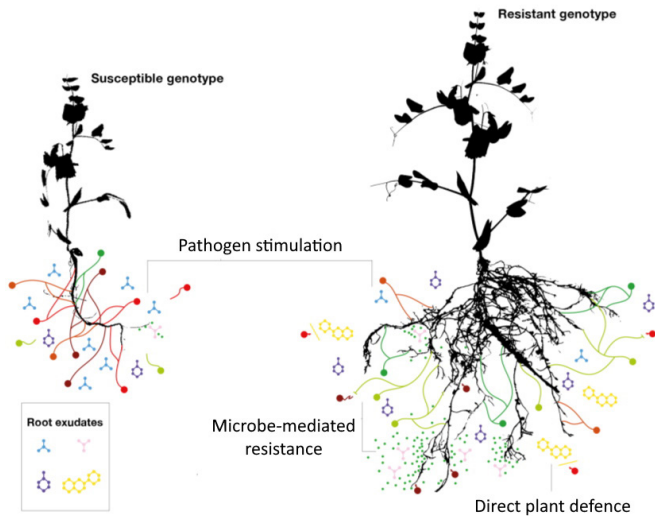


3rd EUCARPIA WORKSHOP ON IMPLEMENTING PLANT-MICROBE INTERACTIONS IN PLANT BREEDING

15 July 2022

Universitäts- und Forschungszentrum Tulln
Konrad Lorenz-Str. 24, 3430 Tulln an der Donau, Austria



modified from Wille et al. 2019, *Plant Cell Environ*

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



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DESCRIPTION

The workshop aims to strengthen a network among plant breeders and scientist of different disciplines to explore the use of plant-microbe interactions in plant breeding.

Plant-associated microbes have received considerable attention in research for their ability to improve crop productivity and yield stability. Knowledge on plant genetic determinants for beneficial interactions with individual microbes (incl. biologicals) and entire communities is growing rapidly. Several 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 members of the microbial community.

However, to what extent genetic factors are responsible for shaping beneficial plant microbiomes is still poorly understood. Similarly, plant microbiome manipulation via the introduction of biologicals offers great promise, but still suffers from variable outcomes due to insufficient knowledge of the factors involved for successful applications. In conclusion, there are still many uncertainties on how to implement this knowledge into plant breeding and propagation programmes.

The Workshop is organised by the EUCARPIA Working Group on Plant-Microbe Interactions of the Section Organic and Low-Input Agriculture and will continue to discuss the potential and limitations of implementing the growing knowledge on plant-microbe interactions in plant breeding. The 2nd workshop in 2019 led to fruitful discussions on related opportunities and challenges,

e.g. emphasising the importance of high-throughput phenotyping, modelling, genetic markers, standards for -omics protocols, microbiome functions (beyond description) and decision tools for genotype selection.

The workshop outputs were synthesized in a perspective article on emerging research priorities towards microbe-assisted crop production (Hohmann et al. 2020, FEMS Micr. Ecol). This year's 3rd EUCARPIA workshop will continue the discussion and foster the dialogue between the different research disciplines and industry in order to develop advanced breeding strategies for future resilient agroecosystems.

Session I:

Genetic determinants of plant-microbe interactions.

Keynote: Victor Carrion (Assistant Professor, Leiden University)

Session II:

Integration of plant-microbe interactions into breeding.

Keynote: Eveline Adam (Head of Oil Pumpkin and Legume Breeding, Saatzucht Gleisdorf)

On behalf of the Organizing Committee:

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Sustainable Plant Protection Programme, IRTA Institute of Agrifood Research and Technology, Lleida, Spain

2. Friederike Trognitz

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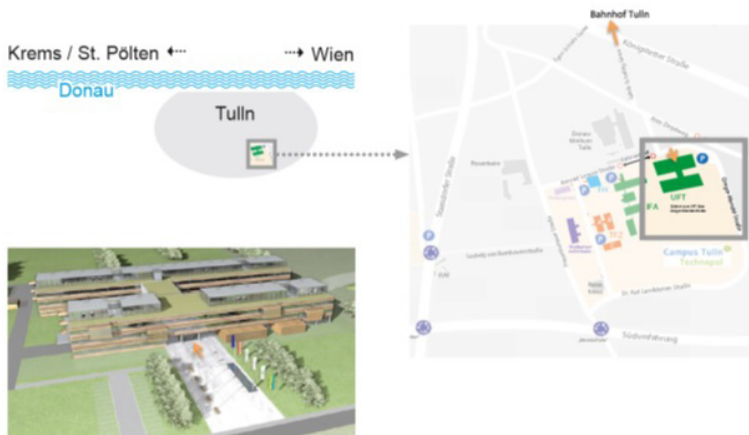
Department of Crop Sciences, Research Institute of Organic Agriculture (FiBL), Frick, Switzerland

Supported by:



LOCATION

The workshop is taking place at Universitäts- und Forschungszentrum Tulln, Konrad Lorenz-Str. 24, 3430 Tulln an der Donau, Austria.



