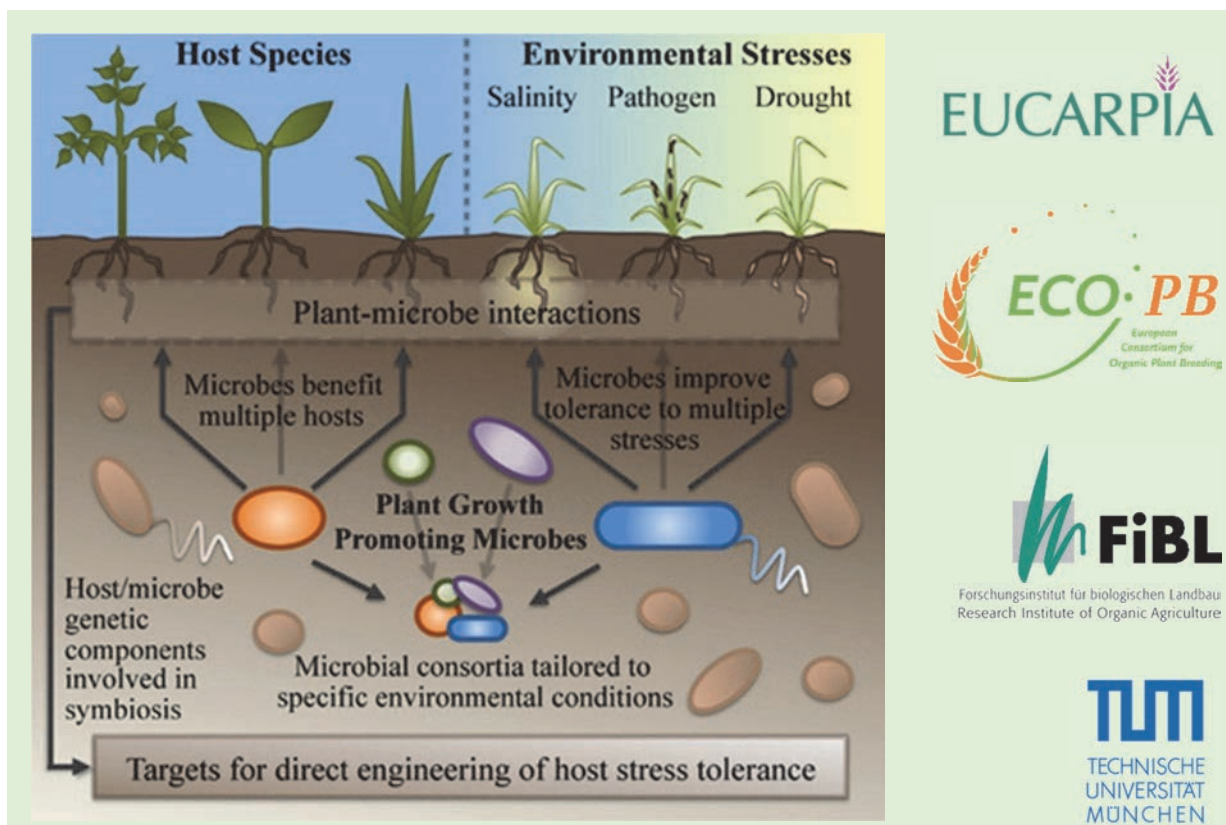


First EUCARPIA Workshop on Implementing Plant – Microbe Interaction in Plant Breeding

25th June - 26th June 2015

Technische Universität München

Freising Weihenstephan, Alte Akademie 8



EUCARPIA Working Group on Plant-Microbe Interactions
Section Organic and Low-Input Agriculture

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ANNOUNCEMENT

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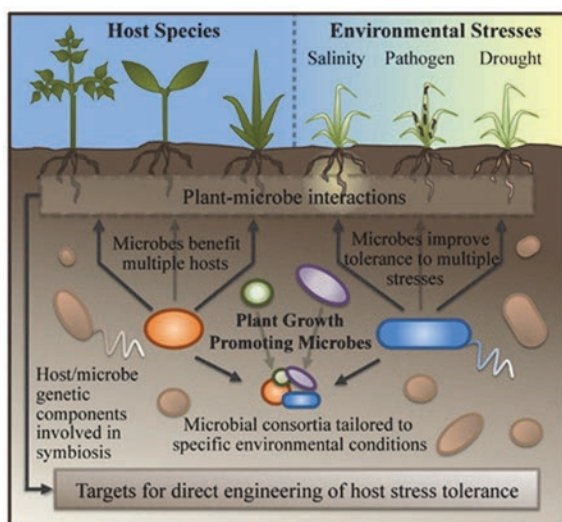
Freising Weihenstephan, Alte Akademie 8

EUCARPIA Working Group on Plant-Microbe Interactions

Section Organic and Low-Input Agriculture

The workshop aims at creating a network among plant breeders and researchers of different disciplines to explore the potential of utilizing plant microbe interaction in plant breeding.

In recent years, plant-associated microbial communities have received considerable attention in research for their ability to improve crop productivity and stability. It is now well recognized that all plants, and nearly all tissues within the plant, are inhabited by a variety of microorganisms. Many of them offer benefits to the host, improving nutrient uptake, preventing pathogen attack, and increasing plant growth under adverse environmental conditions. In return these microorganisms receive shelter from the surrounding environment and access to a carbon-rich food supply. The interaction between plant and microorganism is quite complex. Best elucidated symbiotic systems are legumes and the nitrogen fixing rhizobium and host plants and mycorrhiza fungi. Influence of crop management, soil parameters and climatic effects are well documented. In addition, the knowledge about plant-endophyte, plant-epiphyte, and plant-rhizosphere flora is rapidly growing.



“The fundamental change required is a broader recognition that plants do not exist as autonomous organisms governed entirely by their genetic blueprints, but rather serve as ecological niches for diverse communities of easily overlooked microbes, which work in concert with the plant to survive in a wide range of stressful environmental conditions.”

Coleman-Derr D and Tringe SG (2014) Building the crops of tomorrow: advantages of symbiont-based approaches to improving abiotic stress tolerance. *Front. Microbiol.* 5:283. doi: 10.3389/fmicb.2014.00283

However, little research has been conducted to evaluate the potential to improve the plant microbe symbioses by plant breeding. First reports indicate that not only the host species but also the host genotype play a significant role in driving microbial community composition and activity, selecting for and against particular microbial partners, e.g. by certain root exudates. However, to what extent genetic factors are responsible for the specific associations with beneficial rhizosphere, epiphytic, or endophytic microorganisms is still poorly understood.

The topic is at the crossroads of plant breeding, genetics, plant physiology, nutrition, pathology, entomology, soil microbiology, metabolomics, co-evolution and adaptation.

During this workshop we want to elaborate on the possible implementations of the cutting edge research findings on plant microbe interaction into plant breeding.

We are very happy to have two key note speakers

Prof. Dr. Lori A. Hoagland from Purdue University on “Breeding for beneficial belowground interaction”

Dr. Arjen Biere from the Netherlands Institute of Ecology, NIOO-KNAW will introduce the new COST action “Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production”

A large space will be devoted to discussions on potentials and limitation of implementing the vast growing knowledge on plant microbe interaction in plant breeding in order to improve stress resistance, plant nutrition, plant health and general adaptability, and links between upstream disciplines and breeding. This shall foster the dialogue between the different disciplines in order to develop efficient breeding strategies for the future.

Location

The first workshop is hosted by Dr. Jörg Peter Baresel from Technical University of Munich in Freising-Weihenstephan, Alte Akademie 8.

The meeting is attached to the core-Organic II meeting: Coordinating organic plant breeding activities for diversity (COBRA, <http://www.cobra-div.eu/> and the meeting of the European Consortium for Organic Plant Breeding ECO-PB, www.eco-pb.org)

On behalf of the Organizing Committee:

Dr. Monika Messmer, Research Institute of Organic Agriculture (FiBL) Switzerland

Dr. Maria Finckh, University of Kassel (UK), Germany

Dr. Edith Lammerts van Bueren, Louis Bolk Instituut (LBI), University of Wageningen (WUR), The Netherlands

Dr. Jörg Peter Baresel, Technical University of Munich (TUM), Germany

Supported by:



PROGRAM

Thursday 25th June 2015		TUM Freising-Weihenstephan, Alte Akademie 8
12:00 – 13:15	Registration & Lunch	
13:30	Welcome to the workshop	<i>M. Messmer, M. Finckh, J.P. Baresel, E. Lammerts van Bueren</i>
Session I	<i>Neighbours and inhabitants of our crop plants</i>	<i>Maria Finckh</i>
13:40 – 14:00	SYMBIO Bank – the collection of beneficial soil microorganisms	<i>Lidia Sas Paszt; B. Sumorok; A. Lisek; E. Derkowska; P. Trzciński; S. Głuszek; E. Malusa</i>
14:00 – 14:30	Key note: Introducing new COST Action FA1405: Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production	<i>Arjen Biere</i>
14:30 – 14:50	Effect of plant domestication on the rhizosphere microbiome of common bean (<i>Phaseolus vulgaris</i>)	<i>Juan E. Pérez-Jaramillo, R. Mendes, V.J. Carrion, M. de Hollander, J.M. Raaijmakers</i>
14:50 – 15:10	Influence of terroir on the fungal assemblages associated to common bean seed	<i>Stephanie M. Klaedtke, M.A. Jacques, V. Chable, M. Barret</i>
15:10 – 15:30	Effects of the inoculation with soil microbiota on maize grown in saline soils	<i>H. Moreira, S.A. Pereira, Paula M.L. Castro, A.P.G.C. Marques</i>
15:30 – 15:50	Discussion	
15:50 – 16:20	Coffee Break	
Session II	<i>Genetic determination of plant microbe interaction</i>	<i>Monika Messmer</i>
16:20 – 16:50	Mycorrhiza-mediated disease resistance - A mini-review	<i>Pierre Hohmann, M. R. Finckh, A. Šišić, J. Baćanović, C.J. Coyne, G. Backes</i>
16:50 – 17:10	Degree of root colonization and of induced resistance in wheat is determined by the bacterial strain and wheat genotype	<i>Daniela Villacrés de Papajewski, S. Kellenberger, A. Sharifi-Tehrani, M. Farzaneh, N. Imperiali, M. Pechy-Tarr, Ch. Keel, F. Mascher</i>
17:10- 17:30	The impact of the host genotype on the structure of the seed and rhizosphere microbiome: sugar beet and lettuce as model plants	<i>Christin Zachow, H. Müller, M. Cardinale, A. Erlacher, M. Grube, R. Tilcher, G. Berg</i>
17:30 – 18:00	Discussion	

18:00 – 18:30	Poster Session	
Poster 1	Metagenomic mining of the endophytic plant microbiome	<i>Victor J. Carrion, M. Lupatini, J.E. Perez-Jaramillo, K.S. Janssen, M. de Hollander, V. De Jager, J.M. Raaijmakers</i>
Poster 2	Beneficial interactions of endophytic <i>Herbaspirillum frisingense</i> with <i>Miscanthus</i> and other plants	<i>Michael Rothballer, D. Straub, A. Hartmann, M. Schmid, U. Ludewig</i>
Poster 3	The influence of bioproducts on mycorrhizal occurrence and biodiversity in the rhizosphere of strawberry	<i>L. Sas Paszt, Paweł Trzcinski, E. Malusa, B. Sumorok, E. Derkowska, S. Gluszek</i>

19:30	Common Diner	
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Friday 26th June 2015		TUM Freising-Weihenstephan, Alte Akademie 8
Session III	<i>How to integrate plant microbe interaction into breeding</i>	<i>Edith Lammerts van Bueren</i>
8:30 – 9:10	Key note: Breeding for beneficial root-microbial relationships: how do we get there?	<i>Lori Hoagland</i>
9:10 – 9:30	Genotype-dependent interaction with beneficial plant-associated bacteria	<i>Friederike Trognitz, H. Mayerhof, B. Mitter, A. Sessitsch</i>
9:30 – 9:50	Screening concept for plant-microbe interactions on the Styrian oil pumpkin as basis for an advanced breeding strategy	<i>Eveline Adam, M. Bernhart, H. Müller, J. Winkler, G. Berg</i>
9:50 – 10:10	Barley variety selection for enhanced root colonisation by beneficial soil microbes	<i>J. Murray, J. Malone, M. Wearing, S. DeVos, Christopher J. Ridout</i>
10:10 – 10:40	Coffee Break	
Session IV	<i>Future activities of EUCARPIA Working group on plant microbe interaction</i>	
10:40 – 11:30	Group work	
11:30 – 11:50	Plenum discussion	
11:50 – 12:00	Closing of the Workshop	
12:00	Lunch	

SYMBIO BANK - THE COLLECTION OF BENEFICIAL SOIL MICROORGANISMS

L. Sas Paszt¹; B. Sumorok¹; A. Lisek¹; E. Derkowska¹; P. Trzciński¹; S. Głuszek¹; E. Malusa¹

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Introduction

An important part of the project called EcoTechProduct, which is carried out at the Research Institute of Horticulture in Skierniewice (Poland), is to establish and maintain a Bank of Symbiotic Microorganisms, called SYMBIO BANK. The collected material of isolated spores of mycorrhizal fungi and PGPR bacteria comes from organic orchards and plantations in Central Poland, the Bieszczady and Białowieża areas (less polluted regions in Poland). Results of studies to date have shown that there are large differences in the occurrence of mycorrhizal fungi depending on the species and plant cultivation method.

Plant-soil microorganisms can modulate the uptake of mineral nutrients through feedback processes that reflect plant responses to environmental conditions. The intimate interrelation between the root and symbiotic arbuscular mycorrhizal fungi and the resulting enhancement in the uptake of N and P by the plant are further expanded by the interactions between the fungus and bacteria present in both the rhizosphere and mycorrhizosphere. Numerous species of plant growth promoting bacteria form biofilm when colonizing roots, which can affect bio-geochemical processes and can result in increased availability of poorly available mineral nutrients. The soil biotic communities are formed by several kinds of microorganisms that can live symbiotically or in association with roots. Four major groups of microorganisms are considered as beneficial to plants: arbuscular mycorrhizal fungi (AMF, Jeffries *et al.* 2003), plant growth promoting rhizobacteria (PGPR, Vessey 2003), nitrogen-fixing rhizobia, which are usually not considered to be PGPR, and microbial biocontrol agents, which are composed of viruses, bacteria, yeasts and fungi.

Methods

To distinguish more than 80 isolates of *Pseudomonas* bacteria and bacteria dissolving phosphorus compounds, acquired from the soil in the root zone of apple and sour cherry trees, the technique of rep-PCR was employed, based on an analysis of DNA polymorphism. The tests allowed the selection of bacterial isolates that were different or belonged to the same strain. For the detection of arbuscular mycorrhizal fungi (AMF) in the roots of strawberry plants, the nested PCR technique was used, based on the amplification of fragments of the large subunit ribosomal gene (LSU rDNA) using specific primers. The analyses were performed on the DNA extracted from the roots of strawberry cultivars 'Honeoye', 'Elsanta' and 'Elkat' that had been treated with bio-preparations and fertilized with NPK (control). The tests helped to determine the presence or absence of mycorrhizal fungi of the genera *Glomus*, *Acaulospora* and *Scutellospora* in the roots. The effect of the bio-preparations on the presence of mycorrhizal fungi in the roots of strawberry plants was determined. Over 600 strains of *Pseudomonas fluorescens* and other beneficial bacteria and fungi (*Rahnella aquatilis*, *Bacillus* sp., *Trichoderma* sp.) have been collected. *Pseudomonas fluorescens* strains were isolated from selective S1 medium (Gould *et al.* 1984). Other beneficial bacteria were isolated from differentiating CAS agar medium (siderophores production) or Pikovska medium (dissolving phosphate compounds, Husen *et al.* 2003).

