



Bonar Hall | Dundee, Scotland, UK

# 3<sup>rd</sup> Plant Microbiome Symposium

24th - 26th May 2022



**Abstracts**

## Session 1: Plant microbiome assembly

<b>Number</b>	<b>S1.K1</b>
<b>Authors</b>	Thomas Bell
<b>Affiliations</b>	Imperial College London
<b>Presenting author</b>	Thomas Bell
<b>Email address</b>	<a href="mailto:thomas.bell@imperial.ac.uk">thomas.bell@imperial.ac.uk</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Invasion ecology of plant pathogens
<b>Abstract text</b>	<p>Many plant pathogens spend much of their life history away from plants. Plant pathogens often need to disperse through an environmental matrix (soil, air, water), during which time they are interacting and competing with a resident microbial community. The importance of these interactions with free-living organisms has been understudied, and may be important for understanding their ecology and dynamics. I will discuss whether there are any lessons to be learned from the invasion ecology literature for studying plant pathogens that have free-living life history stages, and describe some experiments that we have used to explore the role of resident communities in altering rates of movement of plant pathogens through soil.</p>

<b>Number</b>	<b>S1.K2</b>
<b>Authors</b>	Vanessa Nessner Kavamura <sup>*1</sup> , Ian Clark <sup>1</sup> , Itamar Soares de Melo <sup>2</sup> , Tim Mauchline <sup>1</sup>
<b>Affiliations</b>	<sup>1</sup> Sustainable Agriculture Sciences, Rothamsted Research, West Common, Harpenden, Hertfordshire, AL5 2JQ, UK.
<b>Presenting author</b>	Vanessa Nessner Kavamura
<b>Email address</b>	<a href="mailto:vanessa.nessner-kavamura-noguchi@rothamsted.ac.uk">vanessa.nessner-kavamura-noguchi@rothamsted.ac.uk</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Insights into the rhizosphere microbiome: past and future perspectives
<b>Abstract text</b>	<p>Microorganisms associated to plants can promote plant growth and development through direct and/or indirect mechanisms in addition to enabling them to tolerate biotic and abiotic stresses. Several factors are responsible for shaping the microbiome associated with plants and understanding how they influence the structure and functions of microbial communities is crucial for the development of sustainable agriculture. Using culture-independent methods and soils from Rothamsted Research, I will describe the importance of different factors in determining the root microbiome structure and diversity in wheat. In addition, I will describe a culture-dependent approach that led to the development of a microbial product for maize. I also discuss gaps and benefits of taking a multidisciplinary approach to explore the plant microbiome to generate microorganism-based solutions for sustainable intensification of crop production.</p>

<b>Number</b>	<b>S1.1</b>
<b>Authors</b>	Sanne W.M. Poppeliers: Poppeliers, Sanne; Dr. Bas Dutilh: Dutilh, Bas; Prof. Dr. Corné Pieterse: Pieterse, Corné; Dr. Ronnie de Jonge: de Jonge, Ronnie
<b>Affiliations</b>	Utrecht University, Utrecht, Netherlands;
<b>Presenting author</b>	Sanne W.M. Poppeliers: Poppeliers, Sanne
<b>Email address</b>	<a href="mailto:s.w.m.poppeliers@uu.nl">s.w.m.poppeliers@uu.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Digging deep into <i>Arabidopsis thaliana</i> roots: quantifying the rhizosphere effect along a soil-to-root gradient
<b>Abstract text</b>	Plants secrete a complex array of organic compounds into the surrounding soil, the rhizosphere. Consequently, concentration gradients are established from the roots into the bulk soil. Since soil microbes benefit from the root exudates for their survival, rhizosphere microbial community composition follows the gradient of available compounds, oftentimes referred to as the rhizosphere effect. How microbial community composition differs along this soil-root gradient on a fine-grained scale has not been well described, yet such insights would allow us to underpin the critical, ecological rules underlying root community assembly. Therefore, here we harvested the roots of <i>Arabidopsis thaliana</i> plants grown in natural soil in a way such that we could interrogate community assembly across consecutive, fine-grained, 'compartments'. To this end, we stripped the roots of more and more soil and adhering microbes. We found that the strength of the rhizosphere effect is dependent on root proximity and that microbial communities closer to the roots harbour phylogenetically, physiologically, and likely, functionally redundant microbes. As we sampled closer to the roots, microbial community assembly became less random and clearly more driven by selection-based processes. Surprisingly, we observed that priority effects determined which specific microbes were found on individual plants, independent from starting conditions.

<b>Number</b>	<b>S1.2</b>
<b>Authors</b>	Odelade, Kehinde Abraham and Babalola, Olubukola Oluranti
<b>Affiliations</b>	North-West University, Mmabatho, South Africa
<b>Presenting author</b>	Babalola, Olubukola Oluranti
<b>Email address</b>	<a href="mailto:olubukola.babalola@nwu.ac.za">olubukola.babalola@nwu.ac.za</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Cowpea ecological niche harbored microbial phyla of varied nutrient preferences and metabolic properties
<b>Abstract text</b>	The microbial communities' diversity patterns of cowpea rhizosphere and the driving factors responsible for their compositions and structures are important for agricultural sustainability and improvement for food security. In this study, high throughput NovaSeq 6000 illumina sequencing was adopted to examine the variations in the bacterial, fungal and archaeal communities between winter season (WS) and summer season (SS). The bacterial distributions in SS with 98.06% relative abundance were higher than WS with 87.69%, while eukaryal distributions in WS with 11.11% relative abundance was higher than SS with 1.24%, and archaeal

	<p>distributions in SS with 0.57% relative abundance were higher than WS with 0.49%. Also, in the WS, Bacteroidetes, Proteobacteria, Firmicutes and Ascomycota composed of 70%, 8%, 7% and 6% relative abundance respectively, while in the SS, Proteobacteria, Actinobacteria, Bacteroidetes, Firmicutes, Verrucomicrobia, Planctomycetes, Acidobacteria, Ascomycota and Crenarchaeota were composed of 43%, 34%, 5%, 3%, 3%, 5%, 3% and 1% and 1% relative abundance respectively. Furthermore, the results showed that difference in the seasonal temperature and soil nutrients (pH, OM, organic C, Ca, total C, N, K, P and N-NH<sub>4</sub>) were responsible for differences in the microbial structural composition. The cowpea ecological niche could condone environmental variations under climate change situations.</p>
--	--

<b>Number</b>	<b>S1.3</b>
<b>Authors</b>	Kaur-Bhambra, Jasmeet ; Gubry-Rangin, Cecile
<b>Affiliations</b>	University of Aberdeen, UK
<b>Presenting author</b>	Kaur-Bhambra, Jasmeet
<b>Email address</b>	<a href="mailto:r03jb18@abdn.ac.uk">r03jb18@abdn.ac.uk</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Substantial variations in biological nitrification inhibition activity of different rice genotypes.
<b>Abstract text</b>	<p>The process of nitrification, mediated by ammonia-oxidising archaea (AOA) and ammonia oxidising bacteria (AOB), allows for conversion of ammonia to nitrate. Nitrification process determines the form of nitrogen available in soil and utilized by plants, having major implications on plant productivity and environmental quality. In heavily fertilised soils, nitrification leads to rapid loss of fertilizers, high nitrous oxide emissions contributing to global warming and groundwater pollution. Thus, reducing nitrification activity is paramount to increasing agronomic and environmental sustainability. There has been evidence of biological nitrification inhibition (BNI) activity in most staple crops including rice (<i>Oryza sativa</i>), an important food crop and the largest fertilizer consumer in Asia. Previous studies have shown an increased inhibition of AOA by BNIs in culture, on the other hand, an increased abundance of AOA was observed in rice paddy fields over time. We hypothesized that this could be due to variation in BNI activity within different rice genotypes. To test this, we analysed the effects of different rice genotypes with variable BNI inhibition capability on the growth and abundance of ammonia oxidisers in soils and in culture. We found that AOA and AOB growth was significantly more inhibited by high BNI producing rice genotypes when compared to that of low-BNI producing rice, both in soil and in culture.</p>

<b>Number</b>	<b>S1.4</b>
<b>Authors</b>	Song, Yang; Spooren, Jelle; Jongekrijg, Casper D.; Manders, J.H.H.; Jonge, Ronnie de; Pieterse, Corné M.J.; Bakker, Peter A.H.M.; Berendsen, Roeland L.
<b>Affiliations</b>	Plant-Microbe Interactions, Department of Biology, Utrecht University, Utrecht, NETHERLANDS
<b>Presenting author</b>	Song, Yang
<b>Email address</b>	<a href="mailto:Y.song1@uu.nl">Y.song1@uu.nl</a>
<b>Presentation type</b>	Oral

<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Echoes of the potato seed tuber microbiome
<b>Abstract text</b>	<p>Potatoes are commonly propagated vegetatively by transplanting seed tubers from one field to another. These tubers provide a nutrient rich habitat for microbes, some of which can severely impact plant performance. However, our understanding of potato tuber-associated microbiomes has lagged behind compared to root-associated microbiomes. In this study, we used 16S and ITS amplicon sequencing to characterize the microbiomes of potato seed tubers that were produced on different farms. We observed that potato tuber associated microbiomes are significantly affected by the potato genotype but also by the field in which the potato was produced. These differential tuber-associated microbiomes persisted during winter storage of the tubers. When seed tubers that were produced on different farms were planted in one field, the microbiomes of newly formed potato plant roots and tubers could be distinguished by their field of origin. However, we found little evidence of direct vertical inheritance of microbes that colonize the seed tuber surface to the daughter tuber or root. Furthermore, we analysed the microbial communities associated with different tuber compartments (peel, eye, heel end, flesh, and adhering soil), and observed significant differences in microbiome composition between the different compartments. When seed tubers were sprouted in the air under controlled conditions, specific members of the sprout associated microbiome were observed to be inherited from all compartments. Thus, potato seed tuber associated microbiomes leave their marks on rhizosphere and tuber associated microbiomes of plants that develop from these seed potatoes, but the driving cause of this effect is likely not a direct inheritance of specific microbes and remains to be elucidated.</p>

<b>Number</b>	<b>S1.5</b>
<b>Authors</b>	Gye-ryeong Bak, Ian Clark, Tim Mauchline
<b>Affiliations</b>	1. Rothamsted Research, Harpenden, United Kingdom 2. Highland Agriculture Research Institute, Pyeongchang, South Korea
<b>Presenting author</b>	Gye-ryeong Bak
<b>Email address</b>	<a href="mailto:gye-ryeong.bak@rothamsted.ac.uk">gye-ryeong.bak@rothamsted.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	The identification of the potato cv. Sumi core rhizosphere microbiota and network
<b>Abstract text</b>	<p>Plant microbiota is associated with plant health by carrying out resistance to biotic/abiotic stress and plant growth-promoting functions. Various factors influence plant microbiota including niche occupancy, environmental conditions, crop management, plant developmental stages, and crop varieties. Here, we identified the core and the network of potato rhizosphere microbiota associated with the cultivar Sumi, one of the most widely grown potato crops in South Korea. Soil and rhizosphere samples were collected at the flowering stage from three different regions and from two different pot trials. Based on ASVs, we carried out taxonomic assignment using QIIME2 from sequencing data of Illumina MiSeq amplicons with bacteria and fungi targeted primers. From the total of 15,706 bacterial ASVs and 4,089 fungal ASVs, 20 bacterial and 24 fungal ASVs were identified as core ASVs. Some of these taxa; Bradyrhizobium, Devosia, Fusarium, and Alternaria were also detected as major taxa of potato rhizosphere from previous studies. The resultant network analysis showed that 97% of edges are positively related to each other with rare interaction between bacteria and fungi. There are</p>

	three main taxa; Conexibacter, Mortierella, and Cladophialophora, described as hub taxa with 98% of degree, closeness and betweenness centrality.
--	---

<b>Number</b>	<b>S1.6</b>
<b>Authors</b>	Ren Wenzi; Penttilä Reijo; Kasanen Risto; Asiegbu Fred O.
<b>Affiliations</b>	University of Helsinki; Natural Resources Institute of Finland (Luke)
<b>Presenting author</b>	Ren Wenzi
<b>Email address</b>	<a href="mailto:wenzi.ren@helsinki.fi">wenzi.ren@helsinki.fi</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Bacteria community inhabiting <i>Heterobasidion</i> fruit body and associated wood of different decay classes
<b>Abstract text</b>	As little is known about the bacteria flora of <i>Heterobasidion's</i> perennial fruit body and the adhering wood tissue, we investigated the bacteria flora of its fruit body and adhering deadwood. An average of 52.6% of bacteria flora in fruit bodies were shared with the associated deadwood. The overall and unique OTUs had trends of decreasing from decay classes one to three but increasing in decay class four. Fruit body had the highest overall and unique OTUs number in the fourth decay class, while wood in the first. The functional analysis revealed nutrition, energy, degradation, and plant-pathogen-related functions of the communities. Our results also showed that bacteria communities in both substrates experienced a process of a new community re-construction through decay. The process was not synchronic in the two substrates, but the community structures and functions were well-differentiated in the final decay class. The bacteria community was highly dynamic, the flora activeness, community stability, and functions changed with the decay process. The third decay class was an important turning point for community re-structuring. Host properties, environmental factors, and microbial interactions jointly influenced the final community structure.