Universitäts- und Forschungszentrum Tulln (UFT)

Universität für Bodenkultur
Konrad Lorenz-Str. 24, 3430 Tulln an der Donau
(Zufahrt über Gregor-Mendel-Str.)

PROGRAMME

9:00 - 9:30 **Registration & coffee**

9:30 **Welcome note**

Session 1

9:40 - 10:05 **Keynote: Back to the roots**

Ben Oyserman, Juan E. Pérez-Jaramillo, Lucas W. Mendes, Jos M. Raaijmakers and Victor J. Carrión

10:05 - 10:20 **Interactions of root anatomical, architectural, and metabolic phenotypes with root microbiomes in maize growing under suboptimal nitrogen fertilization**

Tania Galindo-Castañeda, Elena Kost, Elias Barmettler, Elena Giuliano, Rafaela Conz, Hannier Pulido, Alan Pacheco, Consuelo De Moraes, Johan Six and Martin Hartmann

10:20 - 10:35 **Standardized metagenomic analyses of bacterial plant-beneficial raits**

Sascha Patz, A. Gautam, M. Becker, S. Ruppel and P. Huson

10:35 - 10:50 **Maize root bacteria metabolize host secondary metabolites**

Lisa Thoenen, Marco Kreuzer, Tobias Zuest, Pierre Mateo, Mirco Hecht, Rémy Bruggmann, Matthias Erb and Klaus Schlaeppi

10:50 - 11:10 **Coffee break**

11:10 - 11:25 **Effects of pea breeding history on root microbiome attributes under pea root rot stress**

Valentin Gfeller, Monika M. Messmer, Natacha Bodenhausen, Matthew W. Horton, Lukas Wille, Agata Leska, Klaus Oldach, Bruno Studer and Pierre Hohmann

11:25 - 11:40 **The Brassica napus seed microbiota is cultivar-specific, vertically transmitted, and contributes to host health**

Birgit Wassermann, Ahmed Abdelfatta, Tomislav Cernava, Simon Goertz, Steffen Rietz, Amine Abbadi and Gabriele Ber

11:40 - 11:55 **Coevolution and domestication of the apple microbiome**

Ahmed Abdelfattah, Ayco J.M. Tack, Birgit Wasserman, Jia Liu, Gabriele Berg, John Norelli Samir Droby, Michael Wisniewski

11:55 - 13:00 **Lunch break**

Session 2

13:00 - 13:25 **Keynote: Integration of plant-microbe interactions into breeding**

Eveline Adam, Maria Bernhart and Gabriele Berg

13:25 - 13:40 **Microbiome of Eucalyptus cuttings and its association with rooting capacity: strategy and challenges**

Andrés Villar, Pablo Fresia, Carmelo Centurión and Eduardo Abreo

13:40 - 13:55 **Investigating genetic pathways involved in the beneficial *Ensifer adhaerens* – plant interaction**

Elena Grosu, Dheeraj Rathore, Guiomar Garcia-Cabellos, Anne-Marie Enright and Ewen Mullins

13:55 - 14:10 **Biologicals as seed treatments – benefits and (current) limitations**

Nora Temme

14:10 - 14:25 **Bridging between academia and industry: a view from the seed industry sector**

Javier Carrillo-Reche, I. Brouwer, G. Mos and A. Verhage

Session 3

14:25 - 14:45 **Coffee break**

14:45 - 15:30 **Group work**

15:30 - 15:45 **Group work wrap-up**

15:45 - 16:10 **Plenum discussion**

16:10 - 16:15 **Closing of the workshop**

ABSTRACTS

Back to the roots

Ben Oyserman^{1,2}, *Juan E. Pérez-Jaramillo*³, *Lucas W. Mendes*^{4,5}, *Jos M. Raaijmakers*^{1,6}, *Marnix H. Medema*⁷ and *Víctor J. Carrión*^{1,6,8}

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Plant domestication was pivotal achievement for human civilization and subsequent improvement of 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 microbiomes play a pivotal role in plant growth and health, but the genetic factors involved in microbiome assembly remain largely elusive.