Ten bacterial strains with most potent beneficial abilities were identified and characterized by the BIOLOG system (Holmes *et al.* 1994; Pires & Seldin 1995) and used in further screening studies under greenhouse conditions. The studies indicate that three strains (Ps49A - *Pseudomonas fluorescens*, Pi3A and Pi5A - *Rahnella aquatilis*) enhance growth of strawberry plants. However, further and more complex studies must be conducted. Identification of spores: Trap cultures were set up with narrowleaf plantain in 0.5 L pots filled with a mixture of rhizosphere soil and autoclaved sand, at a ratio of 1:1 v/v (Błaszowski 2003). After six months, 200g samples of the pot substrate were taken from the trap culture combinations and spores were isolated by wet sieving and centrifuging in a sucrose gradient (Brundrett *et al.* 1996). The

isolated spores were divided into morphotypes according to size, shape, and colour of spores. The layer thickness of spore walls and germination walls was measured in freshly isolated spores which were crushed in PVLG or PVLG+Melzer's reagent (1:1, v/v) and observed under a light microscope with a micrometer eyepiece (Błaszowski 2003). The AMF species were named according to Schüßler *et al.* (2001) & Błaszowski (2003).

Results and discussion

The collection in SYMBIO BANK contains: spores isolated from the soil of the following plant species: strawberry 18.0 thousand, apple 10.5 thousand, sour cherry 1.5 thousand, pear 14.0 thousand, wild strawberry 9.0 thousand; Isolates of bacteria: *Pseudomonas fluorescens* -300, producing siderophores 500, dissolving phosphorus compounds - 200, digesting cellulose - 40, producing spores - 110, fixing atmospheric nitrogen - 100, *Actinomycetes* – 100; Isolates of microscopic fungi - 50, including *Trichoderma* sp. - 30. Trap cultures have been used to isolate and identify spores of the following species of arbuscular mycorrhizal fungi: *Ambispora fennica*, *A. gerdemannii*, *Gigaspora margarita*, *Glomus aggregatum*, *G. caledonium*, *G. claroideum*, *G. constrictum*, *G. drummondii*, *G. fasciculatum*, *G. macrocarpum*, *G. microaggregatum*, *G. mosseae*, *G. pallidum*, *G. rubiforme*, *Scutellospora dipurpureus*. The identified species and strains of AM fungi and PGPR bacteria are catalogued and stored in a Bank of Symbiotic Microorganisms, called SYMBIO BANK (stored in a cryoprotectant (glycerol) at the temp. of -80°C). A website of SYMBIO BANK will be launched, which will contain a list of the isolates held in the collection and their descriptions, which will serve as a source of key information for the identification of the species of AM fungi and PGPR bacteria. This will contribute to the knowledge of the biodiversity of these symbionts and help in the formulation of microbiologically-enriched bioproducts for use in fruit-growing practice. The most effective strains and species of microorganisms will be registered in Poland as bacterial and mycorrhizal inocula to be used in fruit production and in phytoremediation of heavy metal pollution.

Acknowledgements

The work has been supported by the EU Regional Development Fund through the Polish Innovation Economy Operational Programme (UDA-POIG.01.03.01-10-109/08-00).

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INTRODUCING NEW COST ACTION FA1405: USING THREE-WAY INTERACTIONS BETWEEN PLANTS, MICROBES AND ARTHROPODS TO ENHANCE CROP PROTECTION AND PRODUCTION

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Introduction

Recently, we initiated a new COST Action, entitled “using three-way interactions between plants, microbes and arthropods to enhance crop protection and production”. I will introduce the objectives of this new COST Action and discuss how it could link up with the new EUCARPIA Working Group on Plant-Microbe Interactions. COST (Cooperation in Science and Technology) is a European framework supporting trans-national cooperation among researchers, engineers and scholars across Europe to jointly develop new ideas and initiatives through pan-European networking of nationally funded research activities.

Plant-Arthropod-Microbe interactions

Crop plants interact with both arthropods and microorganisms, including pests that reduce yields (in Europe up to 20% annually) and mutualists that promote yield. Although much of our research efforts are devoted to studying either plant-microbe interactions or plant-arthropod interactions, often these organisms co-occur on plants and, more importantly, their effects are not independent of each other (Biere and Bennett

2013). Direct and indirect interactions between microorganisms and arthropods on crops lead to three-way interactions that can strongly modify their impacts on yield (e.g. Hauser et al. 2013). For instance, herbivores and pathogens can facilitate each other, causing additional yield loss, e.g. in the case of insect-vectored pathogens or secondary pathogens gaining access to crops through wounds created by herbivores. On the other hand, three-way interactions between plants, microbes and arthropods can also be beneficial to the crop, e.g. when beneficial microorganisms induce defenses that protect crops against particular types of herbivores (e.g. Zamioudis & Pieterse 2012). There is thus potential to enhance crop production and reduce pesticide use if we can better predict and manage such Crop-Arthropod-Microorganism (CAMo) interactions to our advantage. This is the overall aim of the COST Action. Recently there has been an enormous increase in our understanding of how plants integrate responses to multiple environmental signals at the molecular level, including hormonal regulation /crosstalk involved in responses to different types of microbes and arthropods, and how these are modulated by the abiotic environment, that can be helpful to better exploit such interactions.

Links with improving plant microbial symbiosis by plant breeders

Especially in low-input agriculture, plant/ rhizosphere-associated microbes such as plant growth-promoting rhizobacteria or fungi (PGPR/F), arbuscular mycorrhizal fungi (AMF), endophytes, and rhizobia can enhance crop productivity and stability by improving (1) plant nutrition, (2) tolerance to abiotic stress, and (3) resistance/tolerance to below- and aboveground pests and pathogens. As part of the COST Action, we are interested in optimizing interactions with beneficial microbes that can combine nutritional and stress tolerance benefits with enhanced direct and indirect (i.e. altered attraction/efficacy of pest

biocontrol agents) defense against arthropod pests. We can thus view our interest in the effects of beneficial microbes on arthropod pest resistance just as one specific component of how to use beneficial microbes to enhance crop productivity and stability.

Although there are not many plant breeders involved yet, the role of plant breeders seems to be promising as there is potential for exploiting genetic variation related to several components of symbiosis functioning. First, we can exploit variation in the ability of plants to exert selective enhancement/suppression of members of the rhizosphere community e.g. based on specific exudation patterns, root traits that maximize symbiotic interaction, or by selecting on traits underlying specific signaling and recognition interactions allowing only particular symbionts to associate (e.g. Kiers et al. 2010). Second, for specific applications (e.g. seed coating with PGPR) there is scope for breeding for specific cultivar/ strain combinations that provide the highest extent of (stability of) productivity benefit under prevailing conditions. Interestingly, studies in barley have shown that for instance the extent of rhizobacteria-induced aphid resistance is a function of both plant and aphid genotype, indicating the potential to select for traits underlying such more complex interactions (Tétard-Jones et al. 2007).

We hope the parallel interest can spark interactions between the new EUCARPIA working group and the COST Action. The Action will have three working groups (WGs) that can be joined. WG1 aims at understanding the **impact** of interactive effects of microbes and arthropod on yield under different environmental conditions, and how predictable these impacts are across cultivars/ strains, focusing on, but not restricted to tomato and oilseed rape. WG 2 aims at understanding the molecular and physiological **mechanisms** underlying crop-arthropod-microbe interactions. WG3 aims at **utilization** of our knowledge of such interactions to foster development of new strategies and products for improving crop protection and production.

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EFFECT OF PLANT DOMESTICATION ON THE RHIZOSPHERE MICROBIOME OF COMMON BEAN (*PHASEOLUS VULGARIS*)

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Introduction

Plant domestication was a pivotal achievement for human civilization and subsequent plant improvement increased crop productivity and quality. However, domestication also caused a strong reduction in the genetic diversity of modern cultivars compared to their wild relatives. It is known that plants rely, in part, on the rhizosphere microbial community for growth, development and tolerance to (a)biotic stresses. Assuming the plant dependence on the rhizosphere microbiome as a product of natural selection, it has been postulated that modern cultivars of crop plants may have lost some of the traits needed to recruit host-specific root microbiota as compared to their wild relatives, which are genetically more diverse and adapted to pre-agricultural soils (Wissuwa et al. 2009; Bulgarelli et al. 2013). Whether the ability of crop plants to recruit beneficial rhizosphere microbes was undermined by plant domestication and plant breeding is not known to date. The objective of this work was to analyse the rhizosphere microbiome of wild relatives, landraces and modern varieties of common bean in its native habitat and in agricultural soils, and to assess whether wild relatives and landraces recruits with higher frequency beneficial microbes as compared with modern cultivars.

Material and Methods

Two wild relatives, three landraces and three modern cultivars of common bean (*Phaseolus vulgaris*) were selected for this study (Table 1.). These different lines belong to the Mesoamerican bean gene pool of Colombia and were selected amongst more than 37,000 accessions kept in the Genetic Resources Program of the International Centre for Tropical Agriculture (CIAT, Colombia). The eight accessions were grown in both native and in agricultural soils collected in the province of Antioquia (Colombia). At flowering stage, plants were harvested, the rhizospheric soil was collected and DNA was extracted. To assess the bacterial taxonomic diversity the V3-V4 region of the 16S rRNA was sequenced using MiSeq technology. With the resulting OTU table, statistical analyses were performed using Phyloseq (McMurdie and Holmes, 2013) and Vegan (Oksanen et al, 2013) packages in R.

Results and discussion

In the agricultural soil all the accessions showed enrichment in Proteobacteria as compared to the bulk soil, explained by the recruitment of the genus *Rhizobium*. An enrichment of Bacteroidetes was observed in the wild accession G22304 and in the landrace G23998, specially of the Chitinophagaceae and Cytophagaceae families. Also unclassified Chitinophagaceae were enriched in both accessions. It is interesting to note that these accessions were collected in the same geographic region from Colombia, and also clustered together after genotypification using DArT microarrays. Although the wild accession G51283K1 showed significant differences in the statistical analysis, not clear trends could be detected. The modern cultivar G5773 was enriched in Actinobacteria, mostly explained by a higher relative abundance of the genus *Streptomyces*.

Accession number	Status
G22304	Wild
G51283K1	Wild
G5063211	Landrace
G50398	Landrace
G23998	Landrace
G14947	Modern
G51695	Modern
G5773	Modern

Table 1. Common bean accessions used in the study. The seeds were kindly provided by the Genetic Resources Program of the International Center for Tropical Agriculture (CIAT) in Palmira, Colombia.

In the native soil all the accessions showed significant differences with the bulk soil, although the rhizosphere effect was less pronounced than in the agricultural soil. No differences between the genotypes were detected in the native soil. To assess whether the enrichment of Chitinophagaceae and Cytophagaceae family in wild relatives and old landraces is related with a defensive mechanism against soil pathogenic microbes, targeted isolation of bacteria as well bioassays with phytopathogens will be performed.

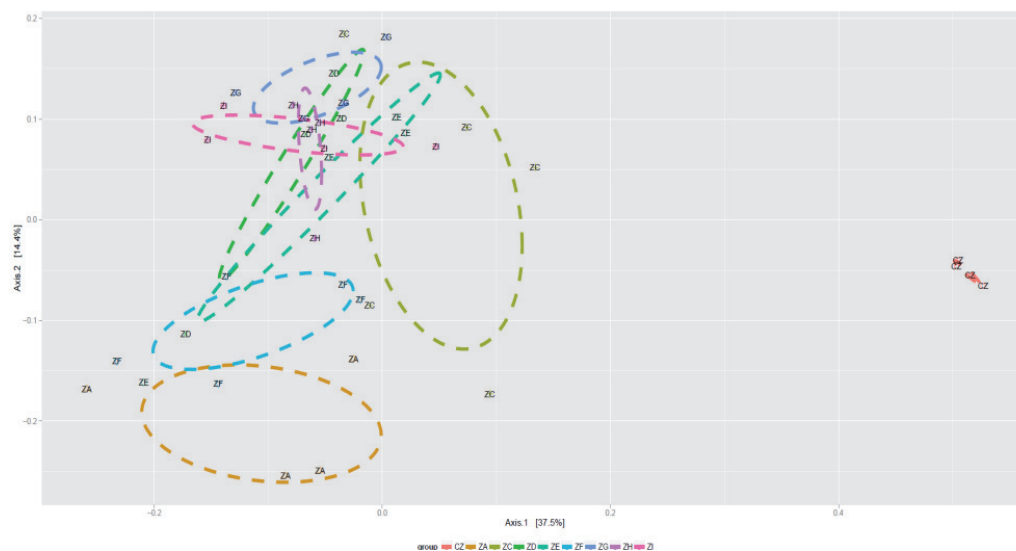


Figure 1. PCoA-Bray centroids plot showing the distance between the accessions and the bulk soil (CZ). Accessions G22304 (ZA) and G51283K1 (ZC), both wild, as well the landrace G23998 (ZF), displaying higher distance with respect to the other two landraces and the modern varieties: G5063211(ZD); G50398 (ZE); G5773 (ZG); G14947(ZH) and G51695 (ZI).

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INFLUENCE OF TERROIR ON THE FUNGAL ASSEMBLAGES ASSOCIATED TO COMMON BEAN SEED

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Introduction

Plants have evolved in association with microbial assemblages, also known as microbiota, which can affect plant growth and health. In contrast with other plant habitats, microbiota associated to seeds have only recently become an object of research. First surveys reveal that seed-associated microbial assemblages are composed of 50 to 1000 bacterial and fungal operational taxonomic units (OTUs) (Barret *et al.*, 2015), including plant pathogens. Common bean (*Phaseolus vulgaris* L.) is affected by several seed-borne pathogens representing a phytosanitary challenge for common bean seed production. In a participatory research project (Farm Seed Opportunities, a European FP6 project), small scale organic seed producers emitted the hypothesis that seed microbiota in their integrity, including pathogens, play a role in shaping the crop as it adapts to local environments, leading to more resilience (Döring *et al.*, 2014). As a first step to investigating this hypothesis, we analyzed 27 bean seed samples to assess whether the seed microbiota are indeed site-dependant or in contrary transmitted from one plant generation to the next within each cultivar.