<b>Number</b>	<b>S1.7</b>
<b>Authors</b>	Holmes, Ashleigh; Jones, Susan; Watts, Lauren; Humphris, Sonia; Cheetam, Andrew; Toth, Ian
<b>Affiliations</b>	The James Hutton Institute, Dundee, UK; Ceres Agri Services, Fraserburgh, UK
<b>Presenting author</b>	Holmes, Ashleigh
<b>Email address</b>	<a href="mailto:ashleigh.holmes@hutton.ac.uk">ashleigh.holmes@hutton.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	Can microbiome profiles be used as an indicator of soil health to investigate the impacts from compaction and potato cropping
<b>Abstract text</b>	Soil compaction is a growing issue in soil health due to the intensification of farming and increased dependence on heavy machinery. The effects of compaction on the soil have been well documented, such as increasing mechanical resistance, but less is understood about the impact to the soil microbiome, where microbial richness and metabolically diverse species demonstrate a healthy soil. Soil compaction causes reduction in pore space and oxygen availability which can alter the metabolic activity of the soil, e.g denitrification of the soil, but may also lead to an increase in

	<p>pathogen populations that favour low oxygen conditions, eg <i>Pectobacterium</i> (blackleg) and <i>Spongospora</i> (powdery scab). These metabolic changes can impact the chemical composition of the soil, e.g. sulphur and calcium concentrations. Making targeted soil amendments to correct these changes, therefore, may help to reduce the negative effects of soil compaction on disease development.</p> <p>Over the next three years, this study aims to investigate the impact of soil amendments, such as organic matter and mineral rebalancing, applied to alleviate the effects of soil compaction on the microbiomes of bulk soil and potato rhizosphere and the incidence of potato and tuber diseases.</p>
--	--

<b>Number</b>	<b>S1.8</b>
<b>Authors</b>	Alegria Terrazas, Rodrigo <sup>1,2.</sup> , Reid, Tessa <sup>2.</sup> , Nesser-Kavamura-Noguchi, Vanessa <sup>2.</sup> , Rchiad, Zineb <sup>1.</sup> , Ndour, Papa Mamadou Sitor <sup>1,3.</sup> , Pawlett, Mark <sup>3.</sup> , Lyamlouli, Karim <sup>1.</sup> , Harris, Jim <sup>3.</sup> , Clark, Ian <sup>2.</sup> , Bargaz, Adnane <sup>1.</sup> , Mauchline, Tim <sup>2</sup>
<b>Affiliations</b>	1. Mohammed VI Polytechnic University, Agrobiosciences Program, Plant & Soil Microbiome Subprogram, Bengueurir, Morocco. 2. Rothamsted Research, Harpenden, UK. 3. School of Water, Energy and Environment, Cranfield University, Cranfield, UK
<b>Presenting author</b>	Alegria Terrazas, Rodrigo
<b>Email address</b>	<a href="mailto:rodrigo.alegria-terrazas@rothamsted.ac.uk">rodrigo.alegria-terrazas@rothamsted.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome assembly
<b>Title</b>	“Exploiting the rhizosphere microbiome diversity in the wheat Moroccan agroecosystem”
<b>Abstract text</b>	<p>Wheat is the most economically important crop and staple food grown in Morocco, across a variety of soils and agroclimatic conditions. The plant-soil interface, the rhizosphere, is inhabited by microbial communities with potential beneficial functions for plant growth.</p> <p>At heading stage, wheat plants and unplanted soils nearby were collected. To represent the wheat Moroccan agroecosystems, seven regions were selected, comprising four fields with five sampling points each containing in a pooled sample of five plants. In total 140 sampling points, from 28 fields of 7 regions were sampled. Illumina MiSeq generated 16S rRNA gene bacterial profiles of the rhizosphere and unplanted soils were analysed, in parallel to extensive soil physical and chemical characterization. Microbial and soil profiling information will be used as drivers of high throughput microbial isolation, functional characterization and genome sequencing that will allow us to construct high complexity bacterial synthetic communities from the chosen regions. This framework will facilitate experimental testing of hypothesis and selection of suitable consortia for crop’s inoculation. The final objective is to put into work the bacterial genetic diversity of Morocco to alleviate crop’s nutrient and environmental stresses. This research is supported by the OCP group.</p>

## Session 2: Plant microbiome communication

<b>Number</b>	<b>S2.K1</b>
<b>Authors</b>	Cara Haney
<b>Affiliations</b>	University of British Columbia
<b>Presenting author</b>	Cara Haney
<b>Email address</b>	<a href="mailto:Cara.haney@ubc.ca">Cara.haney@ubc.ca</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Plant-pathogen-mutualist interactions in the rhizosphere microbiome
<b>Abstract text</b>	Bacteria in the microbiome can have dramatically different effects on plant health and range from mutualists to pathogens. Using closely-related <i>Pseudomonas fluorescens</i> strains that include both opportunistic pathogens and mutualists, and the model plant <i>Arabidopsis</i> , we have dissected both plant and bacterial factors that determine the competitive outcomes of plant-pathogen-mutualist interactions. We have found that <i>Pseudomonas</i> strains that are closely-related to pathogens can protect plants from disease in a colonization-dependent manner. We have found that plants play a role in shaping the outcome and can distinguish closely-related <i>Pseudomonas</i> strains and mount an immune response specifically against pathogens. This work has shed light on both plant and bacterial factors that determine the competitive outcomes of host-pathogen-microbiome interactions.

<b>Number</b>	<b>S2.K2</b>
<b>Authors</b>	Kathrin Wippel
<b>Affiliations</b>	Max Planck Institute for Plant Breeding Research
<b>Presenting author</b>	Kathrin Wippel
<b>Email address</b>	<a href="mailto:wippel@mpipz.mpg.de">wippel@mpipz.mpg.de</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Origin of strains matters for SynCom-specific host responses in <i>Lotus japonicus</i> and <i>Arabidopsis thaliana</i>
<b>Abstract text</b>	Plant roots accommodate host species-specific bacterial communities. The ecological and molecular mechanisms by which those communities are assembled are still unclear. To study how commensals may have adapted to a plant species, we use synthetic communities (SynComs) of strains from our <i>Lotus japonicus</i> and <i>Arabidopsis thaliana</i> bacterial culture collections to let them compete for colonization of the two hosts in gnotobiotic experiments. We showed that there is host preference of commensal communities, where strains accumulate to higher abundances on their cognate host, and that they have a competitive advantage to invade established communities. To investigate the effect of bacterial adaptation to their host, we analyzed the transcriptional outputs of <i>Lotus</i> or <i>Arabidopsis</i> plants colonized by their native or non-native bacterial SynComs and observed a SynCom-specific host response. We found clusters of homologous genes in both hosts that were induced upon colonization by their native bacteria, which included known transcriptional regulators of plant immunity. In pathogenicity assays, inoculation with native or non-

	<p>native strains provided a differential protection against colonization by an opportunistic root pathogen. Moreover, the structure of the non-native community seemed to be more robust against pathogen challenge. To decipher the community-specific molecular interplay with the host, we analyzed root exudates after bacterial colonization. In addition, imaging studies with fluorescently tagged strains will provide insights into colonization patterns. Our findings advance our understanding of microbiota assembly, bacterial host adaptation, and are relevant for the design of successful field inocula.</p>
--	---

<b>Number</b>	<b>S2.1</b>
<b>Authors</b>	Bouwmeester, Harro
<b>Affiliations</b>	Plant Hormone Biology lab, Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, the Netherlands
<b>Presenting author</b>	Bouwmeester, Harro
<b>Email address</b>	<a href="mailto:h.j.bouwmeester@uva.nl">h.j.bouwmeester@uva.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Rhizosphere communication by plants drives MiCRopbiome recruitment
<b>Abstract text</b>	<p>Plants secrete a complex blend of thousands of molecules into the rhizosphere. The composition of this blend is highly plastic and is strongly affected by environmental conditions. With a few exceptions, however, we do not have a clue of the biological significance of the release into the soil of most of these molecules. The one or two exceptions, however, paint a picture of enormous complex and intricate relationships. This is illustrated by the strigolactones that were initially identified in the root exudate of just a few plant species and shown to be germination stimulants for root parasitic plants. Several decades later it was discovered that the strigolactones are present in all plants/plant root exudates and play an essential role in the interaction of plants with AM fungi and Rhizobium, symbiotic organisms that are essential in the acquisition of phosphorus and nitrogen by plants. Moreover, the production of strigolactones is upregulated under P and N deficiency, suggesting a 'cry for help' role.</p> <p>We study the biological relevance of the strigolactones and other metabolites exuded by plants into the soil. Our hypothesis is that many more of these molecules have a signaling role in the recruitment of beneficial micro-organisms. Intriguingly, the structural diversity in exuded metabolites suggests the existence of a belowground chemical arms race in which plants evolve specific signaling relationships with beneficial organisms, on which plant enemies listen in. This is illustrated by the large structural diversity in the strigolactones produced by plants, suggesting evolution of chemical diversity in order to ensure specificity. Indeed, in rice and sorghum we were able to demonstrate that different strigolactones recruit different root micro-organisms. I will discuss how we, in a number of projects including MiCRop (<a href="http://www.microp.org">www.microp.org</a>), use targeted and untargeted approaches to further unravel signaling relationships between a range of plant species from different families and the microbiome, particularly under stress. This will increase our understanding about the role of the plant and plant signaling in root microbiome recruitment and should result in tools that will help to optimize the use of beneficial micro-organisms in agriculture.</p>

<b>Number</b>	<b>S2.2</b>
<b>Authors</b>	Zhou, Jiayu 1,2; Uribe Acosta, Melissa 1; Qi, Run 1, de Jonge, Ronnie 1; Pieterse, Corné 1; Stringlis, Ioannis 1
<b>Affiliations</b>	1. Plant-Microbe Interactions, Department of Biology, Science4Life, Utrecht University, Utrecht, the Netherlands; 2. Institute of Botany, Jiangsu Province and Chinese Academy of Sciences, Nanjing, Jiangsu, China
<b>Presenting author</b>	Stringlis, Ioannis (Gioannis)
<b>Email address</b>	<a href="mailto:i.stringlis@uu.nl">i.stringlis@uu.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Interplay between <i>Arabidopsis</i> defenses and root associated microbes
<b>Abstract text</b>	Plant roots interact in soil with both pathogenic and beneficial microbes. Different structural (cutin, suberin, callose and lignin) and chemical (camalexin and glucosinolates) defense components are necessary to maintain a balanced interaction. Here, we screened Arabidopsis mutants for these defense components to find their involvement in sustaining beneficial plant-microbiome interactions following two approaches. First, we focused on the role of defense components in the interaction of Arabidopsis with beneficial rhizobacterium <i>Pseudomonas simiae</i> WCS417. Under in vitro conditions, we found that WCS417 led to reduced beneficial effects in selected mutants compared to wild-type plants. In some of them WCS417 root colonization was affected. Subsequent transcriptomic experiments on both the bacterial and plant side demonstrated a role of camalexin in bacterial chemotaxis and of other defense components on a balanced growth-defense trade off following colonization. In the second approach, we study the role of these defense components in plant-associated microbiome assembly. For this, we grew mutants in soil and harvested unplanted soil, rhizosphere soil and roots for microbiome analysis to identify microbiota enriched in each defense mutant compared to wild-type and in which compartment. Ultimately, we envision to unearth how selected defense components maintain the homeostasis between plants and their associated microbiome.