Here, our newest results are presented, we studied the microbiome assembly in wild and domesticated crop plants, common bean and in a diverse hybrid population of tomato. For common bean, our analysis indicated that along the bean genotypic trajectory, going from wild to modern, there was a gradual decrease in relative abundance of Bacteroidetes, mainly Chitinophagaceae and Cytophagaceae, and an increase in relative abundance of Actinobacteria and Proteobacteria, in particular Nocardioidaceae and Rhizobiaceae, respectively. Collectively, these results establish a link between common bean domestication, specific root morphological traits and rhizobacterial community assembly.

For tomato, we mapped the molecular features of the rhizosphere microbiome as quantitative traits of a diverse hybrid population of wild and domesticated tomato. Gene content analysis of prioritized tomato quantitative trait loci suggests a genetic basis for differential recruitment of various rhizobacterial lineages, including a *Streptomyces*-associated 6.31 Mbp region harboring tomato domestication sweeps and encoding, among others, the iron regulator FIT and the water channel aquaporin SITIP2.3.

Within metagenome-assembled genomes of root-associated *Streptomyces* and *Cellvibrio*, we identify bacterial genes involved in metabolism of plant polysaccharides, iron, sulfur, trehalose, and vitamins, whose genetic variation associates with specific tomato QTLs. By integrating 'microbiomics' and quantitative plant genetics, we pinpoint putative plant and reciprocal rhizobacterial traits underlying microbiome assembly, thereby providing a first step towards plant-microbiome breeding programs.

Interactions of root anatomical, architectural, and metabolic phenotypes with root microbiomes in maize growing under suboptimal nitrogen fertilization

Tania Galindo-Castañeda¹, Elena Kost¹, Elias Barmettler¹, Elena Giuliano¹, Rafaela Conz¹, Hannier Pulido², Alan Pacheco³, Consuelo De Moraes², Johan Six¹, Martin Hartmann¹.

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The associations between root architectural and anatomical traits with soil microorganisms is an important aspect in the selection of plant cultivars with enhanced resource uptake efficiency from soils. Understanding the interactions of root traits that are linked to improved stress-tolerance with root microbes may lead to the discovery of genetic determinants of microbial recruitment associated with specific architectural or anatomical root phenes. However, these associations between roots and microbes are poorly understood. To test the hypothesis that maize plants with contrasting root architecture and anatomy maintain unique root microhabitats that promote recruitment of different microorganisms, we studied the composition of root-associated prokaryotes and metabolic response in greenhouse-grown maize under low-N. We used 1.5m-tall mesocosms containing 30L of mixture, which resemble the soil volume available for maize growing in the field.

We studied the intra- and inter-genotype variability in root traits and their associations with microbiomes in two experiments: (i) We assessed the microbial distribution along the root systems of a single genotype; (ii) we studied four inbred genotypes with contrasting root architecture and anatomy, and associated prokaryotes. Different prokaryotic communities were found in the seminal vs nodal root systems, as well as in nodal roots at 0-40 vs 40-150 cm. Significant effects of lateral root branching density on the prokaryotic beta diversity were observed within a single genotype, and across the four evaluated genotypes, regardless of the fertilization regime. Different root and shoot metabolic responses were found across N levels and genotypes. Significant taxa-phenotype and taxa-metabolite associations are currently being explored to reveal possible mechanisms of associations of microbes with roots under low-N, and the implications of these associations for N cycling.

These results could be integrated within a top-down approach of plant breeding if the genetic control of either the plant metabolites or the plant root traits associated with specific microbial taxa are understood and if the associations between the plant traits and microbial taxa show some stability across different soils with nitrogen deficiencies. Additionally, integrative research of microbiome and root traits under varying levels of N is crucial to understand possible microbial synergies and tradeoffs of the selection of specific root traits linked to improved resource uptake for a more sustainable agriculture.

Standardized metagenomic analyses of bacterial plant-beneficial traits

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Holistic ontologies, such as of KEGG, GO or COG, give us insight in the entire functional characteristic of e.g., genomes and metagenomes in a descriptive manner. In contrast, more targeted functional ontologies, such as of CARD for antibiotic resistance gene or of VFDB for virulence factors, might provide a better resolution or a new context regarding a specific fraction of the genome, as these only focus on a subset of genes or proteins.