Material and Methods

The influence of the cultivar and seed production site on the structure of the seed microbiota was assessed on 27 seed samples obtained from two cultivation sites. These seed samples were obtained by multiplying 5 initial seed lots in two organic farms in Brittany and Luxembourg in three replicates in 2012 and 2013. Four of these seed lots consisted of farm seeds of traditional cultivars; one was seed of the commercial variety 'Calima' obtained from a breeding company and used as a commercial control. The initial seed lots were thus exposed to contrasting biotic and abiotic environments for two consecutive years. One cultivar ('Rognon de Coq') did not yield sufficient seed for sampling in Luxembourg. Total genomic DNA extraction was performed on 200-seeds subsamples collected from each seed lot. The composition of the bacterial and fungal communities was analyzed by high-throughput sequencing (Illumina MiSeq v. 2.0 platform, 250 bp paired-end reads) of the bacterial 16S rRNA gene and the fungal ITS1 region, respectively. Low quality reads were removed using the standard operational procedure of Mothur (Schloss *et al.*, 2009; Kozich *et al.*, 2013). High-quality sequences were then grouped in operational taxonomic units (OTUs) at a genetic distance of 0.03. Only OTUs with a minimum threshold of 1 ‰ relative abundance were conserved for further analyses and defined as abundant OTUs (aOTUs). Variation of bacterial and fungal diversity across samples was assessed by calculating Bray-Curtis dissimilarity indexes. Analysis of molecular variance (AMOVA) test was performed

Results and Discussion

The microbiota associated to the seed samples are mainly composed of bacteria belonging to *Proteobacteria* and fungi related to *Dothiodemycetes* and *Sordiariomycetes*, as found for other plant-associated microbiota (Meiser *et al.*, 2013). At OTU level, bacterial assemblages are differ strongly, with only one aOTU conserved across all seed samples, affiliated to *Pseudomonas*. Even bacterial assemblages on samples of the same bean cultivar from same site have few aOTU in common (1-28%). With a minimum of 38000 high quality sequences obtained per sample, we can explain this by the fact that each seed may possess a unique assemblage of bacterial taxa, rather than by a lack in sequencing effort. We conclude

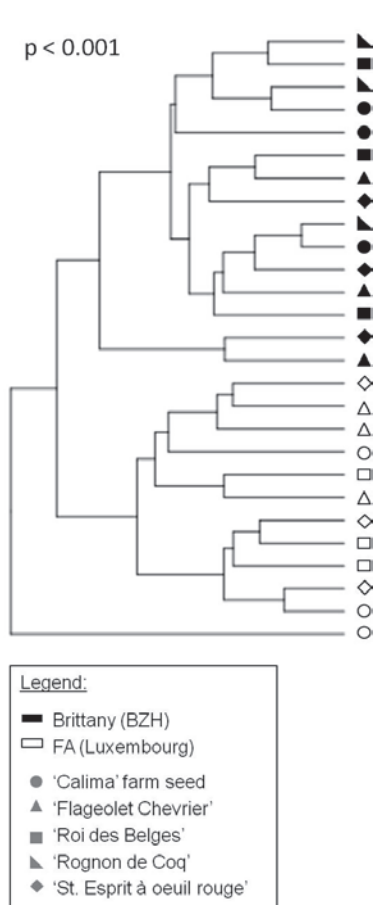


Figure 1. Seed-associated fungal assemblages clustered primarily by experimental site

that the processes driving seed-associated bacterial diversity are neutral ones, such as colonization history and dispersal limitation.

Despite a fairly high similarity between fungal assemblages of seeds of the same bean cultivar harvested on the same site (27.6 to 55.9% of shared aOTUs), only seven fungal aOTUs are conserved across all samples, attesting a strong effect of the experimental site on fungal diversity. In contrast with the bacterial assemblages, the fungal assemblages are affected by deterministic processes dependant on the cultivation site. Such biogeographic patterns have also been observed for soil-associated fungal assemblages (Meiser *et al.*, 2013). The clustering of seed samples according to Bray-Curtis distances (**figure 1**) promotes this hypothesis. Despite the use of genetically diverse cultivars for the analysis, no cultivar effect on fungal assemblages was found.

Hence, the dispersion of seed in different production sites (or terroirs) affected seed-associated fungal assemblage after only 2 years of multiplication. Further research on the evolution of the fungal assemblages in time and the functions of the fungal species is needed to determine whether this may impact seed fitness. In any case, farmers engaged in small-scale, local seed production seem to be safeguarding not only the genetic diversity of traditional cultivars, but also seed-associated fungal assemblages specific of their biogeographic location.

Acknowledgements

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EFFECTS OF THE INOCULATION WITH SOIL MICROBIOTA ON MAIZE GROWN IN SALINE SOILS

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Introduction

According to the UN 2010 predictions, the human population will reach 10 billion by 2080. The food and energetic needs will thus increase dramatically, while conventional agriculture is facing drastic reductions in production yields and/or severe increases in cost to compensate losses in productivity due to lower soil fertility. Soil salinity is a serious problem worldwide causing potential loss of fertility, as plants facing salt stress suffer alterations that adversely affect its growth (Parida and Das, 2005).

A possible strategy for coping with salinity may be the use of crops that are able to survive under the installed saline conditions however the growth of particular crops with high economic valorisation in such soils would be disabled. Therefore, amelioration of the growth of plants with high yield, biomass and economical value such as maize (*Zea mays* L.) should be explored. This work aimed evaluating the effectiveness of combinations of microorganisms for the recovery of maize productivity in saline soils.

Material and Methods

In this study a strategy was set that relied on the culture in greenhouse conditions of a high value food and energetic crop (maize) inoculated with soil plant growth promoting microbiota –an arbuscular mycorrhizal fungi (*Rhizophagus irregularis*), and a rizospheric (*Pseudomonas reactans*) and an endophytic (*Pantoea alli*) plant growth promoting bacteria (PGPB), exposed to soils with different salinity levels (0, 2.5 and 5 mg NaCl kg⁻¹). A randomized design of 5 treatments for each tested concentration was conducted as follows: 0) non-inoculated control soil with maize ; B) soil with maize inoculated with *P. reactans*; F) soil with maize inoculated with *R. irregularis*; E) soil with maize inoculated with *P. alli*; and MIX) soil with maize inoculated with *R. irregularis*, *P. reactans* and *P.alli*.

Roots and shoots of maize plants were harvested 60 days after seeding, washed with deionized water, followed by HCl 0.1 M and again with deionized water. Samples were placed in an oven at 70 °C for 48 h to determine their dry weights. As the work also aimed at relating the effects of bioinoculation with alterations in plant response to salt stress, tissue, root and shoot's samples were then grinded and sieved to <1 mm and digested in a PerkinElmer Microwave 3000 (Waltham, USA) following the 3052 USEPA method. Sodium content was determined using Inducted Couple Plasma by Optic Emission Spectrometry (ICP-OES) of the digests (Wallinga et al., 1989).

Results and Discussion

Increasing salt concentration decreased plant biomass production (Table 1). However, all microbial treatments induced increases in maize shoots and roots biomass, with the mixed inocula (MIX) including all tested microbiota generally outperforming the other treatments.

Table 1: Effects of microbial inoculation and salt concentration on maize biomass (g) (n=4).

SHOOT	sample	biomass (g)			sample	biomass (g)			sample	biomass (g)				
	0C	2,06	±	0,02	^c	2.5C	1,55	±	0,16	^c	5C	0,92	±	0,05
0B	2,68	±	0,28	^b	2.5B	1,74	±	0,09	^b	5B	1,39	±	0,12	^b
0F	2,40	±	0,36	^b	2.5F	2,41	±	0,06	^a	5F	1,50	±	0,08	^b
0E	2,65	±	0,23	^b	2.5E	1,90	±	0,08	^b	5E	1,40	±	0,15	^b
0MIX	3,00	±	0,11	^a	2.5MIX	2,32	±	0,08	^a	5MIX	1,86	±	0,13	^a
F=11,158 (sig=0)				F=69,501 (sig=0)				F=45,943 (sig=0)						
ROOT	sample	biomass (g)			sample	biomass (g)			sample	biomass (g)				
	0C	0,75	±	0,09	^d	2.5C	0,44	±	0,11	^d	5C	0,37	±	0,02
0B	1,14	±	0,09	^b	2.5B	0,54	±	0,08	^c	5B	0,46	±	0,01	^c
0F	1,27	±	0,14	^a	2.5F	0,75	±	0,08	^b	5F	0,57	±	0,02	^b
0E	0,90	±	0,09	^c	2.5E	0,42	±	0,03	^d	5E	0,40	±	0,01	^d
0MIX	1,08	±	0,08	^b	2.5MIX	0,99	±	0,02	^a	5MIX	0,61	±	0,04	^a
F=20,891 (sig=0);				F=54,606 (sig=0)				F=120,565 (sig=0)						

Concerning sodium uptake by maize, it increased with increasing soil concentrations, being the accumulations in roots and shoots generally of the similar order. Generally, microbial inoculation prevented Na uptake in maize roots or shoots, and again the treatment with the mixture of all tested organisms (MIX) showed significantly ($P < 0.05$) higher effects, although in some cases treatment with *Rhizopagus irregularis* (F) showed a similar effect.

Table 2: Effects of microbial inoculation and salt concentration in sodium uptake (g/kg plant fry weight) by maize (n=4).

SHOOT	sample	Na (g/kg)			sample	Na (g/kg)			sample	Na (g/kg)				
	0C	0,018	±	0,004	^{ab}	2.5C	7,4	±	0,2	^a	5C	13,2	±	1,1
0B	0,021	±	0,001	^a	2.5B	7,2	±	1,2	^a	5B	11,1	±	0,8	^b
0F	0,007	±	0,005	^c	2.5F	4,6	±	0,3	^b	5F	4,7	±	0,4	^d
0E	0,015	±	0,001	^b	2.5E	7,2	±	0,1	^a	5E	9,2	±	0,7	^c
0MIX	0,009	±	0,002	^c	2.5MIX	5,2	±	0,8	^b	5MIX	3,9	±	0,2	^d
F=13,395 (sig=0)				F=11,873 (sig=0)				F=92,763 (sig=0)						
ROOT	sample	Na (g/kg)			sample	Na (g/kg)			sample	Na (g/kg)				
	0C	1,17	±	0,14	^a	2.5C	7,6	±	0,9	^a	5C	11,5	±	1,9
0B	1,06	±	0,1	^{ab}	2.5B	7,3	±	0,7	^a	5B	10	±	0,9	^{ab}
0F	0,93	±	0,04	^{bc}	2.5F	5,8	±	0,8	^b	5F	10,1	±	1,3	^{ab}
0E	1,06	±	0,11	^{ab}	2.5E	5,5	±	0,5	^b	5E	9,06	±	0,7	^{bc}
0MIX	0,76	±	0,08	^c	2.5MIX	5,5	±	0,3	^b	5MIX	7,4	±	0,6	^c
F=7,785 (sig=0,001)				F=6,703 (sig=0,003)				F=4,975 (sig=0,009)						

This study supports that adequate inoculation is determinant for the recovery of saline soils, and that a combination of soil microbiota including rhizospheric, endophytic bacteria and mycorrhizal fungi can allow a glycophyte as maize to proliferate in such land, rendering it prone to economic valorisation. The adequate combination of AMF, PGPR and host plants is determinant for the result of their interaction under stress and consequently for their potential use in management of saline soils.

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MYCORRHIZA-MEDIATED DISEASE RESISTANCE - A MINI-REVIEW

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Abstract

Arbuscular mycorrhizal fungi (AMF) play an essential role as one of the primary mutualistic plant-microbe symbioses. Plants benefit from root endophytes that extend their zone of activity beyond the rhizosphere (Feddermann *et al.*, 2010; Hohmann *et al.*, 2011, 2012). The main known benefits of mycorrhiza involve nutrient mobilisation (mainly phosphorus), improved tolerance against abiotic (mainly drought) and biotic stresses (mainly soil-borne pathogens) (Azcón-Aguilar & Barea, 1996; Parniske, 2008). An increasing number of studies highlight a significant role of AMF in the mediation of disease resistances. Besides an improved phosphorus use efficiency, individual reports have shown enhanced levels of defence-related compounds (such as glucanases, chitinases and phenolics) in mycorrhizal plants, and there is first evidence of certain phytohormone pathways (in particular jasmonate signalling) to be involved in mycorrhiza-mediated disease resistance (Jung *et al.*, 2012).

Despite their ecological and nutritional importance, legume crops receive less and less attention in breeding programmes and crop rotations. Increasing problems with fungal diseases seem to be a main cause for the decline in yield (Wilbois, 2011; Finckh *et al.*, 2013). However, legumes are known to show particularly strong interactions with important symbionts such as AMF and *Rhizobium* spp. and, therefore, provide a valuable model system to identify genotypes that interact efficiently with symbiotic microbes.

Linkage mapping was used to identify quantitative trait loci (QTL) and genes in pea that are linked to resistance against various pathogens (Prioul-Gervais *et al.*, 2007; Pereira *et al.*, 2009; Fondevilla *et al.*, 2011; Hamon *et al.*, 2011; Li *et al.*, 2012). The ability of plants to respond to AMF can vary widely between plant species and among genotypes (Parke & Kaeppler, 2000; Sawers *et al.*, 2010). Genotypic differences in the response to AMF have been observed in various crops (Powell *et al.*, 1982; Hetrick *et al.*, 1993; Kaeppler *et al.*, 2000; Tawaraya *et al.*, 2001). Such differences in mycorrhizal responsiveness indicate a genetic basis for plant-AMF interactions. Galván *et al.* (2011) were the first to report on QTL governing responses of onion species to AMF based on shoot biomass. However, little is known about the genetic basis for mycorrhiza-mediated disease resistance and more research is needed to exploit genotypic differences, e.g., via marker-assisted selection.

For legume crops, the use of association mapping has been restricted in the past due to insufficient genome-wide marker coverage. Most recently, 384 pea accessions of the United States Department of Agriculture – Agricultural Research Service (USDA-ARS) pea core collection were genotyped for 20.000+ single nucleotide polymorphism (SNP) marker using genotyping-by-sequencing. These SNP markers are currently being mapped *in silico* using *M. truncatula* to establish a physical genetic map. Further, a linkage map of a portion of these SNP markers will also soon be created using a pea recombinant inbred population. This high density genotyped association mapping panel can now be used for genome-wide association studies as demonstrated for barley (Pasam *et al.*, 2012; Shu *et al.*, 2012).

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DEGREE OF ROOT COLONIZATION AND OF INDUCED RESISTANCE IN WHEAT IS DETERMINED BY THE BACTERIAL STRAIN AND THE WHEAT GENOTYPE

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Introduction

Crop plants are colonized by a myriad of micro-organisms on all plant organs. These micro-organism can interact in many different ways as beneficials, as pathogens or as saprophytes with their host. By this interplay, they probably play a primordial role in the adaptation to environmental conditions, resilience to abiotic stresses and in the resistance against diseases and pests. The present experiments explored the effects of several rhizosphere-borne biocontrol strains of *Pseudomonas protegens* and *P. fluorescens* on the resistance of wheat varieties against brown rust disease caused by *Puccinia triticina*.

Material and Methods

Plant material: The tests have been realized with susceptible (CIMETTA and ARINA) and intermediate resistant (ZINAL, FORNO) cultivars.

Beneficial root colonizers: Seeds have been coated with a suspension of beneficial *Pseudomonas* strains (tab.2) and planted into peat soil in plastic pots.

Experimental procedure: Inoculated pots were placed in the greenhouse (temp. 20°C with light 12/12h). At the 3 leaf stadium (BBCA 20), a mixture of uredospores from Swiss brown rust strains was sprayed on the plants and incubated until appearance of pustules. Number of pustules were counted on each infected leaf and disease severity was expressed as percentage of the average number of pustules per leaf compared with the control treatment (without bacterial inoculant).

Results and Discussion

Inoculation of roots with biocontrol pseudomonads reduced significantly the severity of symptoms on the leaves in all wheat cultivars. Interestingly, the degree of disease reduction was lowest in Forno but highest in Zinal. The plant response depended on the degree of colonization of the root, the state of health of the plant and the wheat cultivar used (not shown). These results suggest a straight interaction between plant and beneficial bacteria at the molecular level.

Tab 1. Beneficial *Pseudomonads* used to trigger induced resistance.

Strain	Description	Reference
<i>P. protegens</i> CHAO	wild type	Keel et al., 1989
<i>P. protegens</i> CHAO gfp*	tagged with the GFP protein	Péchy-Tarr & Keel, unpublished
<i>P. fluorescens</i> PF153 gfp*	tagged with the GFP protein	Péchy-Tarr & Keel, unpublished
<i>P. fluorescens</i> Q2-87 gfp*	tagged with the GFP protein	Péchy-Tarr & Keel, unpublished

Reference

Keel, C., Voisard, C., Berling, C.-H., Kahr, G. and Défago, G. 1989. Iron sufficiency, a prerequisite for suppression of tobacco black root rot by *Pseudomonas fluorescens* strain CHA0 under gnotobiotic conditions. *Phytopathology* 79: 584–589.