<b>Number</b>	<b>S2.3</b>
<b>Authors</b>	Shimels, Mahdere Z. 1; Elsayed Somayah S. 2; Thiombiano, Benjamin 3; Bouwmeester, Harro 3, Raaijmakers, Jos M. 1,2
<b>Affiliations</b>	1. Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands. 2. Institute of Biology, Leiden University, Leiden, Netherlands. 3Plant Hormone Biology, Swammerdam Institute for Life Sciences, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, The Netherlands.
<b>Presenting author</b>	Shimels, Mahdere Z.
<b>Email address</b>	<a href="mailto:M.Shimels@nioo.knaw.nl">M.Shimels@nioo.knaw.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Interruption of the life-cycle of the root parasitic weed <i>Striga hermonthica</i> by root-associated microbes
<b>Abstract text</b>	Sorghum is predominantly grown in areas with low rainfall and low soil fertility. Although sorghum is resilient to abiotic stresses, its production in Sub-Saharan

	<p>Africa faces substantial yield losses by the root parasitic weed <i>Striga hermonthica</i>. Current control measures are not singularly effective and have largely ignored the functional potential of the microbiome associated with sorghum roots. To harness the functional potential of root-associated microorganisms to interfere in the chemical communication between the host plant and <i>Striga</i>, we characterized taxonomically diverse bacterial species from Ethiopian soils for their abilities to suppress or stimulate <i>Striga</i> seed germination. To this end, we extracted root exudates from a <i>Striga</i>-susceptible sorghum genotype and tested if these indigenous bacterial species could grow in these exudates and metabolize specific <i>Striga</i> germination stimulants present in these root exudates. We identified several bacterial species that can disrupt this pre-attachment stage of the parasite's life cycle. Furthermore, we have substantial evidence that these microbe-associated phenotype is linked to compositional changes in the chemistry of the sorghum root exudates. Current work is focused on assessing the efficacy of these bacterial species to control <i>Striga</i> infections of sorghum and to disentangle the underlying mechanisms and genes involved in the signal interference.</p>
--	---

<b>Number</b>	<b>S2.4</b>
<b>Authors</b>	Schäfer, Martin; Vogel, Christine; Bortfeld-Miller, Miriam; Mittelviefhaus Maximilian; Vorholt, Julia
<b>Affiliations</b>	Institute of Microbiology, ETH Zurich, Zurich, Switzerland
<b>Presenting author</b>	Schäfer, Martin
<b>Email address</b>	<a href="mailto:martin.schaefer@biol.ethz.ch">martin.schaefer@biol.ethz.ch</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Mapping and characterizing bacterial interactions in the <i>Arabidopsis</i> phyllosphere
<b>Abstract text</b>	<p>The phyllosphere (aerial parts of plants) hosts a taxonomically structured bacterial community. Interactions between colonizing bacteria are one possible driver of community assembly. Here, we screened for interactions in a gnotobiotic model system by adding 200 strains individually to a 15-member synthetic community and tracked changes in community composition after plant colonization. We observed that most interactions were negative and phylogenetically closely related strains showed consistent effects on the 15-member community. The majority of interactions also manifested in minimal communities of two strains, suggesting binary interactions. However, we also found a higher order interaction that required the presence of at least three strains to emerge. A particularly promiscuous interaction was found between two members of the Actinobacteria. The presence of an Aeromicrobium strain resulted in a 50-fold reduction of Nocardioideis in planta. This inhibition was also observed in vitro and was due to bacterial lysis. Biochemical and genetic experiments resulted in the identification of a putative peptidase secreted by the Aeromicrobium strain. A mutant defective in this trait restored Nocardioideis colonization in planta, demonstrating that a direct bacteria-bacteria interaction was responsible for the population shift originally observed in the wildtype situation.</p>

<b>Number</b>	<b>S2.5</b>
<b>Authors</b>	Supakan Panturat, Alba Pacheco-Moreno, Sanu Arora, Jacob Malone
<b>Affiliations</b>	John Innes Centre
<b>Presenting author</b>	Supakan Panturat

<b>Email address</b>	<a href="mailto:supakan.panturat@jic.ac.uk">supakan.panturat@jic.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Exploring close-rotation microbiome dysbiosis in legumes
<b>Abstract text</b>	<p>Legumes are a nutrient-rich food crop and an important part of crop rotation cycles. However, a major problem for increasing legume production is the decline in yield caused by close rotation. In a previous study, pea was found to have a significantly higher rhizosphere effect compared to wheat and oat. Thus, the soil microbial community is a key factor that should be considered to maximise productivity. In our study, the effect of soil microbiome on yield was investigated by re-planting pea seeds (<i>Pisum sativum hakuna</i>) using the same soil throughout three harvests. After the second harvest, we observed significant yield loss and negative changes in overall plant health. To investigate further, <i>Rhizobium</i> spp. and <i>Pseudomonas</i> spp. isolated from the rhizosphere were subjected to high-throughput phenotyping assays, and nodulation efficiency was determined by quantification of the <i>nodD</i> gene in soil gDNA samples using qPCR. Our results showed an increase in both <i>nodD</i> and the soil <i>Rhizobium</i> population over the course of the three rotations. Our data suggest that despite increased potential for N-fixing symbiosis, close rotation still leads to soil-microbe induced loss of pea yield and health. Understanding the dynamic interactions within soil microbiota could be a promising strategy for better crop productivity.</p>

<b>Number</b>	<b>S2.6</b>
<b>Authors</b>	Sébastien Jaupitre, Harro Bouwmeester, Lemeng Dong
<b>Affiliations</b>	University of Amsterdam
<b>Presenting author</b>	Sébastien Jaupitre
<b>Email address</b>	<a href="mailto:sebastien.jaupitre@gmail.com">sebastien.jaupitre@gmail.com</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Signaling molecules in the root exudates of cucumbers shape the rhizosphere microbiome under herbivory stresses
<b>Abstract text</b>	<p>The soil abounds with microbial communities displaying a large array of functions able to change soil properties and help the development and stress resilience of the plants. Plants create ecological niches around their root systems for the microbes to thrive and modify them when adapting to environmental stresses using chemical communication. Here we aimed at studying these interactions in the context of biotic stresses in the Cucurbitaceae family with a focus on herbivory feeding on the plants.</p> <p>Several studies have shown that microbes can induce systemic resistance against pests in plants. However, the mechanisms behind resistance-inducing-microbiome recruitment remain obscure and many questions are still pending. To further investigate this interspecies interaction, we grew plants under stress conditions and measured the chemical composition of their root exudates while quantifying the changes in microbial communities. Using omics data integration tools, we aimed at linking molecules from the plants to specific microbial functions. We found that the diversity of the microbial communities in the rhizosphere was significantly increased</p>

	under stress conditions. Additionally, we identified several signalling molecules showing differential abundance between treatments from which we measured their expression profile over time.
--	--

<b>Number</b>	<b>S2.7</b>
<b>Authors</b>	Sanchez-Gil, Juan José; Poppeliers, Sanne; Pieterse, Corné; Dutilh, Bas; de Jonge, Ronnie
<b>Affiliations</b>	Utrecht University, Utrecht, The Netherlands
<b>Presenting author</b>	Sanchez-Gil, Juan José
<b>Email address</b>	<a href="mailto:j.j.sanchezgil@uu.nl">j.j.sanchezgil@uu.nl</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Myo-inositol metabolism enhances rhizosphere competence of root-associated <i>Pseudomonas</i>
<b>Abstract text</b>	The rhizosphere environment comprises the plant roots and the soil layer surrounding them. There, rhizodeposition triggers the assembly of a distinct and complex microbiome, whose composition is greatly determined by the functional potential of the microbes in the surrounding soil. These microbes harbour genetic factors that allow them to colonise and persist in the rhizosphere, an ability known as rhizosphere competence. Studying the genetic determinants of highly competent organisms can help us define the molecular basis of rhizosphere microbiome assembly and build a mechanistic understanding of the process. Here, we selected a set of root-associated isolates from the <i>Pseudomonas</i> genus, which commonly dominates rhizosphere communities, based on their ability to colonise <i>Arabidopsis thaliana</i> roots in natural soil. We identified a conserved gene cluster involved in myo-inositol catabolism, the <i>iol</i> locus, as an enriched feature among the best colonisers. In root colonisation assays <i>in vitro</i> , <i>P. protegens</i> CHA0 $\Delta$ <i>iol</i> mutants showed impaired root colonisation capabilities. Remarkably, myo-inositol supplementation of minimal medium does not alter growth dynamics, but instead we observed an induction of swimming and twitching motility. These results suggest a relevant role for plant-derived myo-inositol, an important exudate, in determining rhizosphere competence of <i>Pseudomonas</i> isolates.

<b>Number</b>	<b>S2.8</b>
<b>Authors</b>	Thoenen Lisa 1,3, Kreuzer Marco2, Matteo Pierre1, Zuest Tobias4, Hecht Mirco1, Bruggmann Rémy2, Erb Matthias1, Schlaeppli Klaus3
<b>Affiliations</b>	1 Institute of Plant Sciences, University of Bern, Bern, Switzerland; 2 Interfaculty Bioinformatics Unit, University of Bern, Bern, Switzerland; 3 Department of Environmental Sciences, University of Basel, Basel, Switzerland; 4 Department of Systematic and Evolutionary Botany, University of Zuerich, Zuerich
<b>Presenting author</b>	Schlaeppli Klaus
<b>Email address</b>	klaus.schlaeppli@unibas.ch
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant microbiome communication
<b>Title</b>	Exudate-microbiome interactions on Maize roots

**Abstract text**

Plants secrete a complex array of compounds that have many functions including to act as semiochemical for the recruitment of specific microbes, to serve as carbon substrates for microbial growth, or to structure the composition of the microbiome. Mechanistically however, relatively little is known how root microbes deal and cope with specialized plant exudates. Here we investigated toxicity, tolerance, and metabolization of plant-derived Benzoxazinoids, a group of bioactive and antimicrobial secondary metabolites of grasses including crops such as maize. We have built a culture collection of maize root bacteria to study their growth and metabolic capabilities towards benzoxazinoids. Using synthetic community experiments we discovered that the maize root microbiota divided labor and cooperated in the degradation and metabolization of Benzoxazinoids. We further found a high functional specialization in metabolizing the typical secondary metabolites of their native host. Our work points to microbial adaptation to host-specific exudates, which could explain the composition host-specific microbiomes.

## Session 3: Biotic and abiotic stress tolerance

<b>Number</b>	<b>S3.K1</b>
<b>Authors</b>	Robert Jackson
<b>Affiliations</b>	University of Birmingham
<b>Presenting author</b>	Robert Jackson
<b>Email address</b>	<a href="mailto:r.w.jackson@bham.ac.uk">r.w.jackson@bham.ac.uk</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Examining the emergence of host-adapted phytopathogens via the role of mobile genetic elements
<b>Abstract text</b>	Bacteria are an important component of plant microbiomes and they interact with a wide range of microbial neighbours on and within plants. Some bacteria are harmless or provide a service to the plant whilst pathogenic bacteria exploit plants for nutrients, reproduction and dispersal. Bacterial evolution to these lifestyles is complex and shaped by a wide range of factors including the host and environment, but neighbouring microbes can be a rich source of genetic material that can move between host cells. In this talk, I will outline the study of <i>Prunus</i> (cherry) – <i>Pseudomonas</i> interactions, including non-pathogenic epiphytes, to study the evolution of bacterial pathogens.

<b>Number</b>	<b>S3.K2</b>
<b>Authors</b>	Matthew T. Agler
<b>Affiliations</b>	Friedrich-Schiller University of Jena
<b>Presenting author</b>	Matthew T. Agler
<b>Email address</b>	<a href="mailto:matthew.agler@uni-jena.de">matthew.agler@uni-jena.de</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Insights from wild leaf microbiomes: Can promoting microbial diversity contribute to plant health?
<b>Abstract text</b>	Leaves are constantly exposed to attack from external threats like herbivory and pathogens, making them the front lines of plant defense. While plant immunity can be highly effective, microbial colonizers extend immune phenotypes by playing important roles in determining plant susceptibility. Therefore, finding host factors that directly structure leaf microbiomes in beneficial ways has been a holy grail for microbiome researchers. However, our success in this has so far been marginal. One possibility is that the motivations of the plants we are studying don't match exactly our motivations. Here, I will discuss our recent findings, where we have observed that some host defenses seem to shape microbiome beta-diversity (variation between individuals) in predictable ways. Our data support the idea that beta diversity could protect plants by presenting leaf invaders and colonizers with a complex, less predictable environment.

