditions

Jack Roach[1]*, Rui Guan[1], Rubén Garrido-Oter[1], Stijn Spaepen[2], Paul Schulze-Lefert[1]
[1]Department of Plant-Microbe Interactions, Max Planck Institute for Plant Breeding Research, Germany
[2]Leuven Institute for Beer Research, Katholieke Universiteit Leuven, Belgium

Soil microbiota transplantation allows the separation of the effects of soil edaphic factors and the soil microbiota on host phenotypes. We transplanted microbial communities from diverse natural and agricultural soils into sterilized recipient soils and grew Arabidopsis thaliana in the repopulated soils. Bacterial and fungal communities were profiled at the various stages of community extraction, inoculation, and repopulation. Actinobacteria, Bacteroidetes, and Firmicutes tended to be enriched in repopulated soils, whereas Acidobacteria and Deltaproteobacteria tended to be depleted; no fungal phyla were affected. This effect was due in part to donor soil available phosphorus and potassium, such that repopulated microbial communities derived from nutrient-rich soils better resembled their donor soil cognates. Repopulated soil microbes had a variable influence on host growth that depended, in part, on the presence or absence of available phosphorus.

Saha 149

AgriVectors: a portal for plant diseases transmitted by insect vectors

Surya Saha*, The AgriVectors Consortium, Wayne Hunter and Lukas Mueller
Boyce Thompson Institute, US

Plant-feeding hemipteran pests are global threats to food security and production. Agricultural disease vector systems are an under-served area of research despite being one of the fundamental challenges for increasing food consumption. We propose to build an open and comprehensive resource for plant disease systems where the pathogen is transmitted by an insect vector. The portal will connect to established public repositories such as NCBI and EMBL together with pathosystem-specific repositories like citrusgreening.org. Furthermore, topical resources such as RNAi, CRISPR, insect feeding assays like EPG, etc. will also be included and leveraged to create a knowledgebase for plant diseases and vector biology. This system will also support privileged access for databases with private and unpublished data. We have created the citrusgreening.org portal as a model for a tritrophic disease system with genomics and bioinformatics resources for the vector Asian citrus psyllid (ACP, Diaphorina citri), the host citrus (C. clementina and C. sinensis) and multiple pathogens including Ca. Liberibacter asiaticus (CLas) for the citrus greening disease. We have used Biocyc Pathway Tools databases to model biochemical pathways within each organism that can be used to explore the entire disease complex. Psyllid Expression Network (PEN) is an expression atlas with proteomics and RNAseq data for ACP from adult and nymph life stages, various conditions and multiple hosts. The citrusgreening.org model will be extended beyond gene-centric omics data to pathosystem-wide data including integrated pest management data, behavioral and climate data in addition to phenotyping information from disease trials to create the AgriVectors portal.

Sanguin 150

The human-driven impacts on a long-term affair between an iconic Mediterranean fruit tree and its microbiome

Hervé Sanguin[1,2]*, Frédéric Mahé[1,2], Lahcen Ouahmane[3], Pierre Tisseyre[1,4], Estelle Tournier[1,2], Hamza Khassali[1,2,3], Christine Le Roux[1,2], Yves Prin[1,2], Lucie Miché[5], Pascal Mirleau[5], Robin Duponnois[1,4], Jean-François Arrighi[1,4], Mohamed Hafidi[3], Ahmed Ouhammou[3], Bruno Vincentelli[6], Carole Anziani[6], Laetitia Hugo[6,7], Katia Diadema[8], Gonzalo Nieto Feliner[9], Fatma Mirleau[5], Magda Bou Dagher Kharrat[10], Stefano La Malfa[11], Frédéric Médail[5], Juan Viruel[12], Alex Baumel[5]
[1]LSTM, Univ Montpellier, CIRAD, IRD, INRA, Montpellier SupAgro, Montpellier, France
[2]CIRAD, UMR LSTM, F-34398 Montpellier, France
[3]University of Cadi Ayyad, Faculty of Sciences Semlalia, Laboratory of Ecology and Environment, 40000 Marrakesh, Morocco
[4]IRD, UMR LSTM, F-34398 Montpellier, France
[5]Aix Marseille Univ, Univ Avignon, CNRS, IRD, IMBE, Marseille, France
[6] Corsican Environmental Office (OEC), 20250, Corte, Corsica, France
[7]National Botanical Conservatory of Corsica (CBNC), 20250, Corte, Corsica, France
[8]National Mediterranean Botanical Conservatory (CBNMed), Hyères, France
[9]Real Jardín Botánico (CSIC), 28014 Madrid, Spain
[10]University of Saint-Joseph, Faculty of Sciences, Laboratory of Plant Genome Characterisation, 11072050 Beiruth, Lebanon
[11]University of Catania, Dipartimento di Agricoltura, Alimentazione e Ambiente (Di3A), 95123 Catania, Italy
[12]Royal Botanic Gardens, Kew, Richmond, Surrey, TW93DS, United Kingdom