THE IMPACT OF THE HOST GENOTYPE ON THE STRUCTURE OF THE SEED AND RHIZOSPHERE MICROBIOME: SUGAR BEET AND LETTUCE AS MODEL PLANTS

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Introduction

The structure and function of the plant microbiome is driven by plant host species and prevailing environmental conditions, but also the host genotype play a significant role in microbial community's formation and activity. Thus, plant breeding efforts instantaneously affect the crosstalk between host plant and microbiome, e.g. mediated by the composition of root exudates, and lead to microbial diversification. Little is known about how breeding of modern crop plants affects the microbiome composition in particular microhabitats such as seed, rhizosphere or phyllosphere, and how the microorganisms contribute to specific characteristics of a cultivar with respect to susceptibility to diseases or abiotic stresses. Our microbiome analyses aim to identify microbial key members with important role in disease defence and plant growth. Moreover, we wanted to understand microbial network structures and co-occurrence patterns in plant-microbe interactions and the impact of domestication. Results could direct to holistic concepts for agricultural management and breeding strategies to improve productivity and sustainability [1].

Material & Methods

To analyse the naturally composed seed and rhizosphere microbiome of various cultivars of both crops, lettuce and sugar beet, we applied a combined analysis comprising an amplicon sequencing approach using Illumina's MiSeq platform and microscopy technologies such as fluorescence *in situ* hybridization (FISH) and confocal laser scanning microscopy (CLSM).

Sugar beet (*Beta vulgaris* L.) cultivars were selected according to their susceptibility to the late root rot caused by the soilborne pathogen *Rhizoctonia solani* (tolerant, susceptible and effective). The study for lettuce (*Lactuca sativa*), the most raw eaten vegetable with benefit for human health, comprised the cultivars *incocta* (cultivar *capitata* and *crispa*) and *sativa* (cultivar *longifolia* and *augustana*) as well as the ancestor *L. serriola*. Data from amplicon sequencing were analysed by a comprehensive bioinformatics workflow including taxonomic assignment, calculation of diversity metrics as well as computation of networks. The sequencing approaches were additionally complemented by visualization of bacterial colonization patterns on leaves and roots using FISH-CLSM and a DsRed-labelled representative of a cultivar-specific sugar beet-associated endophyte.

Results & Discussion

In total, the microbiome of seed and rhizosphere of five sugar beet cultivars with different degree of susceptibility to *R. solani* were studied by 16S rRNA gene amplicon sequencing. Reads covered between 17.6 to 25.9% of the microbial communities. A distinct impact of the sugar beet cultivar on the microbiome composition was observed. According to Principal component analysis of unweighted UniFrac distances the tolerant cultivars clustered together and were shown to be separated from the susceptible and effective cultivars. The results revealed a specific acquirement of bacterial genotypes with potential antagonistic properties, which might be one reason for the lower susceptibility of the *R. solani*-tolerant cultivars. This fact was supported by the cultivar-specific occurrence of antagonistic sugar beet-associated

key species like *Pseudomonas* sp. [2]. By applying microscopy and quantitative real-time PCR, *R. solani*-tolerant and susceptible sugar beet cultivars were characterized by different abundance, enrichment and interaction with a potentially beneficial *Pseudomonas* genotype. In the *Rhizoctonia*-tolerant cultivar, the *Pseudomonas* genotype was enhanced in seed, endorhiza and rhizosphere independent of the surrounding soil. In contrast, the *Rhizoctonia*-sensitive cultivar contained no detectable number of this genotype.

For the four lettuce cultivars and the ancestor *L. serriola* a total of 709,021 reads were obtained. The core of all *L. sativa* microbiomes comprised 68 operational taxonomic units (OTUs) constituting 48.8% of all reads; whereas 71 OTUs showed significantly different relative abundances between lettuce subspecies. The root microbiota differed more between cultivar groups than between convars indicating a prevailing effect of the host genotype over the plant morphology on the structure of the root microbiota [4]. Spearman correlations between OTUs revealed potential interactions between bacteria based on their occurrence patterns. A central position was found for Gammaproteobacteria. We showed that domestication of lettuce is supported by an overall increase of bacterial diversity. Microbial diversity is of importance when it comes to potential pathogen outbreaks, which are results of co-occurrence characterizing the relationships among members of the root microbiota as opposed to co-exclusion of the microbiome members.

Overall, the microbiomes associated with sugar beet and lettuce showed a strong cultivar specificity. Moreover, we were able to identify microbial key species potentially involved in the disease tolerance of sugar beets. Along with the breeding history from wild ancestors to modern plant cultivars the associated microbiome is assumed to co-evolve and to be essentially connected with specific properties of the cultivars with respect to susceptibility to diseases or abiotic stresses [3,4]. Generation-spanning specificity and stability of associated microbiota is ensured by the transmission of beneficial microbial partners via seeds that harbor a representative core community. The results suggest that consideration of microbiomes in plant breeding can contribute to new integrated management strategies in modern sustainable agriculture and further lead to the development of so-called next-generation bio-products for disease control and plant growth promotion with stable field efficacy [1].

Acknowledgement

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BREEDING FOR BENEFICIAL ROOT-MICROBIAL RELATIONSHIPS: HOW DO WE GET THERE?

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Plant breeders have made tremendous strides developing new varieties that maximize plant productivity in the presence of synthetic agrochemical inputs. This has come at a cost, however, in the form of nutrient loss and development of pesticides resistance. In response some are calling for a new paradigm where crops are selected for their potential to thrive in low-input production systems via optimized interaction with the soil resource. To accomplish this goal plant breeders will need to focus on belowground traits, including differences in root architecture and root exudates, and functional interactions with beneficial soil microbes. Soil microbes play a central role in the breakdown of organic matter, the mineralization and immobilization of nutrients in soil, mediating plant pathogens, and in maintaining soil structure. Hence they are crucial to soil function and plant health even though their role tends to be marginalized in current soil fertility and disease management recommendations. Soil microbes also directly influence plant fitness by altering physiological and development processes, facilitating nutrient and water uptake, and helping plants tolerate biotic and abiotic stress (reviewed in Phillippot et al., 2013). These interactions occur largely in the rhizosphere, a narrow zone of soil that surrounds and is influenced by plant roots. The number of microbial cells inhabiting the rhizosphere greatly outnumbers plant cells, and the community present at this interface is now referred to as the 2nd genome of the plant, or its microbiome (Berendsen et al., 2012).

To effectively breed for beneficial root-microbial relationships the following conditions need to be met: 1) there must be clearly identifiable genetic variation, 2) the relationships must be heritable, and 3) selection among breeding populations must be practical. Soil type and management history are key factors shaping soil and rhizosphere biological communities, though it is now clear that plants specifically recruit individual microbial taxa and selectively shape the composition of their rhizosphere. Many studies have provided evidence that plant genotype can also influence rhizosphere community structure, with some indicating that the relationships appear to be heritable (Lundberg et al., 2011; Pfeifer et al., 2013). These studies provide evidence that breeders could begin to select for beneficial root-microbial relationships, but meeting the third condition will be difficult. There is still much uncertainty about how plants signal and actively support rhizosphere microbial communities. It is also unclear whether individual microbial taxa act alone or in a consortium, and whether there is a core set required for successful plant function, or if there is functional redundancy among rhizosphere communities. The genetic and physiological mechanisms regulating plant fitness in response to many root microbes are also not well understood. Hence there is currently a lack of simple and effective methods for direct selection among large numbers of breeding populations, and knowledge of whether varieties could be selected for broad adaptability.

To move forward breeders will need to collaborate with scientists from multiple disciplines including agronomy, plant pathology, soil science, microbial ecology, molecular biology, and bioinformatics. They will need to use utilize new technologies that can overcome culture bias and identify functional relationships between plants and microbes as well as microbe-microbe relationships in the rhizosphere. Controlled experiments, such as a recent study conducted by Zancarini et al., (2012), will be critical to identifying elemental traits that contribute to plant fitness and could be used to screen plants in field environments. Breeders may need to utilize wild type and/or land races to obtain suitable germplasm, and even go back to the site of domestication to identify key microbial taxa for potential inoculants if they are not present in agricultural systems as suggested by Hale et al. (2014). Genome-wide association studies (GWAS) could provide valuable insight into plant loci that regulate key plant-microbial interactions (Horton

et al., 2014). Quantitative trait loci (QTL's) identified using GWAS and mapping populations will be useful in marker assisted selection, though results will need to be confirmed in field trials. Finally, selection will need to occur in low-input production systems. Several studies have provided evidence that selecting in high-input production systems can inadvertently result in the loss of beneficial root-microbial relationships, whereas selecting in low-input and organic production systems could optimize selection for such relationships.

In on-going studies, we are using various combinations of these approaches to identify competent germplasm and elucidate the mechanisms mediating beneficial root-microbial relationships in carrot and tomato. A diverse panel of carrot genotypes are being tested in paired organic and conventional trials in four locations over a period of four years to determine how soil quality influences genotype performance. The composition and functional activity of root endophytes in a subset of carrot genotypes with wide genetic backgrounds are being quantified using culture dependent and independent techniques. An organic tomato breeding program is currently underway, and a diverse set of wild type, land race, and modern genotypes are being evaluated for their responsiveness to induced systemic resistance to foliar pathogens.

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GENOTYPE-DEPENDENT INTERACTION WITH BENEFICIAL PLANT-ASSOCIATED BACTERIA

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Introduction

In the following decade an increase in food demand is projected because of the rapidly increasing world population and changing consumption habits. In the meantime, less arable land will be available due to human activities and climate change. To ensure stable food production, the resources have to be used efficiently and equitably and with a concurrent reduction of food waste. In many regions including Europe, food production is on the verge of exceeding environmental limits. Nitrogen synthesis exceeds the planetary boundary by a factor of four and phosphorus use has reached the planetary boundary (<http://ec.europa.eu/environment/eussd/food.htm>). Sustainable agricultural practices should be developed to ward off to reduce the negative impact of chemicals, like inorganic fertilizers and pesticides. Novel approaches have been proposed, which employ plant-associated microorganisms to improve plant growth and health. Plant growth-promoting rhizobacteria (PGPR) and fungi (PGPF) protect plants from various forms of abiotic and biotic threats (Yang et al. 2009,), antagonize soil-borne pathogens (Raaijmakers et al. 2005) improve host nutrition (Hayat et al. 2010) and/or promote plant growth (Mitter et al. 2014). In addition to PGPR, endophytic bacteria that colonize plants internally and promote plant growth and health may be even more important in agricultural practice because they escape competition with soil microorganisms and are in intimate contact with plant tissues. In order to use endophytes in cropping systems it is essential to know the mode(s) of action inside the plant to fully exploit the beneficial effects of endophytes. It is known that pathogens and beneficial microbes share some similar pathways (Spaepen et al. 2013), but endophytes are able to establish themselves inside the plant without causing negative effects on the plant.

The plant host plays a pivotal role in the beneficial plant microbe interaction. The mechanisms of recognition and signal transduction are mostly unknown. While some of the physiological and molecular mechanisms involved in the positive response of plants to beneficial bacteria have been elucidated (Ait Barka et al. 2006, Fernandez et al. 2012, Poupin et al. 2013), little is known about the signaling mechanisms associated with plant receptiveness to these beneficial bacteria.

Results and Discussion

At AIT several plant species (maize, wheat, soybean, potato) and varieties were treated with different endophytic strains to promote germination and plant biomass production. In all experiments performed a host genotype effect was found regarding the response of the plant to inoculation with plant beneficial strains. In the case of wheat, various bacteria strains were inoculated individually onto various wheat genotypes. The response (i.e. germination improvement) of each variety was different, each variety germinated better in combination with one specific bacterial strain. Furthermore, the potato varieties Russet Burbank and Bionta showed a highly different growth response to inoculation with strain PsJN. Using a custom made potato microarray both varieties showed differences on the transcriptional level suggesting different mechanisms of interactions, which will be discussed.

In addition to different responses to inoculation, several studies performed at our institution as well as elsewhere have shown that different plant varieties host distinct microbial communities (Rasche et al., 2006; Hardoim et al., 2011; Ardanov et al., 2012). This suggests that different plant varieties show genetic and physiological differences, which lead to the uptake and maintenance of different microbiota, which are also likely to show functional differences.

Overall, the variability of different genotype in regard to the interaction with either naturally occurring microbiota or to inoculated individual strains suggests that the potential is high to make better use of plant genetic diversity for a more efficient interaction with beneficial microorganisms. On the one hand varieties could be selected for a better response with inoculant strains applied as biofertilizers or biopesticides. Furthermore, plants could be improved (e.g. by breeding) to better select beneficial members of naturally occurring microbiota. To achieve this goal a better understanding of the genetic basis of the interaction between plants and microorganisms is needed as well as suitable markers and screening procedures have to be applied.

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SCREENING CONCEPT FOR PLANT-MICROBE INTERACTIONS ON THE STYRIAN OIL PUMPKIN AS BASIS FOR AN ADVANCED BREEDING STRATEGY

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Introduction

The dark-green, healthy pumpkin seed oil is of traditional use in Austria and has also become popular in the international gourmet cuisines. As a consequence, the Styrian oil pumpkin (*Cucurbita pepo* L. subsp. *pepo* var. *styriaca* Greb.) has become an important oil crop world-wide. Due to the lack of lignification of the seed coat this crop is highly susceptible to various fungal and bacterial pathogens during germination. Leaves of adult plants are frequently infested by the fungus *Didymella bryoniae*, powdery mildew and bacterial pathogens. Fruit rot is caused by consortia of *D. bryoniae* and *Pectobacterium carotovorum*. Abiotic stress factors like heat, drought or heavy rainfalls influence the performance of the crop as well. Collectively known as the plant microbiome, plant-associated microbes can help plants to fend off diseases, stimulate growth, occupy space that would otherwise be taken up by pathogens and promote stress resistance. Additionally they influence crop yield and quality (Berg et al. 2013). As a high cultivar-specificity has already been shown for interactions with pathogens it is likely, that there also exists a high cultivar-specificity on the beneficial plant-microbe interactions. The development of a strategy to screen for such interactions should support breeding of new cultivars that are better capable to exploit the beneficial indigenous microbial community as well as artificially added biocontrol agents.

Materials and Methods

Screening methods already established for the evaluation of biocontrol agents should be used for the assessment of differences in plant-microbe interactions of oil pumpkin cultivars. For this purpose five microbial model strains, listed in Table 1, should be applied to the seeds of four homozygous oil pumpkin breeding lines as well as on a F1 squash hybrid with different characteristics concerning growth type, susceptibility to leaf necrosis and to fruit rot.

Table 1. Model strains for the purpose as beneficial microbes

Strain	Reported results
<i>Serratia plymuthica</i> S13	Increased seedling emergence of field grown pumpkins by up to 109 % (Fürnkranz et al. 2012)
<i>Serratia plymuthica</i> 3Rp8	Significant growth promotion in greenhouse trials (Adam, 2015, unpublished data)
<i>Lysobacter gummosus</i> L101 and <i>Paenibacillus polymyxa</i> PB71	Significant suppression of powdery mildew, reproducible increases in harvest yields (Fürnkranz et al. 2012)
<i>Trichoderma velutinum</i> G1/8	Suppression of <i>Didymella bryoniae</i> <i>in vitro</i> (Adam, 2015, unpublished data)

The evaluation of the plant-microbe interactions will include (i) a visualization of root colonization patterns involving determination of cell counts: for confocal laser scanning microscopic analysis, three of the model strains (*Serratia plymuthica* S13 and 3Rp8 as well as *Trichoderma velutinum* G1/8) were transformed with rhizosphere-stable vectors hosting different fluorescent proteins; (ii) greenhouse experiments to evaluate seed germination and early plant development after introduction of varying microbial communities into sterile soil, (iii) field trials for the evaluation of pathogen suppression on adult plants and the influence of a shift in the microbial community on the yield and (iv) metagenome analyses, microbial fingerprints and

fluorescence in situ hybridization microscopy of field samples to determine the enrichment of different taxonomic taxa depending on the cultivar.