<b>Number</b>	<b>S3.1</b>
<b>Authors</b>	Costa, Lilian S A S (1,4); Faria, Mírian R de (1); Chiaramonte, Josiane B (1); Mendes, Lucas W (2); Sepo, Edis (3); Hollander, Mattias de (4); Fernandes, José M C (5); Carrion, Victor J (3); Bettiol, Wagner (1); Raaijmakers, Jos M (3,4); Mendes, Rodrigo (1).
<b>Affiliations</b>	(1) Embrapa Environment, Jaguariúna Brazil; (2) Center for Nuclear Energy in Agriculture, University of Sao Paulo, Piracicaba, Brazil; (3) Leiden University, Leiden, The Netherlands; (4) Netherlands Institute of Ecology NIOO-KNAW, Wageningen, The Netherlands; (5) Embrapa Wheat, Passo Fundo, Brazil.
<b>Presenting author</b>	Mendes, Rodrigo
<b>Email address</b>	<a href="mailto:rodrigo.mendes@embrapa.br">rodrigo.mendes@embrapa.br</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Repeated exposure of wheat to the fungal root pathogen <i>Bipolaris sorokiniana</i> affects rhizosphere microbiome assembly and disease suppressiveness
<b>Abstract text</b>	Soil-borne pathogens induce plant disease suppression by enriching members and activating functions in the rhizosphere microbiome. This is observed in disease suppressive soils, which show a remarkable ability to naturally suppress plant diseases caused by pathogens. Here, we selected two wheat genotypes, contrasting for <i>Bipolaris sorokiniana</i> resistance, to study how the pathogen affects the rhizosphere microbiome. As expected, the cultivation of the susceptible wheat led to a significant reduction in disease severity after five successive cultivation cycles. Conversely, the resistant genotype showed the opposite pattern, increasing disease severity over cycles. While bacterial families <i>Chitinophagaceae</i> , <i>Anaerolineaceae</i> and <i>Nitrosomonadaceae</i> are associated with disease suppression in the susceptible wheat (fourth cycle), <i>Chitinophagaceae</i> and <i>Comamonadaceae</i> are associated with disease resistance in the resistant plant genotype (first cycle). Metagenome analysis revealed that 604 BGCs, out of 2,571 identified by AntiSMASH analysis, were overrepresented during disease suppression in the rhizosphere of the susceptible plant genotype. These BGCs are associated with biosynthesis of terpenes, non-ribosomal peptides, polyketides, aryl polyenes and post-translationally modified peptides. The understanding of the rhizosphere microbiome dynamics during disease suppression allows the identification of key microbes and functions to be used in novel strategies to control soil-borne fungal pathogens. (Support FAPESP 2020/00469-2; 2019/12330-1; 2016/13754-1)

<b>Number</b>	<b>S3.2</b>
<b>Authors</b>	Pfeilmeier, Sebastian; Petti, Gabriella; Bortfeld-Miller, Miriam; Daniel, Benjamin; Field, Christopher; Sunagawa, Shinichi; Vorholt, Julia
<b>Affiliations</b>	ETH Zurich, Zurich, Switzerland
<b>Presenting author</b>	Pfeilmeier, Sebastian
<b>Email address</b>	<a href="mailto:spfeilme@ethz.ch">spfeilme@ethz.ch</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	The interplay between the leaf microbiota, plant immunity and opportunistic pathogens
<b>Abstract text</b>	The plant microbiota affects host health and fitness. However, it is unclear how the plant shapes its leaf microbiota and what role plant immunity plays in this process.

	<p>We identified the NADPH oxidase RBOHD to be required for maintaining microbiota homeostasis in <i>Arabidopsis thaliana</i>. The <i>rbohD</i> knockout resulted in a microbiota shift due to an enrichment of specific bacteria and plant disease. Screening of individual microbiota members for pathogenic potential revealed opportunistic <i>Xanthomonas</i> pathogens that colonized wild-type plants asymptotically but caused disease in <i>rbohD</i> plants. Strain dropout experiments revealed that the lack of RBOHD unlocks the pathogenic potential of <i>Xanthomonas</i> driving dysbiosis in <i>rbohD</i> plants. We can mimic the enrichment of specific bacteria during dysbiosis in binary plant colonization experiments and have identified virulence factors that contribute to the genotype-dependent pathogenicity of <i>Xanthomonas</i>. Overall, our results show that opportunistic pathogens are key players for leaf microbiota assembly and plant health.</p>
--	--

<b>Number</b>	<b>S3.3</b>
<b>Authors</b>	Siyu Song(1), Zayda Morales Moreira(1), Xuecheng Zhang(2), Andrew C. Diener(2), and Cara H. Haney(1)
<b>Affiliations</b>	(1)University of British Columbia, Vancouver, BC, CANADA, (2)Massachusetts General Hospital, Boston, MA, USA
<b>Presenting author</b>	Siyu Song
<b>Email address</b>	<a href="mailto:siyu.song@ubc.ca">siyu.song@ubc.ca</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	PSKR1 helps recruit <i>Pseudomonas fluorescens</i> to the plant rhizosphere microbiome
<b>Abstract text</b>	<p>Beneficial members of the rhizosphere microbiome provide diverse benefits to plants, including growth promotion and enhanced resistance. However, how plants recruit beneficial microbes while preventing microbial overgrowth remains largely unknown. By rescreening an <i>Arabidopsis</i> mutant collection with altered root immune signaling, combined with bulk segregant analysis and next-generation sequencing, we identified a PSKR1 mutant allele <i>hsm7</i> that exhibits reduced beneficial <i>Pseudomonas fluorescens</i> WCS365 colonization in the rhizosphere. Microbiome sequencing with <i>pskr1-3</i> and the over-expression line 35S:PSKR1-GFP suggests that plant PSKR1 expression level correlates with the relative abundance of <i>Pseudomonas</i> in the rhizosphere without causing phylum-level microbiota dysbiosis. Through transcriptional profiling, we found that PSKR1 may balance growth and defence by suppressing salicylic acid (SA) responsive defense gene expression while promoting growth through photosynthesis and cell expansion. Further tests with SA biosynthesis and perception mutants suggest that SA signaling inhibits beneficial <i>P. fluorescens</i> colonization through both regulating plant defense and metabolism. Furthermore, we also found that <i>P. fluorescens</i> WCS365 strongly induces PSKR1 expression in the root, as a potential strategy to manipulate plant response and benefit its colonization in the rhizosphere. Collectively, our data demonstrate that through suppressing SA-mediated defense responses and promoting root growth, PSKR1 recruits beneficial <i>P. fluorescens</i> to plant rhizosphere microbiome.</p>

<b>Number</b>	<b>S3.4</b>
<b>Authors</b>	Van Bentum, Sietske; Van Pelt, Hans A.; Bakker, Peter A.H.M. ; Pieterse, Corné M.J., Berendsen, R.L.
<b>Affiliations</b>	Utrecht University, Utrecht, The Netherlands
<b>Presenting author</b>	Van Bentum, Sietske

<b>Email address</b>	<a href="mailto:s.vanbentum@uu.nl">s.vanbentum@uu.nl</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Selecting microbes in the field: mycorrhiza depletion in naturally-infected soybean plants
<b>Abstract text</b>	<p>The demand for higher crop yields and urgent need for sustainable practices call for innovative solutions, where plant-beneficial microbes can play an important role. Microbes can strongly influence plant health, and plants have been shown to modulate their rhizosphere microbiome in response to attack. The model plant species <i>Arabidopsis thaliana</i> was previously found to recruit a small consortium of disease resistance-inducing microbes upon pathogen infection. Here, we study changes in the soybean rhizosphere (<i>Glycine max</i>) to identify beneficial microbes associated with this economically-important crop. Healthy and diseased soybean plants were sampled from two commercial fields in the Netherlands. The presence of Soybean Mosaic Virus (SMV) was confirmed in leaf material of infected plants, presenting the first official occurrence of this virus in the Netherlands. Based on amplicon sequencing, both bacterial and fungal rhizosphere communities were distinct between healthy and SMV-infected plants. In each field, more than 200 bacterial features were differentially abundant between healthy and infected plants, of which only a small and taxonomically diverse set was enriched on SMV-infected plants. In one field, mycorrhizal features were clearly enriched on healthy plants. We are currently testing whether mycorrhiza and plant nutritional status affect the resistance of soybean to SMV.</p>

<b>Number</b>	<b>S3.5</b>
<b>Authors</b>	Lund, George <sup>1</sup> ; Mosquito, Susan <sup>1</sup> ; Hughes, David <sup>2</sup> ; Withall, David <sup>3</sup> ; Clark, Ian <sup>1</sup> ; Rudd, Jason <sup>3</sup> ; Mauchline, Tim <sup>1</sup>
<b>Affiliations</b>	1 Sustainable Agricultural Sciences, Rothamsted Research, Harpenden, UK, AL5 5NX. 2 Computational and Analytical Sciences, Rothamsted Research, Harpenden, UK, AL5 5NX. 3 Biointeractions and Crop Protection, Rothamsted Research, Harpenden, UK, AL5 5NX.
<b>Presenting author</b>	Lund, George
<b>Email address</b>	<a href="mailto:george.lund@rothamsted.ac.uk">george.lund@rothamsted.ac.uk</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Microbial natural product discovery pipeline for next generation fungicides effective against <i>Z. tritici</i>
<b>Abstract text</b>	<p>Wheat is the UK's most widely grown crop, but yield is diminished due to diseases caused by pathogenic fungi. The most important disease of wheat in the UK is <i>Septoria tritici</i> blotch, caused by the fungus <i>Zymoseptoria tritici</i>, resulting in up to 50% yield losses. Wheat has no resistance to infection - the fungus has become insensitive to all known classes of fungicides and new ways to protect wheat are urgently needed.</p> <p><i>Pseudomonas fluorescens</i> are ubiquitous, psychrophilic gram-negative bacteria that can act as biocontrol agents of a range of plant pathogens and produce a range of antimicrobial compounds. Relatively little work has investigated the ability of <i>P. fluorescens</i> to inhibit <i>Z. tritici</i>, with four antifungal compounds previously reported in literature. <i>Pseudomonas</i> bacteria possess a largely untapped diverse secondary</p>

	<p>metabolite repertoire, which has potential for the discovery of new high value fungicides.</p> <p>Using a combination of a newly developed high-throughput in vitro screening methodology, genome-mining approaches, and gene disruption, we are working to identify and characterise bacterial secondary metabolite biosynthetic gene clusters involved in the interaction between antagonistic <i>Pseudomonas</i> isolates and <i>Z. tritici</i>. These combined approaches may lead to novel mechanisms to control <i>Z. tritici</i>.</p>
--	---

<b>Number</b>	<b>S3.6</b>
<b>Authors</b>	Bhardwaj Priyanka <sup>1,2</sup> , Jain Rahul <sup>1</sup> , Kumar Sanjay <sup>1</sup>
<b>Affiliations</b>	1. Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology, Palampur- 176061, Himachal Pradesh, India, 2. Academy of Scientific and Innovative Research, Ghaziabad, Uttar Pradesh- 201002, India
<b>Presenting author</b>	Bhardwaj Priyanka
<b>Email address</b>	<a href="mailto:pari169396@gmail.com">pari169396@gmail.com</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Beneficial endophytes of a cold desert plant, <i>Arnebia euchroma</i> alleviate cold stress tolerance in <i>Arabidopsis</i>
<b>Abstract text</b>	<p>The mutualism of plants with endophytic microorganisms often leads to several benefits to its host including plant health and survival under extreme conditions. <i>Arnebia euchroma</i> is an endangered medicinal plant that grows naturally in extreme cold and arid environments in the Himalayas. The present study was conducted to decipher the endophytic diversity associated with <i>A. euchroma</i> and to explore the role of endophytes under low temperature (LT) stress conditions. A total of 60 bacteria and 33 fungi including nine yeasts were isolated and characterized at the molecular level. Among these, Proteobacteria was the most abundant bacterial phylum with the dominance of Gammaproteobacteria (76.67%) and genus <i>Pseudomonas</i>. Ascomycota was the most abundant fungal phylum (72.73%) dominated by class Eurotiales (42.42%) and genus <i>Penicillium</i>. Leaf tissues showed a higher richness (Shao1) of endophytes as compared to root tissues. Isolated endophytes displayed plant growth promotion through phosphorus and potassium solubilisation, ACC deaminase, indole acetic acid and siderophore production. Among all, an auxin and salicylic acid producing yeast namely <i>Naganishia liquefaciens</i> strain ARY7, previously reported from deep-sea Japan trench (Han et al., 2020), was investigated for its role in conferring LT (10°C) tolerance in <i>Arabidopsis</i>. Interestingly, ARY7 treated plants showed enhanced plant performance and biomass as compared to un-inoculated plants at LT suggesting a reduced sensitivity of inoculated plants to LT. Furthermore, biochemical assays, gene expression and metabolome analysis of inoculated plants are under process. The present study provides insights to explore plant-endophyte interaction to alleviate cold stress in crops and medicinal plants.</p>

<b>Number</b>	<b>S3.7</b>
<b>Authors</b>	Abedini Davar, Bouwmeester Harro, Dong Lemeng
<b>Affiliations</b>	Plant Hormone Biology Group, Green Life Sciences Cluster, Swammerdam Institute for Life Science, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, The Netherlands