Similarly, the ontology for bacterial plant growth-promoting traits (PGPT) aims at achieving standardized annotation and classification results for plant-beneficial functions of related bacterial genome-wide proteins. Its application in single genome or metagenome analysis, but also in (meta-) transcriptomics, might improve statistical validation and machine learning approaches to better understand bacterial single strain or community PGPT composition and its plasticity in response to the host e.g., by the host genotype, host microbiome or other parameters that influence the entire holobiont.

Here, we present the use of the web resource PLaBAsE and its tools, as well as a metagenomic analysis pipeline to assist modern crop breeding systems that consider the plant microbiome and sustainable phytosanitary practices against phyto- and food-borne pathogen and pest eradication.

Maize root bacteria metabolize host secondary metabolites

Lisa Thoenen¹, Marco Kreuzer², Tobias Zuest^{1, 4}, Pierre Mateo¹, Mirco Hecht¹, Rémy Bruggmann², Matthias Erb¹, Klaus Schlaeppi^{1, 3}

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4. Department of Systematic and Evolutionary Botany, University of Zuerich, Zuerich

Plant roots release diverse primary and specialized metabolites to the surrounding rhizosphere. These root exudates structure root-associated microbiomes by acting as semiochemicals for microbial recruitment, as carbon sources for microbial growth, and as antibiotic compounds that selectively inhibit specific microbes. The mechanisms by which root microbes metabolize root exudates are still largely unknown.

Benzoxazinoids are a group of bioactive secondary metabolites produced by grasses including crops such as maize, wheat, and rye. Benzoxazinoids protect plants from insect pests, and pathogens and were shown to structure microbial communities. We built a culture collection of maize root bacteria to investigate the interaction of root microbes with specialized plant exudates. We found that MBOA, the main benzoxazinoid accumulating in the maize rhizosphere, inhibits the growth of many of these isolates.

We found a positive correlation between tolerance to benzoxazinoids and abundance in the community, suggesting that tolerance of maize root bacteria to maize exudates may explain the composition of host-specific microbiomes. A handful of bacteria can convert MBOA to AMPO, a stable degradation product that accumulates in soil and functions allelopathically. Bacteria that form AMPO belong to few and taxonomically distinct lineages and are abundant community members on maize roots and are depleted on roots of a benzoxazinoid-deficient maize mutant. To unravel the genetic basis of bacterial benzoxazinoid metabolism, we performed comparative genomics and identified a candidate gene cluster for benzoxazinoid metabolism.

Future work is needed to uncover the ecological functions of benzoxazinoid metabolizing bacteria in the maize root microbiome. Enhancing the capacity of the maize root microbiome to metabolize benzoxazinoids through crop engineering may improve pathogen and weed control in maize fields or crop rotation systems with non-benzoxazinoid producing plants.

Effects of pea breeding history on root microbiome attributes under pea root rot stress

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The pea root rot complex (PRRC) poses a major threat to pea (*Pisum sativum*), one of the most important crops for plant-based protein production. The co-occurrence of various soil-borne pathogens within a PRRC triggers soil fatigue, and thereby constrains cultivation. Even though resistant cultivars against single pathogens exist, the complexity of interactions among the pathogens can still lead to root infections.

In order to make further breeding progress, it is necessary to consider this complexity and link to interactions of the host with the entire root microbial community, including the pathobiome and plant beneficial members. In a previous study, we characterised several known taxa involved in the PRRC (Wille et al. 2021). It is however not known how the PRRC interacts with other members of the microbial community and how these interactions were steered by pea breeding. To shed light on this, we compare the root microbiome of pea landraces and modern European breeding material grown in PRRC-affected field soil. For this, 250 pea genotypes consisting of 174 landraces of the USDA pea core collection, 31 registered cultivars from Europe, and 45 advanced breeding lines from Getreidezüchtung Peter Kunz (CH) were grown in a controlled phenotyping assay that previously identified field-relevant resistance (Wille et al. 2020).

Harvested roots were processed to characterise root bacteria and fungi by 16S and ITS amplicon sequencing, respectively. To evaluate potential effect of plant breeding on microbiome characteristics in response to soil infestation, we investigate alpha diversity indices, microbial community composition, and network characteristics. Furthermore, we present potential microbial hubs and individual taxa associated with breeding history. This will provide valuable information about the selection effects of plant breeding on PRRC-related microbiome attributes and thus help to evaluate the potential of microbe-assisted breeding for disease resistance against pea root rot. In a next step, we aim to exploit genome-wide association studies (GWAS) to seek genetic loci involved in microbe-mediated disease resistance. Markers linked to such loci will be validated in additional genetic material by the KWS breeding company.