The Mediterranean thermophilous woodlands were shaped by human activities for millenia, mainly for forage and fruits harvest. The recurring exchanges that followed between forests and cultivated areas have constituted a pivotal aspect in the process of Mediterranean fruit tree domestication. Since its domestication in the Middle-East around 6,000-4,000 years BP, the carob tree, Ceratonia siliqua L. (Leguminosae), has probably experienced extensive genetic and physiological modifications conducing to potential changes of a major compartment of its functioning: the microbiome. The carob tree is highly dependent of arbuscular mycorrhizal (AM) symbiosis, but some evidences tends to demonstrate bacterial endophytes as a second major symbiotic partner. In the framework of the international project DYNAMIC (Deciphering sYmbiotic Networks in cArob-based MedIterranean agro-eCosystems), high-throughput sequencing methods were applied to estimate several proxies of the carob tree-microbiome diversity and to correlate it to carob tree ecology and phylogeography at the Mediterranean scale. The results provide new insights into the characterization of a Mediterranean core and accessory carob tree-microbiome, highlighting geographical patterns, as well as the contribution of host genetic diversity, habitat and edaphic parameters. New avenues for reflexion regarding the relative role of history and habitat (cultivated vs wild) as drivers of tree-microbiome are also proposed. The conclusions open up promising perspectives for the development of more efficient strategies in conservation and agroecology based on tree-microbiome management.

Sapkota 151

Unravelling the Wheat Mycobiome

Mogens Nicolaisen, Rumakanta Sapkota*

Wheat is widely grown and a major crop for global crop production. As plant are associated with a complex microbial community and these communities are important for plant health and productivity. While the studies of such complex plant microbes are being unfolded, although mostly limited in the bacterial communities. The other part of microbes- the fungal community although being the major player in the plant diseases, understanding the fungal community dynamics in cereal crops such as wheat is limited. Using metabarcoding, we reported the fungal community structure not only in different parts of wheat but also how it changes through the course of different growth stages. In our first experiment where we sampled wheat leaves at three growth stages, we described that the fungal communities being influence by leaf position, growth stage and cultivar. In addition, the effect of cultivar was important in explaining variation in older leaves. Network analysis revealed positive interaction among yeast species and negative interaction with pathogens. In our second experiment, we have sampled whole wheat plants every week and investigated the dynamics of community assembly in detail with growth stage. Our results reveal the major fungal communities harboring in the wheat plant, and the further describes the fungal composition shift as the plant matures.

Sarniguet 152

Influence of soil microbial diversity and host plant genotype on the structure and diversity of root microbiota of Brassica napus infected with Plasmodiophora brassicae

Alain SARNIGUET[1]*, Lionel LEBRETON[1], Kévin GAZENGEL[1], Anne-Yvonne GYUILLERM-ERCKELBOUDT[1], Juliette LINGLIN[1], Stéphanie DAVAL[1], Maria MANZANARES-DAULEUX[1], Christophe MOUGEL[1]
[1]INRA, Université de Rennes 1, Agrocampus-Ouest, UMR 1349 IGEPP (Institute of Genetics, Environment and Plant Protection) – Le Rheu, France

Plant responses to diseases are variable with environmental conditions including plant associated microbiota. Thus we started to explore the respective influence of plant genotype and soil microbiota and their potential synergisms to control root diseases and to select root microbiota. We compared the expression of clubroot disease, caused by the protist Plasmodiophora brassicae, on two Brassica napus genotypes known for their different partial resistance. Plants were grown in a soil recolonized with microbial assemblage of three levels of diversity and infested or not with the pathogen. In parallel with disease expression kinetics, the taxonomic structures of rhizosphere and root microbiota were estimated with two molecular markers, 16S and 18S rRNA at intermediate and final plant growth experimental steps. The microbial soil diversity affected differently the disease extent on the B. napus genotypes. The beta-diversity analysis revealed that soil diversity, disease and plant genotype factors were important driving-forces for the selection of bacterial OTU, but the soil diversity factor is more important in rhizosphere than in roots whereas the disease factor is more important in roots than in rhizosphere. The plant genotype factor had significant but lower influence but with a higher influence on fungi than on bacteria. Next challenge will be to characterize the selected bacterial functions with regards to disease variation and genotype hosting.

Schachtman 153

Natural variation in Zea mays root exudates and their impact on the root bacterial microbiome

Daniel P. Schachtman*, Peng Wang, Sophie Alvarez, Martha Lopez-Guerrero and Karin van Dijk

Root exudates are known to play important roles in the communication between plants and microbes. However, little is known about the genetic variation of exudates in maize and whether the composition of root exudates impacts the assembly of root-associated bacterial communities. To gain a better understanding of the diversity in the chemical composition of root exudates in maize, we developed a semi-hydroponic plant growth system for exudate collection. Targeted analysis, using GC-MS and LC-MS, was done to analyze root exudates of the Goodman-Buckler maize diversity panel for hormones, amino acids, organic acids, sugars, and other compounds. Results showed there is genotypic variation for some exudates and heritability analysis showed that the variation of some exudates may be attributed to genetic factors. Based on the measured variation we chose several lines for studies in the field to determine whether exudates impact the assembly of bacterial communities. Results from the field studies using 16S amplicon sequencing will be presented along with the growth chamber results from the exudate screening.