<b>Presenting author</b>	Abedini Davar
<b>Email address</b>	<a href="mailto:d.abedini@uva.nl">d.abedini@uva.nl</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Nitrogen deficiency results in changes in the microbiome composition and functionality in tomato rhizosphere
<b>Abstract text</b>	<p>Nitrogen (N) is a critical element for plant growth and development and plants have evolved a number of different strategies to deal with N deficiency. One of these, the recruitment of plant growth-promoting bacteria (PGPB) is a fascinating example of such strategies. In legumes, for example, symbiotic Rhizobia are recruited and fix atmospheric nitrogen (N<sub>2</sub>) into ammonia that can be utilized by the plant. The strategy used by non-legume species to mitigate N deficiency is less well explored. In this study, an aeroponics system was adopted to allow us to grow tomato plants under well-controlled, N deficient, conditions and allowing for time-resolved sampling. High-throughput 16S rRNA and ITS sequencing data of the root microbiome revealed that N deficiency strongly changed the root bacterial <math>\alpha</math>- and <math>\beta</math>-diversity. The microbial composition displayed clear changes over time and with N availability. Specifically, tomato plants growing under N-free conditions recruited N-fixing bacteria from Comamonadaceae and Rhizobiaceae families. Functional prediction by PICRUSt2 revealed a clear enrichment of N cycling genes/enzymes such as nitrogenase and amino acid-ammonia lyase under N deficiency. These results demonstrate that tomato plants recruit beneficial microbes involved in N cycling to overcome N deficiency. These findings may facilitate further developments towards a more sustainable agriculture.</p>

<b>Number</b>	<b>S3.8</b>
<b>Authors</b>	Macdonald, Ashleigh; Crozier, Louise; Holden, Nicola; Preston, Gail
<b>Affiliations</b>	Macdonald, Ashleigh and Preston, Gail: University of Oxford, Oxford, UK; Crozier, Louise: Food Standards Scotland, Aberdeen, UK; Holden, Nicola: Scotland's Rural College, Aberdeen, UK
<b>Presenting author</b>	Macdonald, Ashleigh
<b>Email address</b>	<a href="mailto:ashleigh.macdonald@linacre.ox.ac.uk">ashleigh.macdonald@linacre.ox.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Ozone-Mediated Control of Food Spoilage and Food-Borne Pathogens
<b>Abstract text</b>	<p>Post-harvest produce is subject to contamination by food spoilage and food-borne pathogens, and this is controlled in the food industry by surface sanitation steps. Disinfectants, which are currently used for this, can form toxic compounds, therefore ozone, which is a form of reactive oxygen species (ROS), may be a better alternative because it kills a broad range of micro-organisms without the formation of toxic residues. The use of ozone in the food industry has been limited because it is harmful to human health if inhaled, however in-pack ozone technology, developed at Glasgow University, mitigates the risks associated with ozone by containing the ozone within a sealed pack. The aim of the project is to investigate if in-pack ozone technology can be used to control plant and food-borne pathogens in the food industry. It was first important to determine how ozone impacted the native microbial community of post-harvest produce, therefore a large-scale 16S rRNA experiment was completed. Results showed that in-pack ozone technology</p>

	altered the microbiome of the tomato calyx and pedicel by causing significant changes in the abundance of specific genera.
--	--

<b>Number</b>	<b>S3.9</b>
<b>Authors</b>	Uribe Acosta, Melissa 1*. Beschoren da Costa, Pedro 2*. Aragón Gómez, Marcela 2*. Carracedo Lorenzo, Zulema 2,3*. Zhou, Xing 1,4. Spooren, Jelle 1. van Bentum, Sietske 1. Gols, Rieta 2. Kloth, Karen 2. Karlova, Romyana 3. Testerink, Christa 3. Berendsen, Roeland R.L. 1. Dicke, Marcel 2. Pieterse, Corné M.J. 1. Stringlis, Ioannis A. 1.
<b>Affiliations</b>	*Shared first authors 1 Plant-Microbe Interactions, Department of Biology, Utrecht University, Utrecht, the Netherlands 2 Laboratory of Entomology, Wageningen University, Wageningen, the Netherlands 3 Laboratory of Plant Physiology, Wageningen University, Wageningen, the Netherlands 4 School of Geography Science, Nanjing Normal University, Nanjing, China
<b>Presenting author</b>	Uribe Acosta, Melissa.
<b>Email address</b>	<a href="mailto:m.uribeacosta@uu.nl">m.uribeacosta@uu.nl</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	"Cry for help" upon pathogen attack across plant lineages
<b>Abstract text</b>	Under pathogen attack of the leaves, <i>Arabidopsis thaliana</i> recruits beneficial root-associated microbiota that can stimulate the plant immune system against the invader, a phenomenon termed "cry for help". The host-genotype can affect microbiome assembly in the absence of stress, but it's unknown whether microbiome recruitment to pathogen attack across plant lineages is conserved. Therefore, we treated 10 members of the Brassicaceae family with salicylic acid (SA), to mimic pathogen attack, and compared their growth response in vitro to that of <i>Arabidopsis</i> . We observed that all species, apart from <i>Brassica oleraceae</i> , showed significantly affected growth in response to SA, suggesting that the different species are responsive to SA. We then studied in soil if root microbiome recruitment upon foliar treatment with SA across 33 plant species, mostly Brassicaceae, would also vary in a phylogenetic dependent manner. Preliminary Beta-diversity analyses indicate that most species, but not all, assemble different microbial communities as a response to the hormone treatment. Our next analyses will reveal which specific taxa are being recruited and whether we can identify a plant phylogenetic signature in this response. In follow-up experiments we will test whether these microbes can better prepare different plant species for pathogen attack.

<b>Number</b>	<b>S3.10</b>
<b>Authors</b>	Ramirez-Villacis, Dario X. 1,2,3; Tello, Cristina 4; Rivadeneira, Jorge 4; Leon-Reyes; Antonio3, Pieterse, Corné 2; Raaijmakers, Jos M.1
<b>Affiliations</b>	1 Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands. 2 Plant-Microbe Interactions, Department of Biology, Science for Life, Utrecht University, Utrecht, Netherlands. 3 Laboratorio de Biotecnología Agrícola y de Alimentos, Universidad San Francisco de Quito USFQ, Quito, Ecuador. 4 Instituto Nacional de Investigaciones Agropecuarias – INIAP. Est. Exp. Santa Catalina, Quito, Ecuador
<b>Presenting author</b>	Ramirez-Villacis, Dario X.
<b>Email address</b>	<a href="mailto:d.ramirez@nioo.knaw.nl">d.ramirez@nioo.knaw.nl</a>

<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	A walk on the wild side: exploring the functional potential of Andean soil microbiomes to enhance tolerance of potato to late blight disease
<b>Abstract text</b>	Plant domestication is a complex process affecting plant genetics, plant phenotype and habitat relocation collectively referred to as the domestication syndrome. How these changes impact the microbiome and their functions is largely unknown for most plant species. Here, we studied the impact of domestication on the potato microbiome and tolerance to late blight disease caused by the oomycete pathogen <i>Phytophthora infestans</i> . For the experimental work, we collected native and agricultural soils from 14 sites along the Ecuadorian Andes and brought these soils to the greenhouse for controlled bioassays. Potato plants (var. Superchola) were grown in these soils and after 6 weeks challenged with <i>P. infestans</i> . Although differences in growth between potato plants grown in native and agricultural soils were not significant, we observed that potato plants grown in native soil suffered, overall, less from late blight than plants grown in agricultural soils. Collectively, these results show the functional potential of native soils to enhance crop resilience to a specific disease. The potential contribution of the soil and root microbiome to this disease-suppressive phenotype is currently analyzed and will be presented at the meeting.

<b>Number</b>	<b>S3.11</b>
<b>Authors</b>	Thornton, Owen (1,2), Barrett, Glyn (2), Clark, Ian (1), Jackson, Robert (2,3), Mauchline, Tim (1).
<b>Affiliations</b>	1: Rothamsted Research, Harpenden, UK. 2: University of Reading, Reading, UK. 3: University of Birmingham and Birmingham Institute of Forest Research (BIFOR), Birmingham, UK.
<b>Presenting author</b>	Thornton, Owen
<b>Email address</b>	<a href="mailto:owen.thornton@rothamsted.ac.uk">owen.thornton@rothamsted.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Bio-Prospecting For Plant-Growth-Promoting Microbes: Rich Seams in Long-Term Agricultural Field Experiments?
<b>Abstract text</b>	Naturally occurring soil microbes – especially the subset that can live associatively with plant roots – offer the potential to contribute to the sustainable intensification of agriculture by a variety of means, including the suppression of plant diseases and provision of limiting nutrients. However, the effects of different agricultural management practices and cropping systems on the proliferation of particular sets of microbes may determine the manifestation of these beneficial functions. The design of the Broadbalk winter wheat experiment at Rothamsted has ensured that a diverse range of biotic and abiotic selective pressures associated with each of the many combinations of these treatments have acted continuously on resident soil microbes over the last 175+ years. Moreover, crop plants repeatedly cultivated under these specific conditions may promote or suppress specific members of their associated microbial communities accordingly, further increasing the diversity of relevant plant-microbe associations fostered by the experiment. High-throughput in vitro characterisation of a library of ~5000 root-associated microbes recently isolated from a limited selection of Broadbalk treatment plots has begun to reveal the distribution of key functional traits and will enhance our interpretation of a

	comprehensive field-wide amplicon sequencing survey aimed at dissecting the determinants of effective microbial plant-growth-promotion in the field.
--	--

<b>Number</b>	<b>S3.12</b>
<b>Authors</b>	Arhazzal Mahassine 1, 2, 3, Nessner Kavamura Vanessa 1, Clark Ian 1, Harris Jim 2, Pawlett Mark 2, Bargaz Adnane 3, Mauchline Tim1
<b>Affiliations</b>	1, Rothamsted Research, Harpenden. 2, Cranfield University. 3, Mohammed VI Polytechnic University
<b>Presenting author</b>	Arhazzal Mahassine
<b>Email address</b>	<a href="mailto:mahassine.arhazzal@rothamsted.ac.uk">mahassine.arhazzal@rothamsted.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Biotic and abiotic stress tolerance
<b>Title</b>	Does wheat select for beneficial soil microbiome when grown under abiotic stresses?
<b>Abstract text</b>	<p>Drought, salinity, and soil degradation are challenges facing African agriculture under climate change and unsustainable agricultural practices. Plants live in association with diverse microbes which can potentially increase plant abiotic stress tolerance, reduce plant disease incidences, as well as sustainably enhance nutrient availability. Previous research showed that the introduction of dwarfing wheat cultivars during the Green Revolution, increased yields, but may affect the composition of the root microbiome, potentially resulting in reduced selection of plant growth-promoting rhizobacteria. This work investigates the ability of 6 different wheat (<i>Triticum aestivum</i>) cultivars (3 tall, 3 short) to select for beneficial root microbiomes when grown under abiotic stresses (drought or salt tolerance) with and without fertilisers. To analyse the plant microbiome, culture independent and dependent methods will be adopted. The culture independent approach involves next generation amplicon sequencing of the 16S rRNA gene and ITS region. In contrast, culture dependent approaches involve the isolation, identification and functional screening (nutrient solubilization activity and abiotic stress tolerance) of microbes from the rhizospheres of plants grown under drought or salt stress. This work will increase our understanding of wheat microbiome structure and function and potentially lead to developing novel microbial inoculants for use in microbiome assisted agriculture.</p>

## Session 4: Plant growth and development

<b>Number</b>	<b>S4.K1</b>
<b>Authors</b>	Giannis Stringlis, Max Stassen, Melissa Uribe-Costa, Jiayu Zhou, Jelle Spooren, Ke Yu, Gilles Vismans, Yang Song, Sietske van Bentum, Eline Verbon, Ronnie de Jonge, Peter A.H.M. Bakker, Roeland L. Berendsen, and Corné M.J. Pieterse
<b>Affiliations</b>	Plant-Microbe Interactions, Department of Biology, Science4Life, Utrecht University, the Netherlands
<b>Presenting author</b>	Corné Pieterse
<b>Email address</b>	<a href="mailto:C.M.J.Pieterse@uu.nl">C.M.J.Pieterse@uu.nl</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Bi-directional communication along the microbiome-root-shoot axis
<b>Abstract text</b>	<p>Plants nurture a large community of root-associated microbiota, which in turn provide them with essential services, such as enhanced nutrient uptake, growth promotion, and protection against pathogens. Our research is focused on understanding plant-beneficial functions encoded by the root microbiome and the role of plant genes and traits that recruit these functions. We demonstrated that upon foliar pathogen infection, plant roots recruit a consortium of synergistic microbes to their rhizosphere that in turn trigger an immune response in the whole plant body, also in the next generation of plants that grow in the microbially conditioned soil. Using the <i>Arabidopsis-Pseudomonas simiae</i> WCS417 model, we identified the root-specific transcription factor MYB72 as a central regulator in the onset of this induced systemic resistance (ISR), which is typically effective against a broad spectrum of plant pathogens. Metabolomics of root extracts and exudates revealed that MYB72 controls the biosynthesis of iron-mobilizing coumarins, such as scopoletin, which are secreted in the rhizosphere where they aid in iron uptake. Scopoletin also has antimicrobial activity that inhibits growth of soil-borne fungal pathogens, but to which beneficial rhizobacteria such as <i>P. simiae</i> WCS417 are insensitive. Microbiome analysis of coumarin-deficient <i>Arabidopsis</i> mutants revealed that scopoletin functions in rhizosphere community assembly, possibly to promote recruitment of immunity-stimulating rhizobacteria to the roots. Whole genome expression profiling of <i>P. simiae</i> WCS417 exposed to root exudates of wild-type and coumarin-deficient mutants revealed that coumarins have strong effects on bacterial functions such as motility, which may steer the transition of the free-living phase to growth in biofilm on the root surface. Recent data show that rhizobacteria-induced coumarins can also be transported from the roots to the shoots, where they may serve as players in the onset of ISR in the leaves, highlighting coumarins as central players in bi-directional communication along the microbiome-root-shoot axis. Besides coumarins, also other chemical and structural root defense barriers emerged as players in plant-microbiome interactions. Using a defined set of <i>Arabidopsis</i> mutants affected in specific chemical and structural root defense barriers we are currently investigating their role in root-microbiome interactions. Understanding the mechanistic basis of mutually beneficial plant-microbiome interactions provides a firm knowledge basis for the development of future crops that maximize profitable functions from the root microbiome.</p>