This work could pave the way to microbiome-smart breeding that harnesses beneficial plant-microbiome interactions to promote sustainable agriculture.

Acknowledgements:

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The Brassica napus seed microbiota is cultivar-specific, vertically transmitted, and contributes to host health

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The role of seed microbiomes for germination, plant growth and health is being intensively investigated. Successful usage of seed microbes in agriculture, however, requires in depth research on the underlying factors that determine microbial structure and functions. We analyzed the impact of plant-related (genotype, germination rate, pathogen resistance) and external factors (field site, year of harvest, country of harvest) on seed endophyte communities of ten different oilseed rape (*Brassica napus* L.) cultivars from 26 field sites across Europe.

All seed lots harbored a high endophyte abundance and diversity, and consisted of 265 bacterial ASVs on average, which were dominated by six genera: *Ralstonia*, *Serratia*, *Enterobacter*, *Pseudomonas*, *Pantoea*, and *Sphingomonas*. The cultivar was the main factor explaining the variations in bacterial diversity, abundance, and composition. In addition, the latter was significantly influenced by diverse biotic and abiotic factors. A set of bacterial biomarkers was identified to discriminate between host functional characteristics, e.g. *Sphingomonas* for optimal germination and *Brevundimonas* for resistance. Applying a Bayesian community approach suggested vertical transmission of seed endophytes, where the paternal parent plays a major role and might even determine the germination performance of the offspring.

This study contributes to the understanding of seed microbiomes in general and underlines the potential of the microbiome to be implemented in crop breeding and biocontrol programs.

Coevolution and domestication of the apple microbiome

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Plants developed in the presence of a plethora of microbes. However, it is unclear how plant phylogeny and domestication affected host–microbiome co-evolutionary dynamics. The impact of domestication and plant lineage on the endophytic microbiome composition of 11 *Malus* species, representing three major groups: domesticated apple (*M. domestica*), wild apple progenitors, and wild *Malus* species, was investigated in this study. Microbial diversity and abundance were greater in *M. domestica* and its wild ancestors' endophytic communities than in wild *Malus* species. The community makeup of heirloom and contemporary cultivars differed, although with no statistical significance. The endophytic microbiome of domesticated apples is an amalgam of its wild ancestors, according to a community-wide Bayesian model, with clear evidence for microbiome introgression, particularly in for bacteria. The evolutionary distance between *Malus* species and their microbiome was shown to be significantly correlated. This study supports co-evolution between *Malus* species and their microbiome during domestication. This finding has major implications for future breeding programs and our understanding of the evolution of plants and their microbiomes.

Integration of plant-microbe interactions into breeding

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Saatzucht Gleisdorf GmbH is the breeder of the typical 'hull-less' Styrian oil pumpkin (*Cucurbita pepo* ssp. *pepo* var. *styriaca* Greb.). Besides maintaining and improving the typical seed quality traits, like oil content and seed colour, the most important breeding targets are seed yield and yield stability. Those can be improved by enhancing yield-component traits such as the number of harvestable fruits, seed weight and seed count.

Yield-related traits such as biomass and plant architecture (e.g. bush vs. vining growth type), adaptation to climatic conditions and current agronomic practices, resistance to biotic and abiotic stresses or root architecture, affect yield as well. Our resistance breeding approaches especially focus on tolerance to viruses (e.g. ZYMV, WMV and CMV) and tolerance to fruit rot (*Didymella bryoniae* and *Pectobacterium carotovorum*).

In cooperation with University of Natural Resources and Life Sciences, Department of Crop Sciences (BOKU, Pachner) tolerances to viruses were introgressed from *C. moschata* Duchesne into oil pumpkin breeding lines by pyramiding various combinations of resistance genes. Nevertheless, many mechanism of other traits or tolerances (e.g. to fruit rot) are still not fully understood. Considering the effect of beneficial plant-microbe interactions in breeding was neglected for most plant species so far.

First experiments on the Styrian oil pumpkin with seed inoculation using biocontrol strains were performed in the greenhouse and in the open field. Promising results could be achieved; nevertheless the effects differed depending on the field or greenhouse conditions and on the cultivar. To get a deeper insight into the mechanisms of those beneficial plant-microbe interactions, the native microbiome of six oil pumpkin genotypes (including the complete pedigree of a three-way-cross hybrid) was accessed using high-throughput amplicon sequencing targeting the 16S rRNA and the ITS1 genes in soil, seeds, rhizosphere and progeny seeds.