Results and Discussion

Already conducted experiments with *Serratia plymuthica* biocontrol strains under axenic conditions revealed a high abundance of the bacteria (10^9 cfu g⁻¹ fresh weight) on the roots and on the leaves after seed priming with those strains. Figure 1a shows a densely colonized root, visualized by confocal laser scanning microscopy. Nevertheless an uneven distribution of the bacteria within the root system was detected, as depicted by the brighter areas of the roots in Figure 1b. The migration of bacteria and fungi in the soil and along the roots was tested in compartment petri dishes showing a fast migration of bacteria on the root surface and a slow migration from the roots to the leaves of the plants. An example of such an experiment setup is shown in Figure 1c.

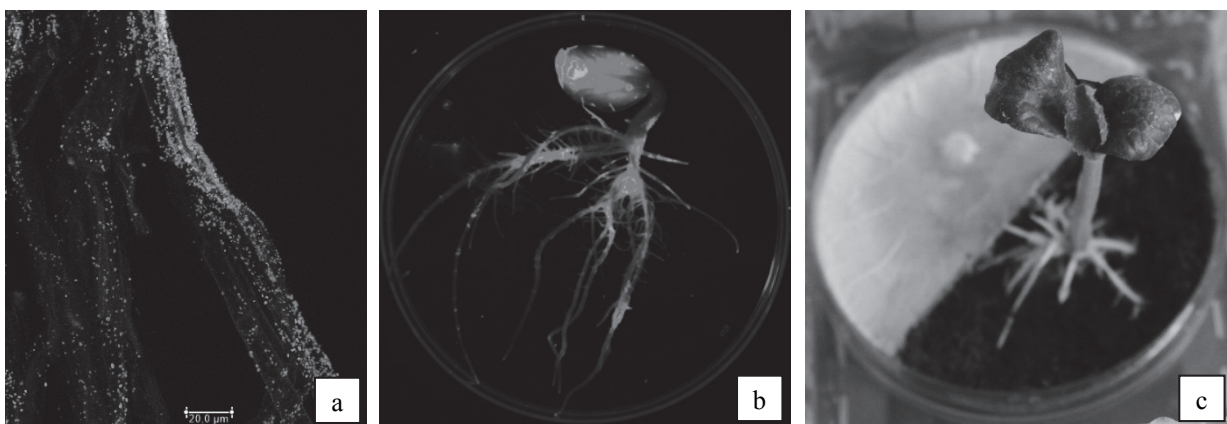


Figure 1. Screening methods of plant-microbe interactions: (a) root colonization visualized by using fluorescent strains and confocal laser scanning microscopy, (b) visualization of the colonization of the entire root system under the Bio-Rad ChemiDoc XRS-System and (c) test of the transport of bacteria on the plant by using two compartment petri dishes.

So far, those experiments were mainly conducted under axenic conditions, but as plants normally have to deal with a complex microbial environment, they should be repeated in greenhouses in heavily infested soils in combination with the fluorescent biocontrol strains. Further, those and other methods should be used to characterize the microbe interactions with the four inbred lines and the F1 hybrid. In this concern possible differences in the interactions depending on the cultivar should be detected and evaluated. Fingerprint and metagenome analysis of field samples of the different breeding lines as well as of plants with and without a biocontrol treatment grown on fields should further lead to a better understanding of the plant-microbe interactions of different cultivars.

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BARLEY VARIETY SELECTION FOR ENHANCED ROOT COLONISATION BY BENEFICIAL SOIL MICROBES

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Introduction

Over the last 50 years, crop breeding has produced elite varieties with high yield and good agronomic features for modern agriculture. This constant selection has narrowed the gene pool, which puts the new varieties at risk from changing environments and crop diseases. Pre-breeding initiatives aim to evaluate crop ancestors, landraces and relatives for new traits for inclusion in breeding programmes. With increasing pressure to reduce agricultural inputs, more efficient nutrient use is becoming an important breeding objective. However, the acquisition of nutrients through the root system has received little attention in variety improvement. Many plant varieties, including barley and other cereals, form beneficial associations with soil microbes that enable the acquisition of nutrients including P and N.

Barley is a major cereal grain, with global production of over 130 million tonnes from a cultivation area of over 550,000 km²; it is the fourth largest grain crop after wheat, rice and corn. Heritage barley varieties and landraces are genetically diverged from modern cultivars, and are a source of new traits for variety improvement. In addition, a range of barley mutants are available to test the role of specific genes in disease resistance and nutrient uptake. For example, the *mlo* gene for powdery mildew resistance is widely used in spring barley cultivars, but little is known about its effect on beneficial associations.

Pseudomonas fluorescens sp. are a diverse group of beneficial, plant-colonizing soil bacteria that promote plant growth, contribute to the uptake of N and P and inhibit pathogen infection. The *P. fluorescens* species group displays significant genetic and phenotypic diversity (Loper *et al.*, PLoS Genetics 2011, e1002784), with each individual *P. fluorescens* strain deploying a different combination of phenotypic outputs including exopolysaccharides, enzymes, motility systems and secreted molecules to effectively colonize the complex rhizosphere environment. Beneficial associations with arbuscular mycorrhiza are established when these fungi colonise roots, and achieve a delicate balance with the host immune system to enable survival. Other fungi are harmful pathogens, causing plant diseases that reduce yield. Breeding efforts are therefore targeted to deploy resistance genes that protect against these harmful pathogens. The trade-off between selection for disease resistance and mycorrhization is largely unknown.

We are investigating the trade-off between disease resistance in barley and the beneficial associations with mycorrhizal fungi and *P. fluorescens*. This will inform breeding to develop varieties with improved nutrient uptake whilst maintaining defence against pathogens.

Material and Methods

To investigate the colonisation of barley roots by *P. fluorescens* strains, GFP and LUX-tagged strains were created to visualise the process. *P. fluorescens* strains used were SBW 25, Pf01 and PF5, transformed using a mini-tn7 and Lux with a *ptas2* helper plasmid. The *P. fluorescens* strains were selected for diverse biosynthetic/catabolic gene clusters. The tagged *P. fluorescens* strains were inoculated onto surface-sterilised and pre-germinated barley cultivar Golden Promise and visualised with a NightOWL in vivo imaging system. With optimised procedures, the experiment will be repeated with barley cultivars selected for genetic diversity and *mlo* resistance: Swanneck, Kneifel, Austrian Early, Ducksbill, Archer, Bavaria, Nurnberg, Scotch Annat, Tipple, Chevallier, Ingrid, *mlo5* Ingrid. The effect of *P. fluorescens* colonisation on resistance to powdery mildew will also be investigated. The barley cultivars will be inoculated with *P. fluorescens* and grown to full leaf stage, and spores of *Blumeria graminis* will be applied in a settling tower.

The number of successful colonies and infection structures developing will be compared to the non-inoculated control treatments. To investigate mycorrhizal associations, barley roots were infected by *Glomus intraradices*, stained with ink and visualised by light microscopy.

Results and Discussion

Procedures were optimised by creating LUX and GFP-tagged *P. fluorescens* for visualisation on barley cv Golden Promise. After 144 hours following inoculation, the bacteria had spread from the inoculated seed to the leaf surface of the growing plant; further growth will continue to be monitored. Experiments on the colonisation of the different barley cultivars and *mlo* mutants are in progress. Hyphae, vesicles and arbuscules of *G. intraradices* were observed in varieties Chevallier, Armelle and Tipple, demonstrating successful infection of this mycorrhizal fungus.

These preliminary results demonstrate the possibility of screening barley cultivars for associations with beneficial bacteria and mycorrhizal fungi. We are developing studies on specific genes involved with plant immunity, including chitin perception, and investigating the trade-off between beneficial microbes and pathogenic fungi. An update on progress will be presented at the meeting.

METAGENOMIC MINING OF THE ENDOPHYTIC PLANT MICROBIOME

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Introduction

The plant microbiome represents an enormous untapped resource for discovering novel microorganisms, traits, genes and bioactive compounds. Endophytes were defined by Bacon & White (2000) as "microbes that colonize living, internal tissues of plants without causing any immediate, overt negative effects". Endophytic bacteria can promote plant growth, act as biocontrol agents and can be beneficial to their host by producing a range of natural products (Ryan et al. 2008; Brader et al. 2014). Here we focus on the diversity and metabolic potential of the endophytic community of plants grown in soils that are naturally suppressive to specific plant diseases.

Material and Methods

The endophytic microbiome of sugar beet plants grown in nonsuppressive soil, suppressive soil, and suppressive soil inoculated with the fungal pathogen *Rhizoctonia solani* were investigated by 16S rRNA gene sequencing on Ion Torrent™ technology. Raw sequences were analysed using a Snakemake (Koster and Rahmann 2012) pipeline that runs commands in Mothur (Schloss et al. 2009). Classification has been done against the SILVA database. Statistical analyses were performed using Phyloseq (McMurdie and Holmes, 2013) and DeSeq (Anders and Huber, 2010) packages in R.

Results and Discussion

The results showed that the endophytic community is very similar between the different soil treatments. However, variations in the abundance of certain groups were observed, with *Azospira*, *Chitinophagaceae*, *Devosia* and *Flavobacterium* being more abundant in the roots of sugar beet plants grown in disease suppressive soil (Figure 1). *In vitro* experiments with *Chitinophaga* and *Devosia* isolates obtained from the endophytic community showed a minor inhibitory activity against *R. solani*. *In planta* experiments will be conducted to resolve if these or other endophytic bacterial genera play a role in the natural protection of plants against pathogen infections. Currently we are performing metagenome sequencing of the endophytic community to understand the functional potential of the microorganisms that live inside the plant root tissue.

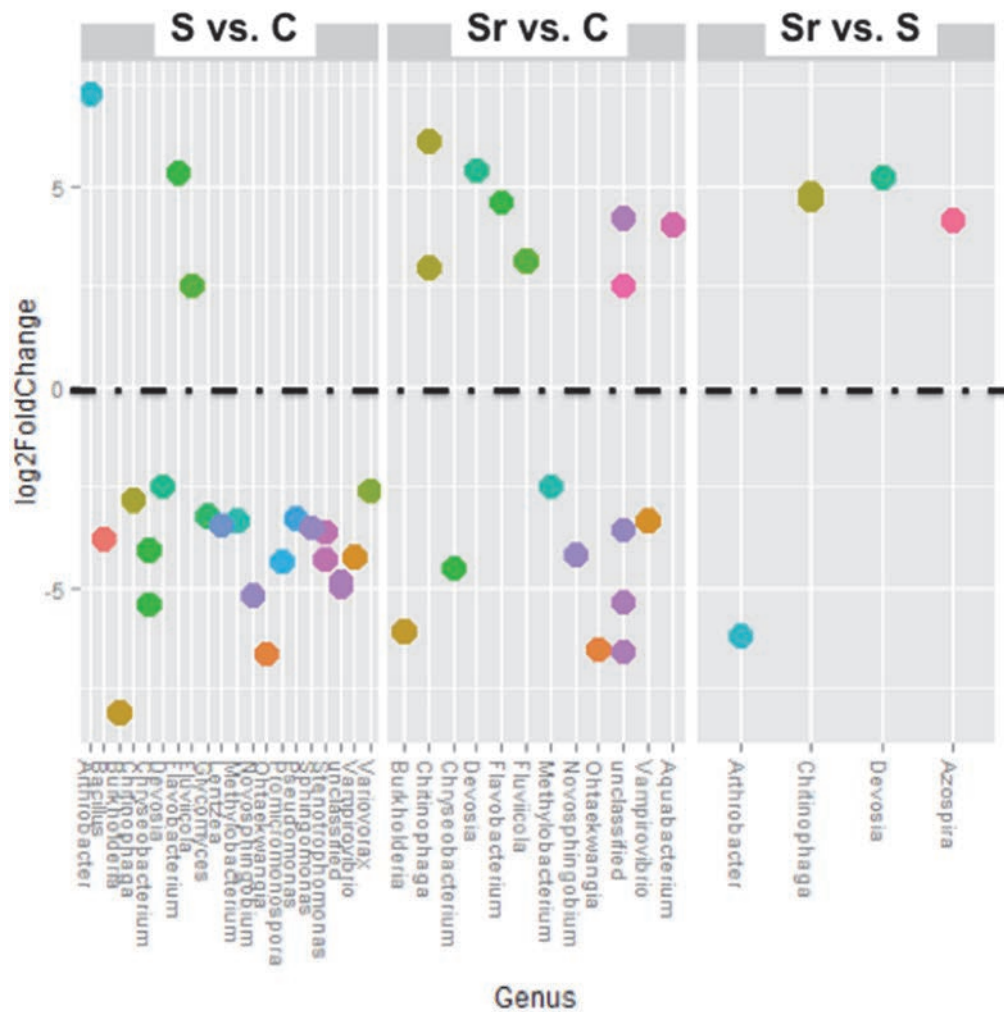


Figure 1. Comparison of the sugar beet endophytic microbiome grown in nonsuppressive soil (C), suppressive soil (S), and suppressive soil inoculated with the fungal pathogen *R. solani* (Sr) using. A positive log2FoldChange value indicates the OTU significantly more abundant and a negative log2FoldChange indicates OTUs less abundant in C, S and Sr.

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BENEFICIAL INTERACTIONS OF ENDOPHYTIC *HERBASPIRILLUM FRISINGENSE* WITH *MISCANTHUS* AND OTHER PLANTS

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Introduction

Plant Growth Promoting Bacteria (PGPB) are getting much attention, when the stimulation of growth and health of non-legumes are concerned. These bacteria are living in the rhizosphere soil, on the root surfaces and even systemically within the plant apoplast as endophytic bacteria without harming the plant. In contrast, the host plants are gaining in multiple ways from their presence. Their beneficial interaction with plants is usually based on several mechanisms. One important mechanism is the production of different phytohormones which stimulate root development, growth of root hairs and also secondary plant hormone responses in the roots. General results of these symbiotic interactions are improved exploration of the soil for water and dissolved nutrients which leads to a better efficiency of fertilizer use and thus significantly less fertilizer application is needed to get the same yield. This not only reduces investments for the farmers but also contributes to improved sustainability and environmental safer crop production. Furthermore, inoculations by certain PGPB results in better control of plant pathogens by successful competition of the inoculants with these pathogens and/or an early acquirement of improved systemic resistance against pathogen attack. Some inoculations with PGPB also lead to more resistance of the plants towards environmental stress like salt stress. The interaction of PGPB with the plants is regulated with several signaling substances produced by the bacteria, including phytohormones, inhibition of ethylene biosynthesis, volatiles and quorum sensing molecules which are also active in beneficial plant responses (Hartmann et al. 2014). Bacteria of the Gram-negative genus *Herbaspirillum*, including *H. frisingense*, colonize many plants on the root surface and endophytically (Rothballer et al. 2008); inoculations frequently lead to improved yields. *H. frisingense* was isolated from roots of the energy plants *Miscanthus sinensis* and *Pennisetum purpureum* in Germany and Brasil (Kirchhof et al. 2001). Many *Herbaspirillum* spp., like *H. frisingense* are diazotrophic, produce plant hormones or interfere with diverse signaling pathways. The genomes of *H. frisingense* GSF30^T (Straub et al. 2013a) and other PGPB have been sequenced. The task of this investigation was to find out more details about the molecular interaction of this PGPB with the energy plant *Miscanthus* (Straub et al. 2013b).