<b>Number</b>	<b>S4.K2</b>
<b>Authors</b>	Maddy Giles
<b>Affiliations</b>	The James Hutton Institute
<b>Presenting author</b>	Maddy Giles
<b>Email address</b>	<a href="mailto:maddy.giles@hutton.ac.uk">maddy.giles@hutton.ac.uk</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Linking nutrient cycling and the soil microbiome – The impact of plant-microbiome interactions on carbon and nitrogen cycling in soils.
<b>Abstract text</b>	Plant-soil interactions are fundamental for regulating nutrient cycling in soils, and the management of these interactions represent a potential means to regulate CO <sub>2</sub> and N <sub>2</sub> O emissions, nutrient retention and storage of C as soil organic matter (SOM). However, microbial controls on soil functioning in the rhizosphere are poorly understood. In particular, it remains unknown how the selection of different microbial communities by different plant varieties can impact rates and products of nutrient cycling. Understanding this interaction will enable the development of management strategies explicitly targeting beneficial plant-soil interactions as a tool for sustainable agriculture and support the maintenance of soil health. Thus, there is a need to understand whether plant driven microbial community selection can affect the rates and products of C and N cycling and the potential mechanisms for this. Here we explore how plant variety, microbial communities and plant derived C inputs interact to determine the fate of C and N in soils.

<b>Number</b>	<b>S4.1</b>
<b>Authors</b>	Reid, Tessa E. (1, 2), Kavamura, Vanessa N. (1), Abadie, Maïder (1), Torres-Ballesteros, Adriana (1), Pawlett, Mark (2), Clark, Ian M. (1), Harris, Jim A. (2), and Mauchline, Tim H. (1)
<b>Affiliations</b>	(1) Rothamsted Research, Harpenden, United Kingdom (2) Cranfield University, Cranfield, United Kindom
<b>Presenting author</b>	Reid, Tessa E.
<b>Email address</b>	<a href="mailto:tessa.reid@rothamsted.ac.uk">tessa.reid@rothamsted.ac.uk</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Has plant domestication decoupled beneficial plant-microbe interactions in wheat?
<b>Abstract text</b>	Transformation of natural habitats to agricultural systems increased food production but was accompanied by reduced wheat genetic diversity by selecting for high-yielding dwarf crops reliant on unsustainable levels of inorganic fertiliser. We investigated the relationship between genetic changes during domestication, and the effect of fertiliser addition, on putative plant growth-promoting rhizobacteria (PGPR). Diploid, tetraploid and hexaploid varieties were grown in nutrient-depleted agricultural soil with and without fertiliser application. Root associated samples were analysed by culture-independent and -dependent techniques. A rhizoplane-derived microbiota culture collection of, approximately 15,000 bacterial isolates, was tested for growth-promoting traits using functional bioassays. Fertilisation was the dominant factor shaping the microbiome. Niche (rhizosphere/rhizoplane), plant species, and plant genotype, contributed significantly, but were associated with less variation in microbial communities. After fertilisation and niche, genome expansion from diploid to allopolyploid caused the

	greatest variation in microbial community structure (between 7-18%). Moreover, differences in the abundance of putative PGPR under contrasting fertilisation conditions were more pronounced in allopolyploid wheat, possibly due to a reduction of plant-microbe signalling pathways. We suggest that the influence of plant genotype on the composition of their associated microbiota is an integral factor and overlooked, during domestication.
--	--

<b>Number</b>	<b>S4.2</b>
<b>Authors</b>	Dong Lemeng, Abedini Davar, White Fred, Guerrieri Alessandra, Zhong Xiaolong, Bouwmeester Harro
<b>Affiliations</b>	Plant Hormone Biology Group, Swammerdam Institute for Life Science, University of Amsterdam, Amsterdam, The Netherlands
<b>Presenting author</b>	Dong, Lemeng
<b>Email address</b>	<a href="mailto:l.dong2@uva.nl">l.dong2@uva.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Nitrogen starvation induced metabolic interactions between plants and microbes
<b>Abstract text</b>	Host-associated microbiomes contribute largely to nutrient acquisition by their hosts. Just as in the mammalian gut, plant nutrition also is a major driver of the microbial composition on the roots. However, our knowledge about the mechanisms underlying the adaptation of the root-associated microbiome in response to plant nutrient (shortage) is only rudimentary. In the past few years, our team has worked on plant adaptation to nitrogen (N) starvation. We revealed that N deficiency induces changes in plant gene expression, root architecture, and root exudate metabolite production, which results in a reshaped microbiome assembly in the rhizosphere. Under these N starvation conditions, N fixing and mineralization functions got enriched in the endophytic and epiphytic microbiome community in an early stage of N starvation, while this did not occur under (semi-)sterile conditions. Using advanced data integration tools (ANOVA Simultaneous Component Analysis, ASCA) and machine learning feature selection methods, we were able to integrate three layers of data, transcriptomic, metabolomic and microbiome data. Two types of terpene derived signaling molecules were subsequently found to be associated with the microbiome community enriched under N deficiency. We are currently engineering these signaling molecules in the root and root exudates to elucidate their function in the rhizosphere.

<b>Number</b>	<b>S4.3</b>
<b>Authors</b>	Escudero-Martinez, Carmen <sup>1</sup> ; Coulter, Max <sup>1</sup> ; Alegria Terrazas, Rodrigo <sup>2</sup> ; Foito, Alexandre <sup>3</sup> ; Kapadia, Rumana <sup>1</sup> ; Pietrangelo, Laura <sup>4</sup> ; Maver, Mauro <sup>5</sup> ; Sharma, Rajiv <sup>6</sup> ; Aprile, Alessio <sup>7</sup> ; Morris, Jenny <sup>3</sup> ; Hedley, Pete <sup>3</sup> ; Maurer, Andreas <sup>7</sup> ; Pillen, Klaus <sup>7</sup> ; Naclerio, Gino <sup>4</sup> ; Mimmo, Tanja <sup>5</sup> ; Abbott, James <sup>1</sup> ; Waugh, Robbie <sup>1,3</sup> ; Barton, Geoffrey <sup>1*</sup> and Bulgarelli, Davide <sup>1*</sup>
<b>Affiliations</b>	<sup>1</sup> University of Dundee, School of Life Sciences, Dundee, UK; <sup>2</sup> Mohammed VI Polytechnic University, Agrobiosciences Program, Plant & Soil Microbiome Subprogram, Bengurir, Morocco; <sup>3</sup> The James Hutton Institute, Invergowrie, UK; <sup>4</sup> Department of Biosciences and Territory, University of Molise, Campobasso, Italy; <sup>5</sup> Faculty of Science and Technology, Free University of Bozen-Bolzano, Bolzano, Italy; <sup>6</sup> Scotland's Rural College, Edinburgh, UK; <sup>7</sup> Department of biological and environmental sciences and technologies, University of Salento, Lecce, Italy;

	10Institute of Agricultural and Food Science and Plant Breeding, Martin Luther University, Halle-Wittenberg, Germany;
<b>Presenting author</b>	Escudero-Martinez, Carmen
<b>Email address</b>	<a href="mailto:c.m.z.escudermartinez@dundee.ac.uk">c.m.z.escudermartinez@dundee.ac.uk</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Plant growth and development
<b>Title</b>	IDENTIFYING PLANT GENES SHAPING MICROBIOTA COMPOSITION IN THE BARLEY RHIZOSPHERE
<b>Abstract text</b>	<p>Harnessing the plant microbiota thriving in the rhizosphere is a promising strategy to enhance sustainable agriculture. A prerequisite for this is to identify plant genes shaping the plant microbiome. Here, we used metagenomics information as an external quantitative phenotype in QTL to map the host genetic determinants of the rhizosphere microbiota in wild and elite genotypes of the global crop barley. We identified a locus on chromosome 3H named QRMC-3HS associated with the recruitment of taxonomically distinct bacteria, possibly representing a major determinant of plant-microbiota interactions. Sibling lines with contrasting alleles, i.e., either elite or wild, at the QRMC-3HS locus shaped the microbial composition, validating the microbial role of this locus. Soil-grown barley RNA-seq of root tissue allowed us to select a limited number of candidate genes for this phenotype. Among those, we identified a Nucleotide-Binding-Leucine-Rich-Repeat (NLR) gene. Further inspection of the barley pangenome, revealed that this NLR falls in a region of structural variation, possibly underlining an important agronomic trait. Overall, our results provide novel insights into the footprint of crop improvement on the plant's capacity of shaping rhizosphere microbes and set the stage for future translation to plant breeding.</p>

<b>Number</b>	<b>S4.4</b>
<b>Authors</b>	Nishisaka, Caroline S (1,2); Quevedo, Helio D (1,2); Mendes, Rodrigo (1)
<b>Affiliations</b>	(1) Embrapa Environment, Jaguariúna, Brazil; (2) Graduate Program in Agricultural Microbiology, University of Sao Paulo, Piracicaba, Brazil.
<b>Presenting author</b>	Nishisaka, Caroline S
<b>Email address</b>	<a href="mailto:csayuri@usp.br">csayuri@usp.br</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Plant growth and development
<b>Title</b>	The impact of soil microbiome diversity on rhizosphere microbial communities' assembly and plant health
<b>Abstract text</b>	<p>The rhizosphere microbiome plays a significant role in the host plant's health, such as defense against soil-borne diseases. However, the understanding of how the rhizosphere soil microbiome diversity impacts plant protection in production systems is still limited. This study aims to evaluate the impact of rhizosphere microbiome diversity in wheat plants inoculated with the soil-borne pathogen <i>Bipolaris sorokiniana</i>, with/without the antagonist <i>Pseudomonas</i> sp. CMAA1741, under a gradient of soil microbiome diversity. We hypothesized that the diversity and functionality of the rhizosphere determine the success of the antagonist bacterium establishment in the rhizosphere. Thus, a bioassay was conducted using natural soil, autoclaved soil, and three different dilutions of natural soil on</p>

	<p>autoclaved soil. The results showed that antagonist inoculated treatments resulted in higher plant height and root dry mass, while, in soils with low diversity, the severity disease index and the biocontrol effect of the antagonist were higher across all treatments that received the fungal pathogen with/without inoculant, respectively. Sterilized soils inoculated with both agents had the most effectiveness in pathogen biocontrol, with enrichment of Chthoniobacter and Chitinophaga bacterial genera in this treatment. Also, an increase of Chitinophaga bacterial genus and Alternaria, Chaetomium, and Waitea fungal genera were observed when just pathogen was inoculated in soils. (Support FAPESP 2020/00469-2; 2020/06077-9; 2021/14711-2).</p>
--	---

<b>Number</b>	<b>S4.5</b>
<b>Authors</b>	Crusciol, Carlos; Siqueira, Gabriela; Fonseca, Mariley; Farias, Marco
<b>Affiliations</b>	São Paulo State University (UNESP), Botucatu, Brazil; Agriresult Assessoria e Consultoria Agrícola, Botucatu, Brazil; Microgeo Biotecnologia Agrícola, Limeira, Brazil
<b>Presenting author</b>	Siqueira, Gabriela
<b>Email address</b>	<a href="mailto:gaferrazsig@gmail.com">gaferrazsig@gmail.com</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Biological fertilizer in sugarcane: physiological effects and stalk yield improvement
<b>Abstract text</b>	<p>The biological management of the agricultural system is the new frontier for high sugarcane yield. Biological fertilizers composed by a pool of beneficial microorganisms may improve the soil biological balance. Its use can be another alternative to improve the use and efficiency of fertilizers, promote soil conservation and increase sugarcane yield in a sustainable way. Thus, this study was carried out to evaluate the agronomic and physiological sugarcane performances and the effect on soil enzyme activity under biological fertilization. Growth, technological and physiological parameters and soil enzymatic activity in surface layer were analyzed. The use of biological fertilizer altered physiological parameters, contributing to a greater assimilation of CO<sub>2</sub>, improving net photosynthesis in the sugarcane crop, in addition to increasing the water use efficiency. There was an increase in the enzymatic activity of soil acid phosphatase. The biometric parameters stalk length, stalk diameter and number of stalks per meter were improved by biological fertilizer application. Consequently, there was an increase of 10% in the stalk yield and 8% in the sugar yield.</p>