Schikora 154

Highly diversified microbiome has the potential to protect crops against human pathogens

Jasper Schierstaedt, Helena J. Barkowski, Sven Jechalke, Abhishek Shrestha, Rita Grosch,Kornelia Smalla and Adam Schikora*

Foodborne diseases are increasingly associated with fresh fruits and vegetables, Salmonella is now their most frequent cause. The biological diversity of soil plays a major role in the establishment of Salmonella in the plant production environment. Antagonists and plant beneficial microbes negatively affect the establishment of Salmonella in the rhizosphere. Here we analyzed the tripartite interactions between the human pathogen Salmonella enterica, the soil microbiome and the crop plants tomato, lettuce and corn salad grown under greenhouse conditions. We observed that Salmonella persisted in the rhizosphere of lettuce and tomato. Very important was the observation that reduction of microbial diversity in soil increased the ability of Salmonella to persist in this environment. These results clearly show a dependency between the microbial diversity and the potential of Salmonella to colonize the rhizosphere. In the following, we focused on the impact of resistance induced in crop plants on the establishment in plant production environment and colonization of plants. In greenhouse experiments, crop plants were primed for induced resistance with the bacterium Ensifer meliloti. This bacterium produces N-acyl-homoserine-lactones, which are known to induce resistance. Our results show that priming has a negative effect on the persistence of Salmonella. Primed plants express the defense-related genes earlier than unprimed plants and are able to close their stomata for longer period. These results indicate the potential of priming for enhanced resistance against Salmonella.

Schmidt 155

How microbial volatiles can help plants to withstand drought

Ruth Schmidt*, Paolina Garbeva and Étienne Yergau

Climate change resulting in higher temperatures leads to enormous losses in yields for major crops, including wheat. A promising and sustainable approach to improve wheat yields under suboptimal conditions stems from volatiles organic compounds (VOCs) producing soil microbes. I have recently shown that VOCs act as a common chemical language between microbes to communicate with each other and alter each other's behavior. For example, the beneficial bacterium Serratia plymuthica PRI-2C induced its motility and produced a unique terpene, called Sodorifen, when exposed to VOCs from the fungal plant pathogen Fusarium culmorum. Further, Sodorifen producing S. plymuthica PRI-2C was able to support the health of maize when under pathogen attack. Similarly, terpenes are likely to play important roles in driving the plants resistance to drought. The next step is to test this hypothesis on the plant holobiont, considering the plant and its microbial community. I have developed a Rhizotron setup that allows to study microbial and plant genes linked to VOC emission along a spatial and temporal resolution. This experiment will show which genes and VOCs are the main players in making plants more resistant to drought and will set the basis for application of VOCs to the field via microbial engineering strategies.

Sergaki 156

The dynamics of microbial and environmental factors in shaping root microbiomes

Chrysi Sergaki[1]*, Patrick Schäfer[1,2]
[1]School of Life Sciences, University of Warwick, Coventry, UK
[2]Warwick Integrative Synthetic Biology Centre, University of Warwick, Coventry, United Kingdom

The root microbiota, consisting of diverse microbial communities in and around plant roots, can significantly influence plant development and stress tolerance. The basic aim of our research is to analyse the communication between microbes in the rhizosphere and between plant roots and microbes. For this purpose, Serendipita indica, a mutualistic fungal root endophyte, which is observed to improve plant performance and disease resistance in host plants, is studied. By analyzing the effect of S. indica on the rhizobiome composition of Arabidopsis thaliana, using a synthetic bacterial community, we aim to reveal plant and/or microbe-derived communication patterns that are involved in shaping root microbiomes. To further test these patterns in a natural environment, a bacterial taxon commonly utilized in agriculture, Rhizobia, is used as a mutualist root symbiont of the legume Medicago truncatula. Rhizobia strains are tested for their abilities to stimulate plant growth and nutrient supply as well as their competitiveness in representative UK soil types and their different natural microbiomes. These analyses will further help in elucidating the stability of beneficial plant-microbe interactions in natural communities and in different environments. Being part of the Warwick Integrative Synthetic Biology Centre, the long-term aim is to integrate molecular and environmental factors to generate customized beneficial microbiomes that can be applied to sustainably support crop production.

Spoelder 157

Studying variation within the PGPR Bacillus mycoides to understand efficacy differences in the field

Jan Spoelder [1,2,3]*, Domenica Philipsen[1], Lo Turkensteen[3], Theo Elzenga[1], Dick van Elsas[2]
[1]Ecophysiology of Plants Group, Groningen Institute for Evolutionary Life Sciences (GELIFES), University of Groningen, P.O. Box 11 103, 9700 CC Groningen, The Netherlands.
[2]Microbial Ecology Group, Groningen Institute for Evolutionary Life Sciences (GELIFES), University of Groningen, P.O. Box 11 103, 9700 CC Groningen, The Netherlands.
[3]Hilbrands Laboratory for Research in Agriculture (HLB), Kampsweg 27, 9418 PD Wijster, The Netherlands

The trend towards more biological approaches in conventional agriculture is obvious. However, efficacy of biologicals is often poor compared to chemical counterparts. We believe that understanding the way microbes, plants and soil vary and interact is crucial to increasing efficacy.

This presentation focuses on the microbe side by studying the plant growth promoting microbe Bacillus mycoides and its intraspecific variation. By means of genetic fingerprinting of 350 isolates we demonstrate a wide variety within the species, even within one square meter of a potato field. This variety is directly linked to the habitat of isolates (endosphere, rhizosphere or bulk soil) and their ability to colonize and stimulate growth of plants in greenhouse and field studies.

A group of plant-associating strains (PA-strains) was selected, as well as a group of poorly colonizing soil strains (S-strains) for further comparative studies to understand what makes a good colonizer.