Material and Methods

Surface sterilized *M. sinensis* seeds were germinated in quartz sand which was washed with HCl to remove traces of nutrients and biological contaminants. Prior to sowing the sand was fertilized with modified Hoagland solution, containing only 1 mM ammonium nitrate. A green fluorescent protein (GFP)-tagged *H. frisingense* GSF30^T strain was used for following the colonization behavior of roots and shoots by confocal microscopy. Three week old plants were inoculated with *H. frisingense* GSF30^T (10⁹ CFU ml⁻¹); for controls, the bacterial inoculum solution was autoclaved. After 3 weeks, the plants were harvested, the sand was washed away and the fresh biomass of roots was determined. The root morphology was analysed with a WinRHIZO system for the number and length of roots with different diameter. After harvest of the plants, roots and shoots were frozen immediately in liquid nitrogen and stored at -80°C. The mRNA was isolated from 100 mg of plant material with an RNeasy Plant Mini kit (Qiagen) and transcribed to cDNA, which was sequenced using Illumina technology (Straub et al. 2013b).

Results and Discussion

Using confocal laser scanning microscopy the GFP-labelled *H. frisingense* strain GSF30^T inoculated to seedlings of *Miscanthus* could be demonstrated to colonize the plant apoplast, where aggregates of cells were detected both in roots and in shoots. In barley, the endophytic colonization by GSF30^T was stronger and more uniform (Rothballer et al. 2008). *Miscanthus* plants inoculated with *H. frisingense* GSF30^T and grown under limited nitrogen supply (100µM nitrogen) reached the same biomass as uninoculated plants when supplied with a higher nitrogen dose (500µM nitrogen); at the higher nitrogen dose, the inoculation had no stimulating effect. The inoculation resulted in an increased dry biomass of both roots and shoots of almost 40% and increased fresh weight of about 20% (Straub et al. 2013b). The roots showed an increase in fine-root structures, laterals and in total root length, yielding a larger root system (Straub et al 2013b). In roots and shoots, the nutrient concentrations were not affected by *H. frisingense* inoculation. However, due to the higher biomass, the total content of all nutrients was increased (Straub et al. 2013b). The investigation of gene expression short (3h) and longer (3 weeks) time after inoculation with *H. frisingense* GSF30^T was investigated with quantitative mRNA sequencing (RNA-Seq) (Straub et al. 2013b). At the short time points, there was a prominent upregulation of genes involved in jasmonate signaling and biosynthesis; also other plant hormonal systems were affected. The altered signaling persisted after 3 weeks only for jasmonate and ethylene. Apparently, the enzyme ACC-deaminase, which was demonstrated in *H. frisingense* GSF30^T (Rothballer et al. 2008) and also other plant hormone affecting activities of *H. frisingense* caused these responses in the hormonal system of the inoculated plants, which had clear consequences in improved nutrient efficiency and growth parameters.

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THE INFLUENCE OF BIOPRODUCTS ON MYCORRHIZAL OCCURRENCE AND BIODIVERSITY IN THE RHIZOSPHERE OF STRAWBERRY PLANTS UNDER CONTROLLED CONDITIONS

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Abstract

An experiment was carried out to evaluate the effect of new organic fertilizers and amendments of very diverse composition on mycorrhizal abundance and biodiversity, as well as on root growth, in strawberry plants cv. 'Honeoye'. The plants were grown in rhizoboxes filled with a podsolc soil collected from an uncultivated field of an experimental organic orchard. The plants were treated with: dry granulated bovine manure, extract of vermicompost (Humus UP), extract of humates (Humus Active + Aktywit PM), solution of titanium (Tytanit), extract from seaweed species reinforced with humic and fulvic acids (BioFeed Quality), a consortium of beneficial soil microorganisms (Micosat) and with two microbiologically enriched products: stillage from yeast production (Vinassa) and a plant extract (BioFeed Amin). Plants treated with foliar fertilizers and the microbial consortium also received half the dose of dry manure. Standard mineral fertilization (NPK) and a non-fertilized control were also included.

The influence of the different products on the development of AMF symbiosis and on the resulting root development could be related to their chemical and biological characteristics. The bioproducts based on humus-like substances and yeast stillage had the greatest positive influence on the colonization of roots by AMF. The highest value of mycorrhizal frequency (F%) was obtained for the treatment with the humate-based product (Humus Active – 38.89), followed by the vermicompost extract (Humus UP – 31.11), the microbiologically enriched yeast stillage (Vinassa – 29.21), and the microbial consortium (Micosat – 26.67). The microbiologically enriched vinassa also induced the highest values of mycorrhizal intensity (m%) (8.20), similar to those for the plant extract (BF Quality – 8.11), Humus UP (6.35), and Micosat (6.05). The lowest values of mycorrhizal frequency and intensity were obtained after the treatment with Tytanit and in the NPK control.

The different treatments affected the biodiversity of AMF species present in the rhizosphere soil. The highest number of species of AM fungi was found in the treatment with manure (4), followed by the treatments with Humus Active, Tytanit, and microbiologically enriched vinassa (3). For the remaining fertilizers, including the zero-fertilization control and the control fertilized with NPK, only two species of AM fungi were found. The most frequently found species, present in all the treatments, was *Claroideoglossum claroideum* (N. C. Schenck & G. S. Sm.) C. Walker & A. Schüßler comb nov. It was followed by *Funneliformis mosseae* (T. H. Nicolson & Gerd.) C. Walker & A. Schüßler comb nov., which was found in eight treatments with the exception of the two controls. The species *Rhizophagus fasciculatus* (Thaxt.) C. Walker & A. Schüßler comb nov. was found in four treatments – the two controls, Humus Active, and Tytanit. The species *Scutellospora dipurpurescens* J. B. Morton & Koske was identified only in the plants treated with manure, while *Funneliformis constrictum* (Trappe) C. Walker & A. Schüßler comb nov. was found in the plants treated with Vinassa.

All of the organic products, even though providing a significantly low amount of nutrients, enhanced more root growth characteristics in comparison with the standard mineral fertilization.

ACKNOWLEDGEMENTS

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INTEREST OF PARTICIPANTS IN EUCARPIA WORKING GROUP ON PLANT MICROBE INTERACTION

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<i>Interest in joining the working group</i>	yes
<i>Member of Eucarpia (Sections)</i>	no
<i>Member of ECO-PB</i>	no
<i>Topic of research related to breeding for plant microbe interaction</i>	Development of a screening concept for plant-microbe interactions on the Styrian oil pumpkin as basis for an advanced breeding strategy.
<i>Related publications</i>	Fürnkranz M, Adam E, Müller H, Grube M, Huss H, Winkler J, Berg G. 2012. Promotion of growth, health and stress tolerance of Styrian oil pumpkins by bacterial endophytes. <i>Eur J Plant Pathol.</i> 134: 509-519. Fürnkranz M, Adam E, Lukesch B, Müller H, Zitzenbacher S, Grube M, Berg G. 2011. Multi-pathogen disease caused by <i>Didymella bryoniae</i> and bacteria on Styrian oil pumpkin: microbial ecology and biocontrol. <i>IOBC/WPRS Bulletin</i> , ISSN 1027-3115. Poster: Adam E, Müller H, Berg G. 2014. Effects of different <i>Serratia</i> genotypes on germination and early plant development of Styrian oil pumpkin and visualization of root colonization patterns. IS-MPMI conference 2014, Greece/Rhodos.
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

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<i>Member of Eucarpia (Sections)</i>	-
<i>Member of ECO-PB</i>	-
<i>Topic of research related to breeding for plant microbe interaction</i>	See publications below
<i>Related publications</i>	http://bfg.oxfordjournals.org/content/early/2014/12/18/bfgp.elu049.full.pdf?keytype=ref&ijkey=JXWlzzazb5sF1nn http://bfg.oxfordjournals.org/content/early/2015/04/22/bfgp.elv008.full.pdf?keytype=ref&ijkey=YCcgWoLMKoXhyN
<i>Can you recommend other persons?</i>	
<i>Remarks</i>	

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Interest in joining the working group	We have expertise and experience working with plant microbiomes and are keen to interact with others who have experience in how these may be utilised in plant breeding efforts. Plants of interest are <i>Trifolium</i> and <i>Lolium</i>
Member of Eucarpia (Sections)	
Member of ECO-PB	
Topic of research related to breeding for plant microbe interaction	Plant microbiomes and impact on invertebrate pest damage
Related publications	We are at the early stages of research in this area for <i>Trifolium</i> so have just three conference publications at this stage (journal manuscripts are in prep): Bell N, Adam K, Fleetwood D, Burch G, Johnson R, Popay A, Mtandavari F, Jones R, Cave V (2015). Microbes From Inner Space: I. Comparison of biological soil suppression potential against invertebrate pests across ten New Zealand pastoral soils. In: <i>Rhizosphere4</i> , Maastricht. 21-25 June 2015. Monk J, Johnson R, Jones R, Adam K, Fleetwood D, Bell N (2015). Microbes From Inner Space: II. Diversity of seed inhabiting endophytes in white clover (<i>Trifolium repens</i>) across continents and their potential as growth promotants and control agents for root pathogens and pests. In: <i>Rhizosphere4</i> Maastricht 21-25 June 2015. Johnson R, Jones R, Monk J, Adam K, Popay A, Bell N, Fleetwood D (2015). Microbes From Inner Space: III. The impact of geography and biotic stress on the root endophytic and rhizospheric microbiomes of <i>Trifolium repens</i> . In: <i>Rhizosphere4</i> Maastricht 21-25 June 2015.
Can you recommend other persons ?	I have circulated this form to colleagues in New Zealand who may also be interested.
Remarks	I am clearly not an EU member but many of the plants used in agriculture are shared across New Zealand and Europe so I see benefit to both parties from establishing links between us.

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<i>Interest in joining the working group</i>	yes
<i>Member of Eucarpia (Sections)</i>	Fodder crops and amenity grasses
<i>Member of ECO-PB</i>	Yes (Agroscope Reckenholz)
<i>Topic of research related to breeding for plant microbe interaction</i>	Breeding of forage grasses and clovers for organic conditions, breeding of clovers relying on symbiotically fixed nitrogen, noxious and beneficial endophytic fungi in grasses, especially <i>Neotyphodium uncinatum</i> , resistance breeding against bacteria (<i>Xanthomonas</i>), bacterial genetics of plant-microbe relationships (ryegrass- <i>Xanthomonas</i> interaction), endophytic bacterial communities in ryegrass
<i>Related publications</i>	
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<i>Remarks</i>	

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Interest in joining the working group	Yes
Member of Eucarpia (Sections)	
Member of ECO-PB	
Topic of research related to breeding for plant microbe interaction	Pre-selection of plant lines which rely their productivity, quality and health on the positive interactions with soil-borne plant-probiotics (PPM). Microbiological markers for heterosis-linked QTLs in <i>Zea mays</i> L., as a basis for assisted plant breeding.
Related publications	<p>PICARD C., FRASCAROLI E., BOSCO M. (2005). Recent knowledge on the ecology of plant-growth-promoting rhizobacteria helps to develop new concepts for organic plant breeding. INTERNATIONAL SEMINAR "Environmental friendly food production system: requirements for plant breeding and seed production". State Stende Plant Breeding Station, Talsi, Latvia May 31 - June 3, 2005 pp.4. ISBN:998497524X. State Stende Plant Breeding Station, Ed.</p> <p>PICARD C., BOSCO M. (2005). Maize heterosis affects the structure and dynamics of indigenous rhizospheric auxin-producing <i>Pseudomonas</i> populations. FEMS MICROBIOLOGY ECOLOGY. vol.53 pp.9 ISSN:0168-6496.</p> <p>Picard C., Frascaroli E., Bosco M. (2005). Maize heterosis affects the frequency and biodiversity of beneficial rhizobacteria. Rhizosphere 2004 – Perspectives and Challenges – A Tribute to Lorenz Hiltner. Munich (D) September 12-17, 2004 ISBN:07211694. GSF-Forschungszentrum, Ed.</p> <p>Bosco M., Baruffa E., Picard C. (2006). Organic breeding should select for plant genotypes able to efficiently exploit indigenous Probiotic Rhizobacteria. European Joint Organic Congress "Organic Farming and European Rural Development". Odense, Denmark May 30-31, 2006 pp.2. ISBN:ISBN: 8799134330. ANDREASEN C.B., Ed.</p> <p>PICARD C., BOSCO M. (2006). Heterozygosis drives maize hybrids to select elite 2,4-diacetylphloroglucinol-producing <i>Pseudomonas</i> strains among resident soil populations. FEMS MICROBIOLOGY ECOLOGY. vol.58 pp.12 ISSN:0168-6496.</p> <p>Picard C., Carriero F., Petrozza A., Zamariola L., Baruffa E., Bosco M. (2007). Selecting tomato (<i>Solanum lycopersicon</i> L.) lines for mycorrhizal</p>