<b>Number</b>	<b>S4.6</b>
<b>Authors</b>	Floss, Luiz
<b>Affiliations</b>	FLOSS Consultoria e Assessoria em Agronegócios, Passo Fundo, Brazil
<b>Presenting author</b>	Floss, Luiz
<b>Email address</b>	<a href="mailto:luiz.gustavo@grupofloss.com">luiz.gustavo@grupofloss.com</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Use of Microgeo and different doses of phosphorus in soybean (Glycine max)

<b>Abstract text</b>	<p>Promoting soybean growth and increasing productivity is influenced by microorganisms that produce metabolites that promote increased availability of nutrients. The objective was to evaluate the use of Microgeo and different doses of phosphorus in soybean (<i>Glycine max</i>), year 2020. The experiment was located in Passo Fundo, Rio Grande do Sul, Brazil, in soil with high phosphorus content. The trial consisted of 8 treatments (double factorial, 1st. with and without Microgeo; and 2nd. 0, 30, 60 and 90 kg.P2O5.ha-1) and 5 repetitions. There was no statistically significant difference between treatments for phosphorus content in the plant, total phosphorus in the soil, phosphorus in Mehlich in the soil and weight of a thousand grains. The highest levels of phosphorus in the grain were at doses of 60 and 90 kg.P2O5.ha-1. The highest activity of the acid phosphatase enzyme was with the use of 90 kg.P2O5.ha-1 with Microgeo. The treatments with Microgeo provided greater amount of acid phosphatase in the soil. The highest grain yield was with the dose of 90 kg.ha-1 with Microgeo, with increasing increase in relation to the phosphorus dose and use of Microgeo.</p>
----------------------	---

<b>Number</b>	<b>S4.7</b>
<b>Authors</b>	Sharma, Rajiv; Powell, Wayne; Mackay, Ian
<b>Affiliations</b>	Scotland's Rural College (SRUC), Kings Buildings, West Mains Road, Edinburgh, EH9 3JG, United Kingdom.
<b>Presenting author</b>	Sharma, Rajiv
<b>Email address</b>	<a href="mailto:rajiv.sharma@sruc.ac.uk">rajiv.sharma@sruc.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Plant growth and development
<b>Title</b>	Microbe-dependent trait expression in wheat
<b>Abstract text</b>	<p>A key to increasing global food production in the wake of global uncertainty is the adoption of hybrids. This remains a target for breeding in cereals such as wheat. Wheat heterosis has long been studied but the routine production of commercially successful hybrid varieties remains elusive. The study of heterosis using fresh perspectives may be informative. A recent study found a link between the microbiome and the heterosis of root biomass and germination in maize (Wagner et al. 2021). These findings are fascinating. This may hold the key to unlocking heterosis in crops such as wheat. In our study, we extend this approach to wheat, testing diverse sets of inbreds and hybrids in a range of microbial colonised and sterile soils. Additionally, we will detect and locate heterotic loci using state of art genomic data in a multi-parent advanced generation inter-cross (MAGIC) population.</p>

## Session 5: Technological advances

<b>Number</b>	<b>S5.K1</b>
<b>Authors</b>	Marnix Medema
<b>Affiliations</b>	Bioinformatics Group, Wageningen University, Wageningen, The Netherlands
<b>Presenting author</b>	Marnix Medema
<b>Email address</b>	<a href="mailto:marnix.medema@wur.nl">marnix.medema@wur.nl</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Technological advances
<b>Title</b>	Computational metagenomics to elucidate functions in plant microbiomes
<b>Abstract text</b>	Plants and their microbiota produce a wealth of specialized metabolites, which mediate molecular interactions and provide a mechanistic basis for many microbe-associated phenotypes. Due to the accelerated accumulation of omics data, computational methods have become more and more important to identify the genes involved in the biosynthesis of these metabolites, and to assess their likely biological activities and ecological roles. Here, I will highlight the work performed in my research group on using these approaches to study microbe-microbe and host-microbe interactions in plant microbiomes. Specifically, I will present recent results on the use of shotgun metagenomics towards elucidating the molecular basis of disease-suppressive phenotypes in wheat rhizosphere microbiomes.

<b>Number</b>	<b>S5.K2</b>
<b>Authors</b>	Laura Lehtovirta Morley
<b>Affiliations</b>	University of East Anglia
<b>Presenting author</b>	Laura Lehtovirta Morley
<b>Email address</b>	<a href="mailto:L.Lehtovirta-Morley@uea.ac.uk">L.Lehtovirta-Morley@uea.ac.uk</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Technological advances
<b>Title</b>	Archaea – important but overlooked players in the plant microbiome?
<b>Abstract text</b>	Archaea are ubiquitous in soil, but often overlooked in microbiome studies. Soil archaeal communities are frequently dominated by ammonia oxidising archaea, which play a vital role in the global biogeochemical nitrogen cycle. Ammonia oxidising archaea are also important for nitrogen fertiliser loss from agricultural ecosystems with consequences for plant growth yield. However, little is known about how archaea interact with plants and how plants shape archaeal communities. There are knowledge gaps in, for instance, how the rhizosphere influences archaeal diversity and abundance, the effect of root exudates on archaea and the potential beneficial role of archaea in promoting plant growth. In this talk, I discuss the current knowledge of the role of archaea in agricultural ecosystems. I will present our recent collaborative work on archaeal communities associated with wheat roots, and discuss the future perspectives of the research into archaea-plant interactions.

<b>Number</b>	<b>S5.1</b>
<b>Authors</b>	Payton Yau; Sue Jones; Nicola Holden
<b>Affiliations</b>	Department of Rural Land Use, Scotland's Rural College (SRUC), Aberdeen, AB21 9YA, UK; Information and Computational Science Department, The James Hutton Institute, Dundee, DD2 5DA, UK
<b>Presenting author</b>	Payton Yau
<b>Email address</b>	<a href="mailto:payton.yau@sruc.ac.uk">payton.yau@sruc.ac.uk</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Technological advances
<b>Title</b>	Microbiome sequence data analysis of the UK Crop Microbiome CryoBank
<b>Abstract text</b>	<p>The UK Crop Microbiome CryoBank Resource intends to underpin national and international crop research on seven major UK crops: (barley, oats, oil seed rape, potato, sugar beet, vining peas and wheat) grown in three different soil types in different regions. The resource consists of preserved microbiomes and culturable isolates focused on crop rhizospheres and genome sequences with providing associated metadata. The complete resource for the ongoing project is discoverable via an online database: <a href="https://agmicrobiomebase.org/">https://agmicrobiomebase.org/</a>.</p> <p>Crop and soil microbiomes are being sequenced for taxonomic groups on bacterial (16S) and fungal communities (ITS - selected samples), and overall community structure by shotgun metagenome sequencing. Culturable isolates are being whole genome sequenced by de novo sequencing. Sequence data analysis pipelines are being optimised for protocol standardisation and to provide the optimal state-of-the-art data outputs. Active involvement with EBI MGNify will serve to improve microbiome datasets utility.</p> <p>The main sequence data analysis aims are to (I) provide an accessible dataset; (II) comparisons of the soil and crop sample type communities; (III) standardised protocols for use with inherently complex microbiota communities. The datasets and resources are openly accessible to provide legacy so that future analyses can be applied for academic, policy and industry interests.</p>

<b>Number</b>	<b>S5.2</b>
<b>Authors</b>	Goossens, Pim; Spooren, Jelle; Pieterse Corné; Van den Ackerveken, Guido and Berendsen, Roeland
<b>Affiliations</b>	Utrecht University- Utrecht
<b>Presenting author</b>	Berendsen, Roeland
<b>Email address</b>	<a href="mailto:r.l.berendsen@uu.nl">r.l.berendsen@uu.nl</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Technological advances
<b>Title</b>	Downy mildew diseased plants are enriched for a disease-associated phyllosphere microbiome that benefits the plant.
<b>Abstract text</b>	<p>Plant microbiomes have the capacity to affect disease resistance but can themselves also be dynamically shapen by both plant and pathogen. Here, we studied the phyllosphere microbiome associated with infection by <i>Hyaloperonospora arabidopsidis</i> (Hpa), the downy mildew of the model-plant <i>Arabidopsis thaliana</i>. In the laboratory, this obligate biotroph is typically cultured by successive weekly passaging over susceptible host plants for long periods of time. We show that the</p>

	<p>plants used for this passaging have dramatically altered phyllosphere microbiomes following the inoculation of Hpa spores and their associated microbiomes. Cultures of distinct Hpa isolates maintained in laboratories in Germany and the Netherlands were dominated by nearly isogenic bacterial genomes. These Hpa-associated bacteria are depleted from the phyllosphere microbiome when inoculated on Hpa-resistant plants and disease-associated bacteria increase in abundance when co-inoculated with gnotobiotic Hpa on susceptible plants. Together, this suggests that these specific disease-associated microbes have been selectively enriched in the phyllosphere of distinct Hpa cultures as a result of downy mildew infection. Moreover, specific members of the Hpa-associated microbiome reduced Hpa spore production, whereas gnotobiotic Hpa consistently outperforms Hpa with its co-inoculated microbiome. This suggests the disease-associated microbiome benefits the plant.</p>
--	---

<b>Number</b>	<b>S5.3</b>
<b>Authors</b>	Richards, Luke; Lagunas, Beatriz; Richmond, Bethany; Jiang, Xue; Buckling, Angus; Gifford, Miriam; Schäfer, Patrick; Soyer, Orkun.
<b>Affiliations</b>	School of Life Sciences, University of Warwick, Coventry, UK. Biosciences, University of Exeter, Penryn, UK. Institute for Molecular Botany, Ulm University, Ulm, Germany
<b>Presenting author</b>	Richards, Luke
<b>Email address</b>	<a href="mailto:Luke.Richards.1@warwick.ac.uk">Luke.Richards.1@warwick.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Translational applications
<b>Title</b>	Environmental conditions influence the overall root microbiome and individual microbial interactions.
<b>Abstract text</b>	<p>Soils host an overwhelming diversity of microorganisms; forming an integral part of the plant holobiont. Understanding plant health in this context is vital to maximising crop health and yield. The wealth of functional capabilities in soil communities could be exploited given sufficient understanding of community assembly, stability, and function. Our research aims to understand microbial interactions using both “top-down”, sequencing-based and “bottom-up” experimental analysis approaches. On the top-down approach, we profiled endophytic, bacterial and fungal, microbiome composition in low and high nutrient regimes and found drastic differences. The extent to which plants are driving this selection remains an open question. From a bottom-up perspective, we are using a known interaction between beneficial endophytes <i>Bacillus subtilis</i> and <i>Seredipita indica</i> as a model system. We have found that <i>S. indica</i> is incapable of taking up nitrate and is therefore dependant on other sources of nitrogen. We have shown that <i>B. subtilis</i> can assimilate nitrate into, yet unknown, nitrogen sources suitable for <i>S. indica</i>. Such interactions could be vital to the growth-promoting capability of <i>S. indica</i> depending on environmental conditions. The complexity, that this interaction displays, highlights the need to understand, intimately, microbe-microbe interactions and the potential impact they have on plant health.</p>