PA-strains can respond to higher concentrations of nutrients with chemotaxis as shown using gradient agar experiments. They also produce more auxins compared to the S-strains. Biolog-microplate analysis characterizes carbohydrate metabolism. We demonstrate the strong ability of the PA-strains to utilize sucrose and pectin, two strongly plant-related compounds.

Full genome analysis of the strains is underway and there is clear distinction between PA-strains and S-strains.

Taken together, we clearly see strains specialized in living with plants that are more suitable candidates for applications in the field. Studies into the effect of variations in plants and soils are ongoing. (Spoiler: the soil will be the decisive factor).

Thijs 158

GenOme Resolution by Density-gradient Isopycnic ANalysis (GORDIAN) for sequence-based microbial community analysis

Thijs S*, Bullen NP, Coyotzi S, Vangronsveld J, Holben WE, Hug LA, Neufeld JD

High-throughput sequencing applied to 16S rRNA gene amplicons or shotgun metagenomes results in high coverage of templates from abundant taxa, yet only low access to extensive diversity that exists at lower relative abundance. Here we adopted a previously developed "GC fractionation" approach for use with high-throughput sequencing, which together we refer to as GenOme Resolution by Density-gradient Isopycnic ANalysis (GORDIAN). Using bisbenzimide to accentuate GC:AT ratio-specific density differences, cesium chloride gradients separated microbial community DNA into distinct fractions based on GC content. We pioneered GORDIAN for comprehensive analysis of DNA extracted from two soil samples (agricultural and forest; high diversity), a wastewater treatment facility (biofilm from a rotating biological contactor; RBC; medium diversity), and a defined community (five pure bacterial cultures; low diversity). All fractions were characterized by 16S rRNA gene sequencing on a MiSeq (Illumina) prior to shotgun metagenomic sequencing. The 16S rRNA gene results demonstrated strong separation of genomic DNA, based on distinct taxonomic profiles associated with the fractions from each gradient. Comparison of 16S rRNA gene profiles to reference genomes with known GC content confirms that GC content governs fraction distributions. Individual fractions represent a subset of the diversity detected in the unfractionated sample. Many rare biosphere taxa (<0.1%) from the original unfractionated samples increased by 10- to 100-fold to become dominant (>1%) within fractions associated with high and low GC contents, such as those affiliated with unclassified bacteria, Nitrososphaeraceae, Chitinophagaceae, and Acidobacteria (subgroup 6). Overall, these 16S rRNA gene results demonstrate the promise of applying GORDIAN for accessing genomes from unique microbial populations within complex microbial communities using shotgun metagenomics, which is currently in progress.

Torres-Cortes 159

Copiotrophic traits drive the assembly of bacterial microbial community during germination and emergence.

Gloria Torres-Cortés[1]*, Sophie Bonneau[1], Martial Briand[1], Marie-Agnès Jacques[1] and Matthieu Barret[1]
[1] IRHS, INRA, AGROCAMPUS-Ouest, Université d'Angers, Beaucouzé, France

Microbial interactions occurring on and within seeds are key for plant fitness since seed associated microorganisms are the primary source of inoculum for the plant. The aim of this study is to uncover microbial traits implicated in the assembly of the seed microbiome during germination and plant emergence. With this purpose, we performed shotgun sequencing of microbial DNA and RNA from seeds, germinating seeds and seedlings of two plant species: bean and radish. We observed an enrichment of Enterobacteriales and Pseudomonadales during emergence and a group of functional traits linked to copiotrophy that could be responsible for this selection due to the increase of nutrient availability after germination. Moreover, representative bacterial isolates of taxa that are selected in seedlings showed faster bacterial growth rate in seed exudates media in comparison to seed-associated bacteria isolates. In addition, multifunctional redundancy analyses showed that radish-associated microbial assemblages are more resistant to invasion by alien species at the seedling stage than bean microbiota. Finally, binning of metagenomics contigs results in the reconstruction of population genomes of the major bacterial taxa associated to the samples. Together, our results demonstrate that, although seed microbiome varied across plant species, nutrient availability during germination elicits changes of the composition of microbial communities by selecting microbial groups with specific copiotrophic functional traits. The data presented here represents the first attempts to empirically assess changes in the microbial community during plant emergence and moves us towards a more holistic understanding of the plant microbiome.

Wolinska 160

Role of the plant innate immune system in controlled accommodation of beneficial microbes in Arabidopsis thaliana roots

Katarzyna W. Wolinska[1], Brigitte Pickel[1], Thorsten Thiergart[1], Stéphane Hacquard[1]
[1]Department of Plant-Microbe Interactions, Max Planck Institute for Plant Breeding Research, 50829 Cologne, Germany

Plants have evolved a complex, multi-layer, immune system that detects microbial invasion and discriminates self from non-self. Paradoxically, the roots of healthy plants are colonized by a staggering diversity of microbes, including bacteria, fungi, and oomycetes (i.e. the root microbiota), forming complex multi-kingdom microbial communities that affect plant productivity[1]. Although plant innate immunity components that shape relationships between specific microbe-plant pairs have been extensively studied under laboratory settings[2–4], our understanding of these complex interactions in natural (i.e. community) contexts remains incomplete, especially in plant roots[5]. Recent studies indicate that certain sectors of the plant immune system, namely phytohormones and tryptophan-derived secondary metabolites play an important role in the establishment of the plant microbiota[6,7]. Our preliminary experiments on a wide variety of immunocompromised mutants show that, different elements of immune system exert subtle but distinct effects on the endophytic root microbiota composition. The mutations have different effect on diverse groups of microbes (bacteria, fungi and oomycete) and this effect seems to be time-dependent. We also find that the function of the microbiota in promoting plant growth is lost in certain immunocompromised mutants, especially those with dysfunctional wrky-mediated basal defence and tryptophan-derived metabolite pathways, indicating the importance of these components in establishing beneficial plant-microbe interactions. Altogether, we anticipate that this research will shed more light on the role of the immune system in plant-microbe interactions in a community context.