	<p>competence: a prerequisite for breeding the plants of the future. RHIZOSPHERE 2, International Conference. Montpellier, France 26-31-5-2007 pp.250. INRA ,Ed.</p> <p>Bosco M., Picard C. (2007). Interactions of cereal varieties with plant-probiotic soil microorganisms. COST SUSVAR Workshop "Varietal characteristics of cereals in different growing systems with special emphasis on below ground traits". Velence, Hungary 29 May – 01 June 2007 pp.108. RISØ National Laboratory, Ed.</p> <p>Bosco M., Picard C. (2007). Breeding the plants for a sustainable future will need to exploit their genotype-specific differential interactions with plant-probiotic microorganisms.</p> <p>EUCARPIA Symposium "Plant breeding for organic and sustainable, low-input agriculture: dealing with genotype-environment interactions".. Wageningen 7–9 November 2007 pp.72. Wageningen University, Plant Breeding Group, Ed.</p> <p>Bosco M., Picard C. (2008). Tools for innovative organic breeding arise from rhizosphere microbial ecology. Cultivate the Future, 16th IFOAM ORGANIC WORLD CONGRESS.. Modena June 16-20, 2008 vol.1 pp.4 ISBN:9783037360231. ISO FAR, Ed.</p> <p>Bosco M., Picard C. (2008). Breeding durum wheat for a sustainable future will need to exploit its genotype-specific differential interactions with plant-probiotic micro-organisms.</p> <p>From Seed to Pasta: the Durum Wheat Chain – International Durum Wheat Symposium. Bologna, June 30 - July 3, 2008.</p>
<i>Can you recommend other persons ?</i>	
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<i>Member of Eucarpia (Sections)</i>	
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	
<i>Related publications</i>	<p>The commercial impact of Neotyphodium endophyte science and technology. Caradus, JR 2012. Proceeding of 8th International grass endophyte symposium. Lanzhou, China. Edited by Zhibiao Nan and Chunjie Li. Pages 203-206.</p> <p>The exploitation of epichloae endophytes for agricultural benefit. Linda J. Johnson & Anouck C. M. de Bonth & Lyn R. Briggs & John R. Caradus & Sarah C. Finch & Damien J. Fleetwood & Lester R. Fletcher & David E. Hume & Richard D. Johnson & Alison J. Popay & Brian A. Tapper & Wayne R. Simpson & Christine R. Voisey & Stuart D. Card. 2013. Fungal Diversity DOI 10.1007/s13225-013-0239-4.</p> <p>Have biopesticides come of age? Travis Glare, John Caradus, Wendy Gelernter, Trevor Jackson, Nemat Keyhani, Jurgen Kohl, Pamela Marrone, Louise Morin and Alison Stewart. 2012. Trends in Biotechnology XX: 1-9.</p>
<i>Can you recommend other persons ?</i>	
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Interest in joining the working group	Working with mycorrhiza, plant growth promoting bacteria and endophytes for successful plant establishment with interest in deepening the association between the microbial symbiosis and plant breeding
Member of Eucarpia	
Member of ECO-PB	
Topic of research related to breeding for plant microbe interaction	Research on the use of microbial inoculants for agro-forestry practices and soil requalification, from pot to nursery and field experiments, and on molecular biology tools to improve design of bioinoculant formulations. Work encompasses the use of plant growth promoting bacteria and mycorrhiza fungi, either in agricultural and forest soils, and in several environmental degraded areas, including metal and pesticide contaminated lands and agricultural nutrient-deficient soils.
Related publications	<p>Nadine R. Sousa, Albina R. Franco, Miguel A. Ramos, Rui S. Oliveira, Paula M.L. Castro. 2015. The response of <i>Betula pubescens</i> to inoculation with an ectomycorrhizal fungus and a plant growth promoting bacteria is substrate-dependent. <i>Ecological Engineering</i>. 81, 439–443</p> <p>Pereira, S.I.A., Castro, P.M.L. 2015. The effect of phosphate-solubilizing rhizobacteria on <i>Zea mays</i> growth on P-deficient soils. <i>Ecological Engineering</i>, 73:526–535.</p> <p>Franco, A.R., Castro, P.M.L. 2014. Inoculation of <i>Pinus pinea</i> seedlings with <i>Pisolithus tinctorius</i> and <i>Suillus bellinii</i> promotes plant growth in benfluralin contaminated soil. <i>Plant and Soil</i>. 386 (1-2): 113-123</p> <p>Pereira, S.I.A., Barbosa, L., P.M.L. Castro. Diversity and characterization of culturable bacterial endophytes from <i>Zea mays</i> and their potential as plant growth-promoting agents in metal-degraded soils. <i>Environmental Science Pollution Research</i>. 21: 14110–14123.</p> <p>Pereira, S.I.A., Barbosa, L.V., Castro, P.M.L. 2014. Rhizobacteria isolated from a metal polluted area enhance plant growth in zinc and cadmium contaminated soil. <i>International Journal Environmental Science and Technology</i>. DOI: 10.1007/s13762-014-0614-z.</p> <p>Moreira, H., Marques, A.P.G.C., Franco, A.R., Rangel, A.O.S.S., Castro, P.M.L. 2014. Phytomanagement do Cd contaminated soils using maize (<i>Zea mays</i> L.) assisted by plant growth promoting rhizobacteria. <i>Environmental Science and Pollution Research</i>. 21 (16) , pp. 9742</p> <p>Nadine R Sousa; Albina R Franco; Rui S Oliveira; Paula M L Castro. Reclamation of an abandoned burned forest using ectomycorrhizal inoculated <i>Quercus rubra</i>. <i>Forest Ecology and Management</i>. 320:50–55.</p> <p>Sousa, N.R., Ramos, M.A., Marques, A.P.G.C. and Castro, P.M.L. 2014. A genotype dependent-response to cadmium contamination in soil is displayed by <i>Pinus pinaster</i> in symbiosis with different mycorrhizal fungi. <i>Applied Soil Ecology</i> 77, pp. 7-13.</p> <p>Marques, A.P.G.C., Moreira, H., Franco, A.R., Rangel, A.O.S.S., Castro, P.M.L. 2013. Inoculating <i>Helianthus annuus</i> (sunflower) grown in zinc and cadmium contaminated soils with plant growth promoting bacteria - Effects on phytoremediation strategies. <i>Chemosphere</i> 92 (1), pp. 74-83</p> <p>Sousa, N.R., Ramos, M.A., Franco, A.R., Oliveira, R.S., Castro, P.M.L. 2012. Mycorrhizal symbiosis affected by different genotypes of <i>Pinus pinaster</i>. <i>Plant and Soil</i> 359 (1-2), pp. 245-253.</p>

	<p>Oliveira, R.S., Franco, A.R., Castro, P.M.L. 2012. Combined use of <i>Pinus pinaster</i> plus and inoculation with selected ectomycorrhizal fungi as an ecotechnology to improve plant performance. <i>Ecological Engineering</i> 43, pp. 95-103.</p> <p>Sousa, N.R., Franco, A.R., Oliveira, R.S., Castro, P.M.L. 2012. Ectomycorrhizal fungi as an alternative to the use of chemical fertilisers in nursery production of <i>Pinus pinaster</i>. <i>Journal of Environmental Management</i> 95 (SUPPL.), pp. S269-S274.</p> <p>Sousa, N.R., Ramos, M.A., Marques, A.P.G.C., Castro, P.M.L. 2012. The effect of ectomycorrhizal fungi forming symbiosis with <i>Pinus pinaster</i> seedlings exposed to cadmium. <i>Science of the Total Environment</i> 414, pp. 63-67.</p> <p>Sousa, N.R., Franco, A.R., Ramos, M.A., Oliveira, R.S., Castro, P.M.L. 2011. Reforestation of burned stands: The effect of ectomycorrhizal fungi on <i>Pinus pinaster</i> establishment. <i>Soil Biology and Biochemistry</i> 43 (10), pp. 2115-2120.</p> <p>Oliveira, R.S., Franco, A.R., Vosátka, M., Castro, P.M.L. 2010. Management of nursery practices for efficient ectomycorrhizal fungi application in the production of <i>Quercus ilex</i>. <i>Symbiosis</i> 52 (2-3), pp. 125-131.</p> <p>Dias, J.M., Oliveira, R.S., Franco, A.R., Ritz, K., Nunan, N., Castro, P.M.L. 2010. Evaluación de la colonización micorrícica y de los nutrientes del suelo en dos zonas de restauración afectadas por fuego. Assessment of mycorrhizal colonisation and soil nutrients in unmanaged fire-impacted soils from two target restoration sites. <i>Spanish Journal of Agricultural Research</i> 8 (SPL ISS.), pp. S86-S95.</p> <p>Calheiros, C.S.C., Teixeira, A., Pires, C., Franco, A.R., Duque, A.F., Crispim, L.F.C., Moura, S.C., Castro, P.M.L. 2010. Bacterial community dynamics in horizontal flow constructed wetlands with different plants for high salinity industrial wastewater polishing. <i>Water Research</i> 44 (17), pp. 5032-5038.</p> <p>Marques, A.P.G.C., Pires, C., Moreira, H., Rangel, A.O.S.S., Castro, P.M.L. 2010. Assessment of the plant growth promotion abilities of six bacterial isolates using <i>Zea mays</i> as indicator plant. <i>Soil Biology and Biochemistry</i> 42 (8), pp. 1229-1235.</p> <p>Oliveira, R.S., Boyer, L.R., Carvalho, M.F., Jeffries, P., Vosátka, M., Castro, P.M.L., Dodd, J.C. 2010. Genetic, phenotypic and functional variation within a <i>Glomus geosporum</i> isolate cultivated with or without the stress of a highly alkaline anthropogenic sediment. <i>Applied Soil Ecology</i> 45 (1), pp. 39-48.</p> <p>Calheiros, C.S.C., Duque, A.F., Moura, A., Henriques, I.S., Correia, A., Rangel, A.O.S.S., Castro, P.M.L. 2009. Changes in the bacterial community structure in two-stage constructed wetlands with different plants for industrial wastewater treatment. <i>Bioresource Technology</i> 100 (13), pp. 3228-3235.</p> <p>Marques, A.P.G.C., Oliveira, R.S., Rangel, A.O.S.S., Castro, P.M.L. 2008. Application of manure and compost to contaminated soils and its effect on zinc accumulation by <i>Solanum nigrum</i> inoculated with arbuscular mycorrhizal fungi. <i>Environmental Pollution</i> 151 (3), pp. 608-620.</p> <p>Marques, A.P.G.C., Oliveira, R.S., Samardjieva, K.A., Pissarra, J., Rangel, A.O.S.S., Castro, P.M.L. 2008. EDDS and EDTA-enhanced zinc accumulation by <i>Solanum nigrum</i> inoculated with arbuscular mycorrhizal fungi grown in contaminated soil. <i>Chemosphere</i> 70 (6), pp. 1002-1014.</p> <p>Marques, A.P.G.C., Oliveira, R.S., Samardjieva, K.A., Pissarra, J., Rangel, A.O.S.S., Castro, P.M.L. 2007. <i>Solanum nigrum</i> grown in contaminated soil: Effect of arbuscular mycorrhizal fungi on zinc accumulation and histolocalisation. <i>Environmental Pollution</i> 145 (3), pp. 691-699.</p> <p>Marques, A.P.G.C., Oliveira, R.S., Rangel, A.O.S.S., Castro, P.M.L. 2006. Zinc accumulation in <i>Solanum nigrum</i> is enhanced by different arbuscular mycorrhizal fungi. <i>Chemosphere</i> 65 (7), pp. 1256-1263.</p> <p>Oliveira, R.S., Castro, P.M.L., Dodd, J.C., Vosátka, M. 2006. Different native arbuscular mycorrhizal fungi influence the coexistence of two plant species in a highly alkaline anthropogenic sediment. <i>Plant and Soil</i> 287 (1-2), pp. 209-221.</p> <p>Oliveira, R.S., Vosátka, M., Dodd, J.C., Castro, P.M.L. 2005. Studies on the diversity of arbuscular mycorrhizal fungi and the efficacy of two native isolates in a highly alkaline anthropogenic sediment. <i>Mycorrhiza</i> 16 (1), pp. 23-31.</p> <p>Oliveira, R.S., Castro, P.M.L., Dodd, J.C., Vosátka, M. 2005. Synergistic effect of <i>Glomus</i> intraradices and <i>Frankia</i> spp. on the growth and stress recovery of <i>Alnus glutinosa</i> in an alkaline anthropogenic sediment. <i>Chemosphere</i> 60 (10), pp. 1462-1470.</p>
Can you recommend other persons ?	Sofia Pereira, Nadine Sousa, Helena Moreira - UCP

<i>Title</i>	Dr
<i>First name</i>	Dionysia
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<i>Webpage</i>	www.ari.gov.cy
<i>Interest in joining the working group</i>	Yes
<i>Member of Eucarpia (Sections)</i>	Yes
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Plant Breeding for improved plant microbe interactions
<i>Related publications</i>	
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr
<i>First name</i>	Abe
<i>Last name</i>	Gerrano
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<i>Webpage</i>	www.arc.agric.za
<i>Interest in joining the working group</i>	I am working on legume crop, cowpea which is under-utilized resource in the country and need to integrate breeding programme with nitrogen fixing ability of the crop
<i>Member of Eucarpia (Sections)</i>	
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Involved in germplasm collection, conservation, characterization, evaluation, cultivar development, maintenance, nutritional quality study and technology promotion and documentation of germplasm accessions (African Leafy Vegetables Breeding Programme such as Amaranthus, Bambara Groundnut, Cowpea, Corchorus, Okra and Taro).
<i>Related publications</i>	Shegro, A., Atilaw, A., Pal, U.R. and Geleta, N. 2010. Influence of varieties and planting dates on growth and development of soybean (<i>Glycine max</i> L. Merr) in Metekel zone, North Western Ethiopia. Journal of Agronomy 9 (3): 146-156.
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr
<i>First name</i>	Ioannis M.
<i>Last name</i>	Ioannides
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<i>Webpage</i>	www.ari.gov.cy
<i>Interest in joining the working group</i>	Yes
<i>Member of Eucarpia (Sections)</i>	No
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Molecular Biology
<i>Related publications</i>	Omirou Michalis... I.M. Ioannides et al. (2013) Mycorrhizal inoculation affects arbuscular mycorrhizal diversity in watermelon roots, but leads to improved colonization and plant response under water stress only. Applied Soil Ecology 63: 112-119.
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr.
<i>First name</i>	Pierre
<i>Last name</i>	Hohmann
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<i>Webpage</i>	www.uni-kassel.de/go/fb11-opb
<i>Interest in joining the working group</i>	Networking, collaborations
<i>Member of Eucarpia (Sections)</i>	
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Microbial responsiveness Microbe-mediated disease resistance
<i>Related publications</i>	Hohmann P. , Jones E.E., Hill R.A., Stewart A. (2012). Ecological studies of the bio-inoculant <i>Trichoderma hamatum</i> LU592 in the root system of <i>Pinus radiata</i> . <i>FEMS Microbiology Ecology</i> , 80(3): 709-721. Hohmann P. , Jones E.E., Hill R.A., Stewart A. (2011). Understanding <i>Trichoderma</i> in the root system of <i>Pinus radiata</i> : Associations between rhizosphere colonisation and growth promotion for commercially grown seedlings. <i>Fungal Biology</i> , 115(8): 759-767.
<i>Can you recommend other persons ?</i>	Prof. Martin Parniske, TUM, parniske@lmu.de
<i>Remarks</i>	

Title	Dr
First name	Bernd
Last name	Horneburg
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Webpage	
Interest in joining the working group	I want to explore the potential of breeding for plant – microbe interaction, in particular for diverse organic and low-input environments.
Member of Eucarpia (Sections)	Organic and low input, fruit vegetables, legumes / protein plants
Member of ECO-PB	yes
Topic of research related to breeding for plant microbe interaction	<p>We want to support the adaptation of soybean to less favourable climates. The improvement of root performance and symbiotic N fixation may become important approaches.</p> <p>We are preparing a project in pea breeding research. Symbiotic N fixation will most likely be in the focus.</p> <p>A project exploring fruit quality in a very diverse set of tomato cultivars has recently started. Cultivars cover the entire range from heritage cultivars to the most recent organically and conventionally bred cultivars for the production outdoors, in polytunnels, heated greenhouses and hydroponics. The tomatoes will be grown 2015 in organic management in low-input conditions. The trial is suitable to study other aspects of plant – environment interaction above and below ground. We are looking for partners who want to join in the trial now!</p>
Related publications	
Can you recommend other persons ?	
Remarks	