## Session 6: Translational applications

<b>Number</b>	<b>S6.K1</b>
<b>Authors</b>	Matthew J. Ryan
<b>Affiliations</b>	CABI, Bakeham Lane Egham, Surrey, UK TW20 9TY
<b>Presenting author</b>	Matthew J. Ryan
<b>Email address</b>	<a href="mailto:M.Ryan@cabi.org">M.Ryan@cabi.org</a>
<b>Presentation type</b>	Keynote
<b>Session Name</b>	Translational applications
<b>Title</b>	Conserving the microbiome – unravelling the conundrum
<b>Abstract text</b>	<p>There is a fundamental need to underpin crop and soil microbiome research through the provision of a supporting infrastructure. Through projects such as EU Microbiome Support, the research community has started to address and define some key requirements. These include the development of experimental standards; provision of mechanisms to deposit samples to allow others to reproduce research; and the tools to deliver cultures, samples and associated data for future research in both academia and industry. Integral to the above is the need to develop a biobanking approach to conserve and preserve soil and plant samples and their associated microbes.</p> <p>Historically, culture collections have developed protocols to preserve ‘axenic’ microbes, using both freeze-drying and cryopreservation approaches. which involves storage of material at ultralow temperatures. The microbiome presents a significantly more complex conundrum – how do we translate the methodology to environmental samples that may contain many thousands of different species or even ‘simpler’ synthetic communities containing just a handful of different strains? The answer lies in our understanding of how microbial cells respond to the stresses encountered during freezing, thawing and recovery and how methods can be optimised to retain physiological and genomic integrity for different taxa and cell types. Using this approach, we can start to predict the components of the microbiome that may retain viability and, more importantly, retain their functional potential. In this talk I will provide an overview of the approaches being utilised for the UK Crop Microbiome Cryobank and how we are utilising state-of-the-art technologies and adapting them for complex microbial samples.</p>

<b>Number</b>	<b>S6.1</b>
<b>Authors</b>	Javier Martínez-Pérez (1,2), Govind Chandra (1), Joel Vanneste (3), Andrew Truman (1) and Jacob Malone (1)
<b>Affiliations</b>	(1) John Innes Centre, Norwich, United Kingdom, (2) University of East Anglia, Norwich, United Kingdom and (3) Plant & Food Research, Hamilton, New Zealand
<b>Presenting author</b>	Javier Martínez-Pérez
<b>Email address</b>	<a href="mailto:javier.martinez@jic.ac.uk">javier.martinez@jic.ac.uk</a>
<b>Presentation type</b>	Oral
<b>Session Name</b>	Translational applications
<b>Title</b>	Unlocking the biocontrol potential of kiwifruit <i>Pseudomonas</i>

<b>Abstract text</b>	<p><i>Pseudomonas syringae</i> pv. <i>actinidae</i> (Psa) is the major threat to the world kiwifruit industry since 2008. Just in New Zealand, yield losses are well over £1B. Currently, copper compounds and antibiotics are the most common and efficient treatments but bacteria can rapidly evolve, leading to agrochemical resistance.</p> <p>With this project, we are aiming to provide kiwifruit growers with effective, sustainable, and environmentally friendly crop protection agents to control Psa. To do so, we are examining how the naturally occurring population of kiwi-associated <i>Pseudomonas</i> responds to Psa infection, to exploit this knowledge, discover and characterise novel anti-Psa treatments. From a representative 6,000 <i>Pseudomonas</i> collection, 1,000 strains have been tested using laboratory-based assays. As a result, there were identified 33 biocontrol candidates. Additionally, more than 100 <i>Pseudomonas</i> were whole-genome sequenced. This data has been of great value for identifying that published copper resistance genes are missing from most copper resistant strains. Also, with AntiSMASH and molecular biology techniques, we have successfully identified a wide variety of known and unknown natural product (NP) potential within the strains.</p> <p>From the biocontrol candidates, at least three <i>Pseudomonas</i> strains strongly suppress Psa infection in planta and we have identified a novel NP cluster responsible for strongly suppressing Psa. Currently, we are in the process of characterising the compound and examining the impact of this NP by making deletion mutants.</p>
----------------------	---

<b>Number</b>	<b>S6.2</b>
<b>Authors</b>	Robertson-Albertyn Senga, Abbott James, Corral Aileen, Alegria Rodrigo, Bulgarelli Davide
<b>Affiliations</b>	University of Dundee, Dundee, Scotland
<b>Presenting author</b>	Robertson-Albertyn Senga
<b>Email address</b>	<a href="mailto:srobertsonalberty002@dundee.ac.uk">srobertsonalberty002@dundee.ac.uk</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Translational applications
<b>Title</b>	Harnessing the spinach bacterial microbiome for sustainable food production and nutrition
<b>Abstract text</b>	<p>Within a multidisciplinary and multinational research project we developed an innovative lab in the field sampling approach exploring both the properties and structure of spinach microbiomes under field conditions. As spinach are fresh produce for which microbiome information is still rather limited, novel insights from this project have the potential to positively impact the farm to fork microbiome nexus. We subjected over 200 spinach samples across microhabitats, host genotypes, farming approaches, harvest periods and geographical locations to a high-throughput amplicon sequencing survey of the 16S rRNA gene. Using ecological indices and multivariate statistical analyses we demonstrated that the plant microhabitat, i.e., roots, leaves or rhizosphere, emerged as a main driver of the spinach microbiome irrespective of host genotype, treatment or geographical location. At a finer scale, we identified taxa putatively associated to differential yield responses and geographically mediated taxonomic shifts putatively associated to nitrate accumulation in leaves. This data, combined with the development of metagenomic investigations will contribute to farming approaches of the future (e.g., targeted inoculation) as well as towards enabling farmers, stakeholders and the public to making informed food choices.</p>

<b>Number</b>	<b>S6.3</b>
<b>Authors</b>	Vogel, Christine; Potthoff Daniel; Schäfer, Martin; Barandun, Niculò; Vorholt, Julia
<b>Affiliations</b>	Institute of Microbiology, ETH Zurich, Zurich, Switzerland
<b>Presenting author</b>	Vogel, Christine
<b>Email address</b>	<a href="mailto:chvogel@ethz.ch">chvogel@ethz.ch</a>
<b>Presentation type</b>	Either
<b>Session Name</b>	Translational applications
<b>Title</b>	Plant protection abilities of the <i>Arabidopsis</i> leaf microbiota
<b>Abstract text</b>	<p>The aerial parts of plants are host to taxonomically structured bacterial communities. Members of the core phyllosphere microbiota are able to protect <i>Arabidopsis thaliana</i> against foliar pathogens. It is, however, unclear whether this phenomenon is widespread and whether modes of plant protection differ. Here, we present a systematic analysis of protection capabilities of the At-LSPHERE, a representative collection of &gt;200 bacterial isolates from <i>Arabidopsis thaliana</i>, against the pathogen <i>Pseudomonas syringae</i> DC3000. The leaf isolates were individually assessed for plant protection in a gnotobiotic model system. The protection potential differed with approximately 10% of strains providing protection, 10% showing intermediate levels of protection and the majority not markedly improving disease phenotypes. The protective strains were distributed across different taxonomic groups. Synthetic community experiments revealed additive effects of strains but also that a single strain can confer protection in a community context. Furthermore, we show that different mechanisms contribute to plant protection. While pattern-triggered immunity co-receptor signaling is involved in protection by a subset of strains, which thus confer indirect plant protection, others did not require functional BAK1 and BKK1. Using a comparative genomics approach followed by mutagenesis, we exemplarily demonstrate that direct bacteria-pathogen interactions contribute to plant protection by <i>Rhizobium</i> Leaf202. This shows that a computational approach based on the data provided can be used to identify genes related to plant protection.</p>

<b>Number</b>	<b>S6.4</b>
<b>Authors</b>	Asunção, Paulo; Trevisanuto, Henrique
<b>Affiliations</b>	PA Consultoria, Diamantino, Brazil
<b>Presenting author</b>	Trevisanuto, Henrique
<b>Email address</b>	<a href="mailto:henrique@paconsultoriaagronomica.com.br">henrique@paconsultoriaagronomica.com.br</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Translational applications
<b>Title</b>	Effect of Microgeo® Biotechnology in different application forms and doses in the soybean crop under water stress conditions
<b>Abstract text</b>	<p>The research was performed with different doses of Microgeo® Biotechnology in sowing and V2 stage of soybean and the impacts on plant height, number of nodules per plant, compaction in the sowing line, number of nematodes and productivity. The experiment were performed in sash blocks with 4 repetitions in each swath. The data were submitted to analysis of variance and the averages were compared by the</p>

	<p>Tukey method at 5%. The results show that there was the presence of nematode only in the T5 treatment (control) and although it did not differ statistically, only the T2 treatment (80 L/ha Furrow + 80 L/ha V2 stage) showed compaction values lower than 2500 KPa in the 16- 20 and 21-25 cm. For productivity, it was possible to conclude that the treatments with the highest response were with the application of Microgeo® Biotechnology in sowing with increments of up to 978 kg/ha. The application of V2 stage was under high temperature and without rain environmental conditions, which may have affected the effect of the product on the system.</p>
--	---

<b>Number</b>	<b>S6.5</b>
<b>Authors</b>	Brierley, Jennie Yau, Tung On. Jones, Susan
<b>Affiliations</b>	The James Hutton Institute, Dundee, UK Scotland's Rural College, Aberdeen, UK
<b>Presenting author</b>	Jones, Susan
<b>Email address</b>	<a href="mailto:sue.jones@hutton.ac.uk">sue.jones@hutton.ac.uk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Translational applications
<b>Title</b>	Disease suppressive soils: comparing the soil microbiome in relation to soil cultivation practices
<b>Abstract text</b>	<p>New research at the James Hutton Institute is exploring the relationship between soil management practices, suppression of potato diseases and the composition of the soil microbiome. One objective of this work is to assess the impact of soil management on the diversity of the soil microbiome. The Centre for Sustainable Cropping, a 6-year experimental rotation set up in 2011 in NE Scotland, has soil managed according to two contrasting strategies, conventional and integrated. The integrated treatment is less extensively cultivated and has annual amendments of organic matter. In this work we extracted DNA from bulk soil taken from the field treatments at two different time points (March and July 2021, before and after potatoes were planted) and conducted 16S amplicon sequencing to assess the diversity of the soil microbiomes. We used a bioinformatics workflow that included Qiime2 to identify the amplicon sequence variants present in the soils. We calculated beta diversity and abundance of bacterial phyla to compare the microbiomes of the two soil types. We observed differences in diversity of the microbiomes from the two soil types which have implications for managing soils for disease suppression and in turn Integrated Pest Management (IPM) and Integrated Farm Management (IFM) strategies.</p>

<b>Number</b>	<b>S6.6</b>
<b>Authors</b>	Frangiosi, Daine
<b>Affiliations</b>	Daine Frangiosi, Campo Florido, Brazil
<b>Presenting author</b>	Frangiosi, Daine
<b>Email address</b>	<a href="mailto:dainefrangiosi@uol.com.br">dainefrangiosi@uol.com.br</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Translational applications
<b>Title</b>	Microorganisms: soil-plant interaction and impacts on plant health
<b>Abstract text</b>	<p>The objective of the research was to evaluate the action of the biological fertilizer produced with Microgeo Biotechnology in the sugarcane crop with the presence of</p>

	<p>pests. The work was carried out in the state of Minas Gerais in Brazil, during the 2019/20 season. Areas with incidence of <i>Colletotrichum falcatrum</i>, <i>Acidovorax avenae</i> and <i>Mahanarva fimbriolata</i> were analyzed. The trial was conducted with five treatments, being a control, without application of biotechnology, and four application method of 300 L/ha of Microgeo Biotechnology. Through molecular report it was possible to identify that the plant selects its own biodiversity of microorganisms. It is also concluded that the Microgeo biotechnology provided better health indices for the plant, resulting in a productivity gain of 3.37 to 20.07 tons of sugarcane.</p>
--	---

<b>Number</b>	<b>S6.7</b>
<b>Authors</b>	Højmark Fischer, Marie; Kjøller, Rasmus; Rzepczynska, Agnieszka Marta; Wong, Tammy
<b>Affiliations</b>	Terrestrial Ecology, Department of Biology, University of Copenhagen, Denmark
<b>Presenting author</b>	Højmark Fischer, Marie
<b>Email address</b>	<a href="mailto:marie.fischer@bio.ku.dk">marie.fischer@bio.ku.dk</a>
<b>Presentation type</b>	Poster
<b>Session Name</b>	Translational applications
<b>Title</b>	Endophytic fungal interactome of the wheat phyllosphere
<b>Abstract text</b>	<p>Wheat (<i>Triticum aestivum</i>) is the most widely cultivated cereal in the world and consequently, one of the most important crops for global food security. Despite the intensive pesticide use, a substantial amount of yield is lost annually due to fungal infections. To achieve sustainable wheat production new management strategies are needed. Here, the wheat phyllobiome fungi may act as both problems and solutions. To explore the wheat phyllosphere microbiome for potentially beneficial fungi, we established a fungal endophyte culture collection from symptom free wheat flag leaves from four winter wheat cultivars. These fungi were explored for their fungal-fungal and fungal-plant interactions. Specifically, we: a) mapped fungal-fungal interactions between the isolated fungi, b) screened interaction of the isolated fungi with the model fungal pathogens <i>Zymoseptoria tritici</i> and <i>Fusarium graminearum</i>, c) tested the host plant phenotypic response to all isolated fungi in leaf assays and d) screened the interaction of a selection of the isolated fungi with <i>Z. tritici</i> in a detached leaf assay. Results will be presented and discussed.</p>