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Young 161

Taming a root rot pathogen: understanding the spatio-temporal dynamics of a root rot disease

Carolyn A. Young[1]*, Chakradhar Mattupalli[1], Corey A. Moffet[2], Larry M. York[1], Kushendra N. Shah[1], Suresh Bhamidimarri[1], Mike R. Komp[1], James K. Rogers[1]
[1]Noble Research Institute, LLC, Ardmore, OK 73401, USA
[2]USDA-ARS, Southern Plains Range Research Station, Woodward, OK 73801, USA

Geospatial technologies can greatly enhance evaluation of large production areas, and when combined with on ground monitoring, can facilitate our understanding of disease. Alfalfa is a valuable forage crop that provides high protein content to livestock. A common problem growing alfalfa in southwest U.S.A. is the presence of a prevalent root rot pathogen, Phymatotrichopsis omnivora. Alfalfa stands affected by the disease Phymatotrichopsis root rot (PRR) decline prematurely. To understand the spatio-temporal dynamics of PRR, we have monitored disease progression in an alfalfa production field utilizing multiple techniques. Aerial imagery provided a bird's eye view of disease spread. During a single growing season (June to October) the disease front moved on average 3 m and over 30% of the stand was lost. The pathogen is readily detected in the roots by PCR but is more abundant at the disease front. Genome sequence of three isolates revealed a heterothallic mating system; however, the observed spatial distribution of isolates with different mating types is limited to sparse interacting points. Plants that have survived PRR have an altered root architecture, where the main taproot is severely damaged but the plant has compensated with development of more crown and lateral roots. We have selected plants with this altered root phenotype to determine if this is a genetic trait that will provide disease tolerance. Combining multiple technologies has provided insight into the P. omnivora-alfalfa disease complex, which will be integrated with decision-making tools associated with breeding and precision agriculture to reduce the severity of this root rot disease.

King 162

Host transcriptional regulations during associative symbioses: Comparative analysis of rice sensing of plant-beneficial Burkholderia

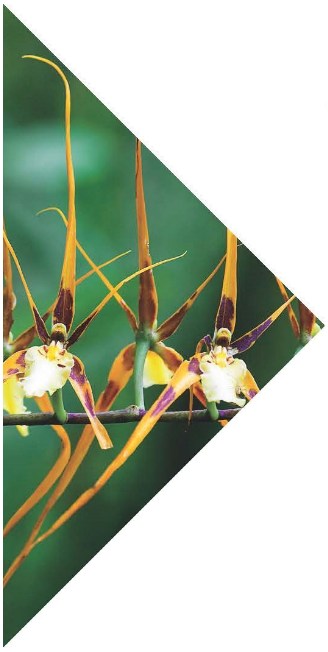
Eoghan King, Lionel Moulin and Pierre Czernic
Interactions Plant-Microbes-Environment (IPME), IRD-CIRAD-UM, 911 Av. Agropolis, Montpellier.

Throughout a plant' life cycle negotiations at the molecular level between microbes and the host plants occur. Although for a number of plant pathogens the underlying molecular bases of the interaction are well described it is not the case for non- mutualistic beneficial interactions or associative symbiosis. Particularly little is known about the transcriptional regulations associated with the "immune tolerance" of crop plants towards beneficial microbes.

In this context, the study of the Burkholderia-rice model is very promising to describe the molecular mechanisms implicated in associative symbiosis. Indeed several species of the Burkholderia genus can colonize rice tissues and have beneficial effects. We produced the transcriptome of rice plants inoculated with different root-associated Burkholderia through RNA-Seq and proceeded to their comparative analysis.

This study revealed that extensive common transcriptional regulations occur in leaves throughout the establishment of the interaction at the root level. However important differences were observed, particularly while the studied Burkholderia species are phylogenetically closely related, some induced much less transcriptional regulations than others also we were able to identify genes showing opposite regulation.

This fundamental work leads the way to the identification of molecular markers associated with the capacity for plants to exploit beneficial effects of their microbiome.