<i>Title</i>	
<i>First name</i>	Stephanie
<i>Last name</i>	Klaedtke
<i>Position</i>	PhD student
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<i>Webpage</i>	http://www.seed.ulg.ac.be/team/stephanie-klaedtke/
<i>Interest in joining the working group</i>	yes
<i>Member of Eucarpia (Sections)</i>	no
<i>Member of ECO-PB</i>	no
<i>Topic of research related to breeding for plant microbe interaction</i>	<p><u>PhD research:</u> Plant adaptation and plant health in a context of on-farm breeding of common bean (<i>Phaseolus vulgaris</i>) in European organic farms</p> <p>In the context of this research, I study interactions of common bean with microorganisms, be they pathogenic or beneficial to the crop. This constitutes a first take on a salutogenic approach to plant health in the context of farm seed. Field trials are complemented with interviews with stakeholders to better understand their point of view on and management of plant health in their seed systems.</p>
<i>Related publications</i>	<p>Klaedtke, S., Barret, M., Chable, V., & Jacques, M.-A. (2014). Microbial communities associated to common bean seed - A mechanism of local adaptation of plants? In V., Chable, I., Goldringer, S., Howlett, P., Barberi, P., Miko, P., Mendes-Moreira, M., Rakszegi, H., Ostergard, A., Borgen, M., Finckh, T., Pedersen, & R., Bocci (Eds.), Diversity strategies for organic and low input agricultures and their food systems. Book of abstracts of Solibam final congress, Nantes, 7-9 July 2014.</p> <p>Klaedtke, S., Stassart, P. M., & Chable, V. (2014). An Alternative Approach to Plant Health: The Procedural Concept Applied to Common Bean Seed Systems. In G., Rahman & U., AKSOY (Eds.), Building organic Bridges (pp. 307-310). Brunschweig, Germany: Johann Heinrich von Thünen-Institut.</p>
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Prof. Dr.
<i>First name</i>	Edith
<i>Last name</i>	Lammerts van Bueren
<i>Position</i>	Senior researcher and professor
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<i>Webpage</i>	
<i>Interest in joining the working group</i>	As participant
<i>Member of Eucarpia (Sections)</i>	yes
<i>Member of ECO-PB</i>	yes
<i>Topic of research related to breeding for plant microbe interaction</i>	Below-ground traits, root system improvement, breeding for improvement nitrogen-use efficiency, but not active in microbe research
<i>Related publications</i>	<p>Kerbiriou, P., E.T. Lammerts van Bueren, T.J. Stomph, P.C. Struik, 2013. Shoot growth, root growth and resource capture under limiting growing conditions for two cultivars of lettuce (<i>Lactuca sativa</i> L.). <i>Plant and Soil</i> 371: 281-297.</p> <p>Kerbiriou, P., T.J. Stomph, E.T. Lammerts van Bueren, P.C. Struik, 2013. Influence of transplant size on the above- and below-ground performance of four contrasting field-grown lettuce cultivars. <i>Front. Plant Sci.</i>, 4, Article 379, 16 pp, doi: 10.3389/fpls.2013.00379.</p> <p>Kerbiriou, PJ, Stomph, TJ, Lammerts van Bueren, ET, Struik, PC, 2014. Modelling concept of lettuce breeding for nutrient efficiency. <i>Euphytica</i> 199(1-2): 167-188.</p> <p>Tiemens-Hulscher, M., E.T. Lammerts van Bueren, P.C. Struik. Identifying nitrogen-efficient potato cultivars for organic farming. <i>Euphytica</i> 199(1-2): 137-154.</p>
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr
<i>First name</i>	Fabio
<i>Last name</i>	Mascher
<i>Position</i>	Researcher; phytopathologist of the wheat breeding programme at Agroscope
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<i>Webpage</i>	www.agroscope.ch
<i>Interest in joining the working group</i>	Yes!
<i>Member of Eucarpia (Sections)</i>	-/-
<i>Member of ECO-PB</i>	-/-
<i>Topic of research related to breeding for plant microbe interaction</i>	Interactions of beneficial Pseudomonads with wheat Study affinity between Pseudomonas strains and wheat variety at the genotype-genotype level. Induced resistance. Implementation in field trials.
<i>Related publications</i>	
<i>Can you recommend other persons ?</i>	Christoph Keel, University of Lausanne, Christoph.Keel@unil.ch; Maurhofer Bringolf Monika, ETH Zürich, monika.maurhofer@usys.ethz.ch Brigitte Mauch-Mani, University of Neuchâtel, brigitte.mauch@unine.ch Katia Gindro, Agroscope IPS, katia.gindro@agroscope.admin.ch Vincent Michel, Agroscope IPS, vincent.michel@agroscope.admin.ch Jean-Laurent Spring, Agroscope IPS, jean-laurent.spring@agroscope.admin.ch Ted Turlings, University of Neuchâtel, ted.turlings@unine.ch Raquel Campos Herrera, University of Neuchâtel, raquel.campos@unine.ch
<i>Remarks</i>	

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Interest in joining the working group	I'm interested in selection tools to improve plant microbe interaction for enhanced nutrition and plant health and the importance of host plant species on beneficial microbial community in intercropping systems
Member of Eucarpia (Sections)	Yes , Organic and Low Input Agriculture, Oil and Protein Crops, Cereals
Member of ECO-PB	Yes
Topic of research related to breeding for plant microbe interaction	Improvement of N fixation by selection of Bradyrhizobia strains adapted to cool growing conditions and early maturing soybean genotypes. Threefold interaction between Soybean- Bradyrhizobia- Mycorrhiza or PGPR under different growing conditions Competition and N fixation of native Bradyrhizobia isolated from cowpea in different geographic regions in Kenya Effect of <i>Trichoderma spp.</i> on lupin tolerance against seed and soil born <i>Colletotrichum</i> infections
Related publications	Hildermann, I.H., Messmer, M.M., Dubois, D., Boller, Th., Wiemken, A., Mäder, P. (2010) Nutrient use efficiency and arbuscular mycorrhizal root colonization of winter wheat cultivars in different farming systems of the DOK long-term trial. <i>Sci Food Agric</i> 90, 2027–2038 Fließbach, A., Messmer, M., Nietlispach, B., Infante, V., Mäder, P. (2012): Effects of conventionally bred and <i>Bacillus thuringiensis</i> (Bt) maize varieties on soil microbial biomass and activity. <i>Biology and Fertility of Soils</i> 3, 315-324. Messmer, M., Hildermann, I., Thorup-Kristensen, K., Rengel, Z., (2012). Nutrient Management in Organic Farming and Consequences for Direct and Indirect Selection Strategies. In: Lammerts van Bueren, E.T., Myers, J.R. (Eds.), <i>Organic Crop Breeding</i> . John Wiley and Sons, pp. 15-38 Messmer, M., Berset, E., Zimmer, S., Haase, T., Habekuss, A., Peláez, S., Thonar, C., Salomé, C., Ordon, F., Hess, J., and Wilbois, K.-P. (2012). Breeding for improved soybean-Bradyrhizobia symbiosis for cool growing conditions in Central Europe. In: Hartmann, A., Ott, T., and Parniske, M., (Eds.), "10th European Nitrogen Fixation Conference ", Munich. 11-16. Mathu, S., Thonar, C., Vanlauwe, B., Messmer, M., and Frossard, E. (2012). Multi-purpose cowpea inoculation for improved yields in small holder farms in Kenya, "Integrated Soil Fertility Management in Africa: From Microbes to Markets", Nairobi, Kenya, 22. - 26. October 2012 Messmer, M., Berset, E., Hertenstein, Peláez, S., Salomé, C., Thonar, C., Zimmer, S., Haase, Th., H., Hess, J., Habekuss, A., Kleemann, M., Ordon, F., Vogt-Kaute, W., Vogel, R., Unsleber, J., Littmann, J., Wilbois, K.-P. (2013) Selection for cold tolerant Bradyrhizobia strains and their Interaktion with early Soybean cultivars. <i>Rhizobia Day</i> , 16th September 2013, Frick Schmidt, J., Messmer, M.M., Wilbois, K.P. (2015) Beneficial microorganisms for soybean (<i>Glycine max</i> (L.) Merr), with a focus on low root-zone temperatures. <i>Plant and Soil</i> (in press)
Can you recommend other persons ?	

<i>Title</i>	Dr
<i>First name</i>	Michalis
<i>Last name</i>	Omirou
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<i>Interest in joining the working group</i>	Yes
<i>Member of Eucarpia (Sections)</i>	No
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Microbial ecology and Plant-Microbe Interactions
<i>Related publications</i>	Omirou Michalis... I.M. Ioannides et al. (2013) Mycorrhizal inoculation affects arbuscular mycorrhizal diversity in watermelon roots, but leads to improved colonization and plant response under water stress only. Applied Soil Ecology 63: 112-119.
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr
<i>First name</i>	Christopher
<i>Last name</i>	Ridout
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<i>Country</i>	UK
<i>e-mail</i>	Christopher.ridout@jic.ac.uk
<i>Webpage</i>	www.jic.ac.uk
<i>Interest in joining the working group</i>	I am interested in root association bacteria and mycorrhizal fungi, and how they affect disease resistance in barley. I also work on brassicas
<i>Member of Eucarpia (Sections)</i>	
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	This is a new topic of research for me and I have a PhD project starting this autumn on mycorrhizal fungi in barley and their effect on disease resistance. I also have started a project on beneficial Pseudomonas species in barley. This recent work builds on my background in resistance mechanisms in cereals and brassicas, and recent collaboration at the John Innes Centre on beneficial bacteria and mycorrhiza. I have a partnering award with America and Canada on 'Genomic selection in cereals for grain quality and improved soil health'. I have an ERA-CAPS grant on mechanistic analysis of quantitative disease resistance in brassica napus by associative transcriptomics
<i>Related publications</i>	Schoonbeek H. J., Wang H. H., Stefanato F. L., Craze M., Bowden S., Wallington E., Zipfel C., Ridout C. J. (2015) Arabidopsis EF-Tu receptor enhances bacterial disease resistance in transgenic wheat. <i>New Phytologist</i> 206 606-613 Goddard R., Peraldi A., Ridout C., Nicholson P. (2014) Enhanced Disease Resistance Caused by BRI1 Mutation Is Conserved Between Brachypodium distachyon and Barley (Hordeum vulgare) <i>Molecular Plant-Microbe Interactions</i> 27 1095-1106 Bryant R. M., McGrann G. R. D., Mitchell A. R., Schoonbeek H., Boyd L. A., Uauy C., Dorling S., Ridout C. (2014) A change in temperature modulates defence to yellow (stripe) rust in wheat line UC1041 independently of resistance gene Yr36 <i>BMC Plant Biology</i> 14 10 Lloyd S., Schoonbeek H., Trick M., Zipfel C., Ridout C. (2014) Methods to Study PAMP-Triggered Immunity in Brassica Species <i>Molecular Plant Microbe Interactions</i> 27 286-295 Boyd L. A., Ridout C., O'Sullivan D. M., Leach J. E., Leung H. (2013) Plant-pathogen interactions: disease resistance in modern agriculture <i>Trends in Genetics</i> 29 233-240
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

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<i>Last name</i>	Rothballer
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<i>Interest in joining the working group</i>	
<i>Member of Eucarpia (Sections)</i>	
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	Molecular Interaction of crops with endophytic plant growth promoting bacteria (PGPB) Colonization efficiency and yield improvement in different cultivars and breeding lines
<i>Related publications</i>	Rothballer, M., Eckert, B., Schmid, M., Klein, I., Fekete, A., Schloter, M., Hartmann, A. (2008) Endophytic root colonization of gramineous plants by <i>Herbaspirillum frisingense</i> . FEMS Microbiol. Ecol. 66, 85-95 Straub, D., Rothballer, M., Hartmann, A., and Ludewig, U. (2013) The genome of endophytic <i>Herbaspirillum frisingense</i> GSF30T identifies diverse strategies in the <i>Herbaspirillum</i> genus to interact with plants. Frontiers in Microbiology. doi: 0.3389/fmicb.2013.00168
<i>Can you recommend other persons ?</i>	Prof. Dr. Uwe Ludewig, Institut für Kulturpflanzenwissenschaften, Ernährungsphysiologie der Kulturpflanzen, Universität Hohenheim, Fruwirthstr. 20, D-70593 Stuttgart, Germany
<i>Remarks</i>	

<i>Title</i>	Dr.
<i>First name</i>	Carolin
<i>Last name</i>	Schneider
<i>Position</i>	CEO
<i>Organisation</i>	Inoq GmbH
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<i>Webpage</i>	www.inoq.de or www.endophytes.eu
<i>Interest in joining the working group</i>	yes, but no member in EUCARPIA
<i>Member of Eucarpia (Sections)</i>	no
<i>Member of ECO-PB</i>	no
<i>Topic of research related to breeding for plant microbe interaction</i>	<p>Inoq is a commercial producer for beneficial plant microbes (mainly mycorrhiza) with high interest (and experience) in applied scientific projects to solve all questions which hamper the widespread use of those microbes. Therefore we are well aware of the impact of plant breeding for effective plant microbe interaction.</p> <p>Carolin Schneider is Chair of COST Action FA1103 “Endophytes for biotechnology and agriculture” and Vice Chair for FA 1405 together with Chair and keynote speaker Arjen Biere.</p>
<i>Related publications</i>	<p>Arnholdt-Schmitt B, Valadas V, Döring M, 2015: Functional marker development is challenged by the ubiquity of endophytes – a practical perspective. Briefings in Functional Genomics, 2014, 1-6, doi:10.1093/bfpg/elu049</p> <p>Morgenstern, K., Döring, M. & Krabel, D., 2014: Rhabdocline needle cast – most recent findings of the occurrence of Rhabdocline pseudotsugae in Douglas-fir seeds. Botany (in press)</p> <p>Döring, M., Schneider, C., 2011: Inoculation of arbuscular mycorrhizal fungi with micropropagated plants during acclimatization. In: Pirttilä, A. M., & Sorvari, S. (eds.) Prospects and Applications for Plant-Associated Microbes. A laboratory manual. Part B: Fungi, Hannover, Germany, S. 118-121</p>
<i>Can you recommend other persons ?</i>	I sent the information to the 260 members of “my” COST Action FA1103, I guess people will contact you in case of interest. I would be happy to spread more information in future.
<i>Remarks</i>	Thanks for bringing the topic on the table ;-), I am sorry that I cannot take part.

<i>Title</i>	Prof.
<i>First name</i>	Marcel
<i>Last name</i>	Van der Heijden
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<i>Webpage</i>	
<i>Interest in joining the working group</i>	
<i>Member of Eucarpia (Sections)</i>	Yes
<i>Member of ECO-PB</i>	
<i>Topic of research related to breeding for plant microbe interaction</i>	<p>Our groups investigates the impact of plant symbionts (arbuscular mycorrhizal fungi, nitrogen fixing bacteria, root associated bacteria and fungi) on plant growth and ecosystem functioning and sustainability.</p> <p>Our expertise (Klaus Schläppi and Marcel van der Heijden):</p> <ul style="list-style-type: none"> -impact of microbes on plant growth -molecular characterisation of microbial communities associating with plant roots (using state of the art high throughput sequencing tools)
<i>Related publications</i>	<p>van der Heijden, M.G.A., & Schläppi, K. (2015) The root surface as a frontier for plant microbiome research. Proceedings of the National Academy of Sciences USA 112: 2299-2300.</p> <p>Wagg, C., Boller, B., Schneider, S., Widmer, F., & van der Heijden, M.G.A., (2015) Intraspecific and intergenerational differences in plant-soil feedbacks. Oikos (in press)</p> <p>Wagg C., Bender S.F., Widmer F., van der Heijden, M.G.A. (2014) Soil biodiversity and soil community composition determine ecosystem multifunctionality. Proceedings of the National Academy of Sciences USA 111 (14): 5266–5270.</p>
<i>Can you recommend other persons ?</i>	
<i>Remarks</i>	

<i>Title</i>	Dr.
<i>First name</i>	Christin
<i>Last name</i>	Zachow
<i>Position</i>	Senior Researcher
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<i>Webpage</i>	
<i>Interest in joining the working group</i>	Get insights in the current state of companies and research in regard to microbiome research, breeding, plant cultivars, sugar beet Potential participation in EU project
<i>Member of Eucarpia (Sections)</i>	-
<i>Member of ECO-PB</i>	-
<i>Topic of research related to breeding for plant microbe interaction</i>	Current research: microbiome of different sugar beet cultivars from seed to rhizosphere and comparison of wild and modern sugar beet cultivars Topic: breeding with cultivar-microbiome interaction, analysis of key species in biocontrol, abiotic and biotic stress resistance
<i>Related publications</i>	Zachow, C., Müller, H., Tilcher, R., & Berg, G. (2014). Differences between the rhizosphere microbiome of <i>Beta vulgaris</i> ssp. <i>maritima</i> -ancestor of all beet crops-and modern sugar beets. <i>Frontiers in microbiology</i> , 5. Berg, G., Zachow, C., Müller, H., Philipps, J., & Tilcher, R. (2013). Next-generation bio-products sowing the seeds of success for sustainable agriculture. <i>Agronomy</i> , 3(4), 648-656.
<i>Can you recommend other persons ?</i>	Dr. Henry Müller, Biotenzz, Graz, Austria; as partner for formulation of microorganisms for field application Dr. Ralf Tilcher, KWS SAAT AG, Einbeck, Germany as contact person for seed production
<i>Remarks</i>	ACIB is an interface of universities and companies

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