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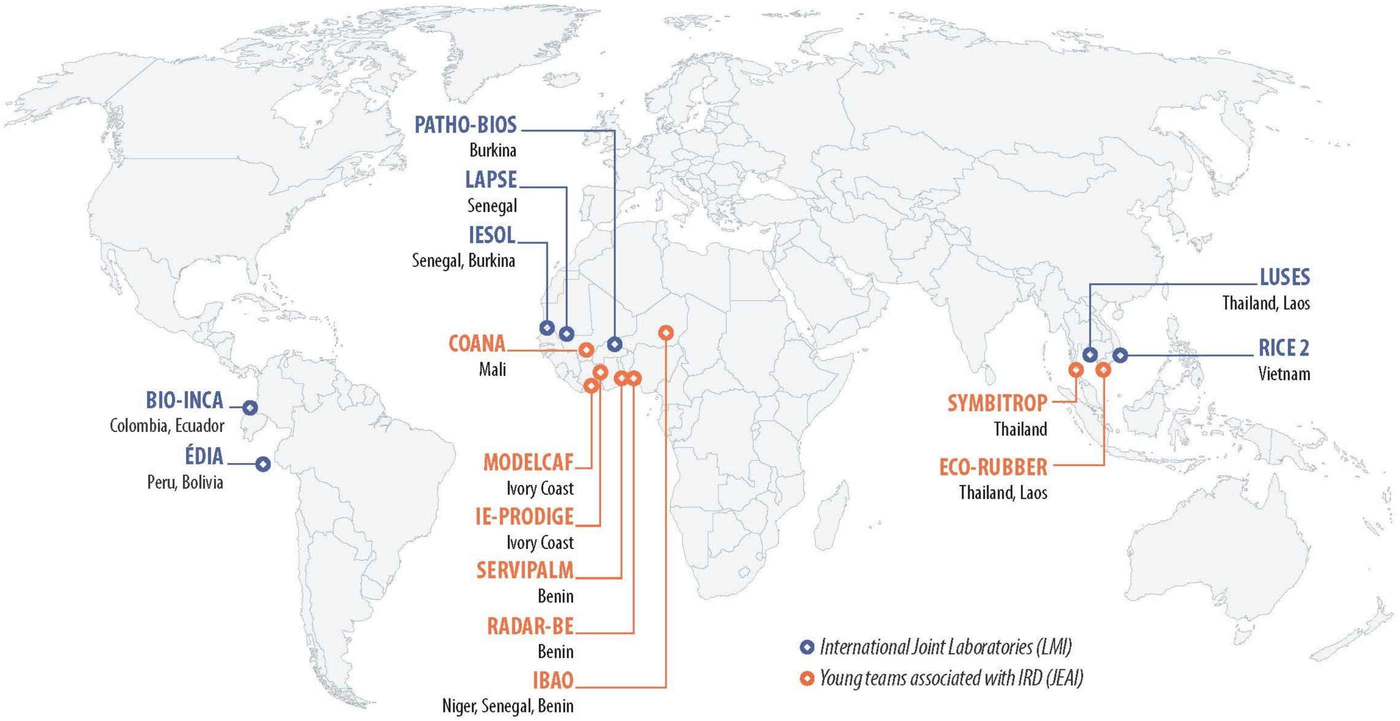

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Conference Participant List *(current as of 12 November)*

Shrestha Abhishek
Julius Kühn Institute
abhishek.shrestha@julius-kuehn.de

Alberto Acedo
Biome Makers
acedo@biomemakers.com

Jonathan Adams
Chinese Academy of Sciences, Nanjing
geog.ecol@gmail.com

Gul Ali
University of Florida
gsali@ufl.edu

Pascal Alonso
CIRAD
pascal.alonso@cirad.fr

Welington Araújo
University of São Paulo
wlaraujo@usp.br

Komi Assigbetse
IRD
Komi.assigbetse@ird.fr

Weronika Babińska
University of Gdańsk, Intercollegiate
Faculty of Biotechnology UG&MUG
werabab@wp.pl

Matthieu Barret
INRA
matthieu.barret@inra.fr

Alejandro del Barrio Duque
AIT
Alejandro.delBarrio-Duque@ait.ac.at

Gwyn Beattie
Iowa State University
gbeattie@iastate.edu

Alberico Bedini
INOQ GmbH
albericobedini@inoq.de

Stien Beirinckx
VIB-PSB
stien.beirinckx@ugent.be

Terrence Bell
Pennsylvania State University
thb15@psu.edu

Stéphane Bellafiore
IRD
stephane.bellafiore@ird.fr

Gilles Béna
IRD
gilles.bena@ird.fr

Annette Berard
INRA
annette.berard@inra.fr

Laurence Blondin
CIRAD
laurence.blondin@cirad.fr

Stéphane Boivin
IRD LSTM
boivinstephane@hotmail.fr

Natalie Breakfield
NewLeaf Symbiotics
nbreakfield@newleafsym.com

Eoin Brodie
Lawrence Berkeley National Lab
elbrodie@lbl.gov

Richard Broglie
Pivot Bio
richard@pivotbio.com

Isabelle Caugant
Eversole Associates
caugant@eversoleassociates.com

Trevor Charles
University of Waterloo /
Metagenom Bio Inc.
tcharles@uwaterloo.ca

Pierre Czernic
IRD
pierre.czernic@umontpellier.fr

Olivier Dangles
IRD
olivier.dangles@ird.fr

Stéphanie Daval
INRA
stephanie.daval@inra.fr

Diegane Diouf
IRD
diegane.diouf@ucad.edu.sn

Stéphane Dupas
IRD
stephane.dupas@ird.fr

Branly Effa Effa
IRD
branlyeffeffa@gmail.com

Kellye Eversole
International Phytobiomes Alliance
eversole@eversoleassociates.com

Gary Felton
Pennsylvania State University
gwf10@psu.edu

Omri Finkel
University of North Carolina
ofinkel@live.unc.edu

Sally Flis
The Fertilizer Institute
sflis@tfi.org

Tania Fort
INRA
fort.vincensini@gmail.com

Zach Foster
Oregon State University
fosterz@oregonstate.edu

Emilie Froussart
VIB
emfro@psb.vib-ugent.be

Tania Galindo-Castañeda
The Pennsylvania State University
tania.camila@gmail.com

Paolina Garbeva
Netherlands Institute of Ecology
(NIOO-KNAW)
p.garbeva@nioo.knaw.nl

Martine Gautier
SBM DEVELOPPEMENT
martine.gautier@sbm-company.com

Jim Germida
University of Saskatchewan
jim.germida@usask.ca

Thaura Ghneim Herrera
Universidad Icesi
tghneim@icesi.edu.co

Simon Goertz
NPZ Innovation GmbH
s.goertz@npz-innovation.de

Nik Grunwald
USDA ARS
grunwaln@oregonstate.edu

David Hallahan
Corteva Agriscience
david.hallahan@pioneer.com

Larry Halverson
Iowa State University
larryh@iastate.edu

Annika Hoffmann
Leibniz Centre for Agricultural
Landscape Research (ZALF) e.V.
annika.hoffmann@zalf.de

Nicola Holden
The James Hutton Institute
nicola.holden@hutton.ac.uk

Shiji Hou
Max Planck Institute for Plant
Breeding Research
hou@mpipz.mpg.de

Charley Hubbard
Indigo Ag
chubbard@indigoag.com

Juan Imperial
CBGP, UPM-INIA
juan.imperial@upm.es

Lilach Isaur Kruh
ORT Braude College
iasur@braude.ac.il

Daniel Jacobson
Oak Ridge National Laboratory
jacobsonda@ornl.gov

Sylwia Jafra
Univerity of Gdansk
sylwia.jafra@biotech.ug.edu.pl

Jihye Jung
Korea Research Institute of
Bioscience & Biotechnology
abcde40@kribb.re.kr

Laura Kaminsky
Pennsylvania State University
lmk52@psu.edu

Presanna Kankanala
Noble Research Institute, LLC.
pkankanala@noble.org

Lydie Kerdraon
INRA
lydie.kerdraon@inra.fr

Jihyun Kim
Yonsei University
jfk1@yonsei.ac.kr

Stephanie Kivlin
University of Tennessee/EEB
skivlin@utk.edu

Agnieszka Klonowska
IRD
agnieszka.klonowska@ird.fr

Enoch Narh Kudjordjie
Aarhus University
enochnarh@agro.au.dk

Jay-Ram Lamichhane
INRA
Jay-Ram.Lamichhane@inra.fr

Chih-Ying Lay
Concentric Agriculture Inc.
clay@concentricag.com

Jan Leach
Colorado State University
Jan.Leach@colostate.edu

Lori Leach
Eversole Associates
leach@eversoleassociates.com

Lionel Lebreton
INRA
lionel.lebreton@inra.fr

Yongjin Lee
Kyung Nong
yjlee1@dongoh.co.kr

Soohyun Lee
Korea Research Institute of
Bioscience & Biotechnology
ysh76@kribb.re.kr

Christolph Lehnen
Bee Vectoring Technology BVT
clehnen@amani-agri.com

Yuxin Ma
INRA
yuxin.ma@inra.fr

Frederic Mahe
CIRAD
frederic.mahe@cirad.fr

Andreas Makiola
INRA
andreas.makiola@inra.fr

Andrea Marino
Advanced Biological Marketing
andreamarino@abm1st.com

Charles Mason
Pennsylvania State University
cjm360@psu.edu

Anne-Sophie Masson
IRD
anne-sophie.masson@etu.umontpellier.fr

Tim Mauchline
Rothamsted Research
tim.mauchline@rothamsted.ac.uk

Marco Mechan Llontop
Virginia Tech University
marcoeml@vt.edu

Conference Participant List *(current as of 12 November)*

Michael Millican
University of Wisconsin - Madison
mmillican@wisc.edu

Andrea Molt
BASF SE
andrea.molt@basf.com

Christina Morauf
bio-ferm GmbH
christina.morauf@bio-ferm.com

Jean-Benoit Morel
CIRAD
jbmorel@cirad.fr

Agata Motyka-Pomagruk
Univeristy of Gdansk
agata.motyka@biotech.ug.edu.pl

Christophe Mougel
INRA
christophe.mougel@inra.fr

Lionel Moulin
IRD
lionel.moulin@ird.fr

Pascal Muelner
ABiTEP GmbH
muelner@abitep.de

Papa Mamadou Sitor Ndour
IRD
sitndour@yahoo.fr

Claire Neema
Montpellier supagro
claire.neema@supagro.fr

Morgane Ourry
INRA
morgane.ourry@inra.fr

Antonio Pandolfi
Res Agraria S.r.l.
antoniopandolfi@resagraria.com

Jacob Parnell
Novozymes
jap@novozymes.com

Charlie Pauvert
INRA
charlie.pauvert@inra.fr

Antoine Persyn
VIB
anper@psb.ugent.be

Isabelle Pieretti
CIRAD
isabelle.pieretti@cirad.fr

Nils Poulicard
IRD
nils.poulicard@ird.fr

Lucie Poulin
Laboratoire de Biologie et Pathologie
Végétales, Université de Nantes
lucie.poulin@univ-nantes.fr

Alberto Prado
INRA
alberto.prado-farias@inra.fr

Claudia Preininger
AIT
claudia.preininger@ait.ac.at

Patrice Rey
INRA
patrice.rey@inra.fr

Jack Roach
Max Planck Institute for Plant
Breeding Research
roach@mpipz.mpg.de

Aude Rochefort
INRA
aude.rochefort@inra.fr

Montufar Rommel
IRD
rjmontufar@puce.edu.ec

Philippe Roumagnac
CIRAD
philippe.roumagnac@cirad.fr

Matthew Ryan
CABI
m.ryan@cabi.org

Surya Saha
Boyce Thompson Institute
ss2489@cornell.edu

Isai Salas-Gonzalez
University of North Carolina
at Chapel Hill
isai@email.unc.edu

Hervé Sanguin
CIRAD
herve.sanguin@cirad.fr

Rumakanta Sapkota
Aarhus Universtiy
rumakanta.sapkota@agro.au.dk

Joelle Sasse-Schlapfer
Lawrence Berkeley National
Laboratory
jschlapfer@lbl.gov

Alain Sarniguet
INRA
alain.sarniguet@inra.fr

Daniel Schachtman
University of Nebraska - Lincoln
daniel.schachtman@unl.edu

Angela Sessitsch
AIT
angela.sessitsch@ait.ac.at

Adam Schikora
Julius Kühn-Institut
adam.schikora@icloud.com

Ruth Schmidt
INRS- Institut Armand Frappier
schmidt.ruth@gmail.com

Chrysi Sergaki
University of Warwick
sergaki.chrysi@gmail.com

Andong Shi
IBG2, Forschungszemtrum Julich
a.shi@fz-juelich.de

Jan Spoelder
HLB / University of Groningen
j.spoelder@rug.nl

Boris Szurek
IRD
boris.szurek@ird.fr

Sofie Thijs
Hasselt University
sofie.thijs@uhasselt.be

Charlotte Tollenaere
IRD
charlotte.tollenaere@ird.fr

Gloria Torres-Cortes
INRA
gloria.torres-cortes@inra.fr

Corinne Vacher
INRA
corinne.vacher@inra.fr

Steven Vandenabeele
Aphea.Bio
steven.vandenabeele@aphea.bio

Leo van Overbeek
Wageningen University and Research
leo.vanoverbeek@wur.nl

Isabel Vercauteren
Aphea.Bio
isabel.vercauteren@aphea.bio

Valérie Verdier
IRD
valerie.verdier@ird.fr

Christian Verniere
CIRAD
christian.verniere@cirad.fr

Gwendolin Wehner
Julius Kühn-Institut
gwendolin.wehner@julius-kuehn.de

Guenter Weiz
Bayer Crop Science Division
guenter.welz@bayer.com

Lisa Wingate
INRA
lisa.wingate@inra.fr

Katarzyna Wolinska
Max Planck Institute for Plant
Breeding Research
wolinska@mpipz.mpg.de

Xu Xiangming
NIAB EMR
xiangming.xu@emr.ac.uk

Carolyn Young
Noble Research Institute, LLC
cayoung@noble.org

Updated Conference Participant List *(current as of 30 November)*

Stefano Colella
INRA
Stefano.colelle@inra.fr

Philippe Dufour
RAGT2n
esabatier@ragt.fr

Jean-Francois Dussart
Elephant Vert
jean-francois.dussart@elephant-vert.com

Carla de la Fuente Cantó
IRD
Carla.de-la-Fuente-canto@ird.fr

Alain Ghesquiere
IRD
alain.ghesquiere@ird.fr

Barry Goldman
Indigo Ag
bgoldman@indigoag.com

Mathilde Hutin
IRD
Mathilde.hutin.ird.fr

Eoghan King
University of Montpellier
Eoghan.king@etu.umontpellier.fr

Pascal Kosuth
Agropolis Foundation
kosuth@agropolis.fr

Soon-Kyeong Kwon
Yonsei University
orionirion@yonsei.ac.kr

Mathias Lorieux
IRD
Mathias.lorieux@ird.fr

Gloria Mosquera
IRD
G.M.Mosquera@CGIAR.org

Julie Orjuela
IRD
Julie.orjuela@ird.fr

Hyein Park
Yonsei University
6457phi@gmail.com

Laurence Pascal
IRD-UM
laurence.pascal@umontpellier.fr

Carola Peters
Incotec Europe B.V.
Carola.peters@incotec.com

Hamidou Tall
IRD
Hamidou.tall@ird.fr

Ngan Phan Thi
IRD
Ngan.phan-thi@ird.fr

Statish Rai
KWS SAAT SE
Satish.rai@kws.com

Quentin Struelens
IRD
Quentin.struelens@ird.fr

Romain Valade
ARVALIS Institut du vegetal
R.valade@aravlis.fr

Vittorio Venturi
International Centre for Genetic Engineering and Biotechnology
venturi@icgeb.org

Adrian Wallner
IRD
adrian.wallner@ird.fr

Hong Zhu
BioConsortia
hzhu@bioconsortia.com

INTERNATIONAL PHYTOBIOMES CONFERENCE 2018

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