Those analyses showed that between genotypes, more substantial changes can be observed for seed microbiomes compared to the rhizosphere and that bacterial signatures are mainly linked from seed to seed, while fungal communities are shaped by the soil and rhizosphere.

This work set the foundation for microbiome-assisted breeding and seed production in the Styrian oil pumpkin.

Microbiome of Eucalyptus cuttings and its association with rooting capacity: strategy and challenges

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Eucalyptus dunnii is cultivated in Uruguay due to particular features of the pulp. Clonal reproduction of this species is possible, so breeding programs run by UPM have produced a series of clones that are being effectively multiplied. However, the multiplication efficiency has reached a plateau partly due to low rooting percentage of some clones. A research project under development is exploring the association among fungi and bacteria with *E. dunnii* clones along the production line, with the objective of identifying key microbial species associated with 1) mother plants of clones with different rooting capacity 2) mother plants of different age whose cuttings show different rooting capacity 3) cuttings with and without rooting 4) substrate used for rooting.

Initial exploration started with the sampling of 15 cuttings from mother plants of each of four *E. dunnii* clones of variable rooting capacity and one clone of *E. grandis* (G_1) with good rooting capacity. Sampling of clone D_1 of *E. dunnii* was done on mother plants younger than 1 year old and older than 3 years, while samplings of clones D_2, D_3, D_4 of *E. dunnii* and G_1 of *E. grandis* were done on mother plants older than 3 years. Segments of 5 mm length were cut from the base and medium part of each cutting and were surface disinfected through immersion for 1 minute in 3% NaClO, 95% ethanol and a final rinse in sterile water. Segments were plated on PDA and LB Petri plates and incubated at 26°C for one week. Colonies were counted to evaluate colonization frequency of segments and streaked to fresh Petri plates to obtain pure cultures for further identification. Interestingly, the most colonized cutting segments were obtained from the *E. grandis* cuttings. Within *E. dunnii*, the clones known for better rooting capacity also showed higher percentage of colonized segments, and mostly at the base of the cutting. Finally, in the case of clone D_1, cuttings from mother plants older than 3 years old produced segments with higher colonization than cuttings from younger mother plants.

After these promissory results a microbiome profiling, based on amplicon sequencing approach, will be carried out with a similar sampling strategy in order to obtain a wider understanding of microbial richness and diversity. This information could then be used to guide the isolation of key species associated with rooting success and to inform the selection criteria applied during crossing and progeny evaluation at the genetic improvement program.

Investigating genetic pathways involved in the beneficial *Ensifer adhaerens* – plant interaction

Elena Grosu^{1, 2}, *Dheeraj Rathore*¹, *Guiomar Garcia-Cabellos*², *Anne-Marie Enright*², *Ewen Mullins*¹

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In the last decade, European Union regulations (EU Directive 2009/128/EC) have oriented the region towards more sustainable crop production, limiting the use of chemical crop improvement products. Moreover, an increase in volatile weather patterns linked to climate change is impacting production systems and further highlights the need for more resilient cropping systems, if we are to achieve the European Farm to Fork goals for 2030.

In light of all the above, the biostimulants field has received increased attention. Microbial inoculants (i.e. plant growth promoting bacteria) have proven to be efficient in improving plant growth and yield via entering the plant nutrient cycle and actively enriching nutrient availability together with activating defence mechanisms.

This project focuses on characterizing the plant growth promoting activity of a new *Ensifer adhaerens* strain Op14 (EaOp14) on a variety of crops (oilseed rape, wheat, barley, faba bean, lupins). Phenotypical data showed that seeds coated with an EaOp14 inoculum develop more vigorous seedlings (oilseed rape and wheat) when germinated under in-vitro conditions and based on replicated experiments under glasshouse conditions.

Trying to understand the molecular mechanisms behind these beneficial effects, we exposed EaOp14 to plant extract and separately to different concentrations of the important plant signalling compound salicylic acid (SA, 50 μ M, 100 μ M, 200 μ M, 400 μ M, 600 μ M, 800 μ M). At several time points up to 12 hr post-treatment (hpt), the activity of pchB and salD was assessed. Previous work by this group (Zuniga et al, 2019) confirmed their involvement in SA synthesis and degradation in *E. adhaerens* respectively. In contrast to pchB, when exposed to plant extract, salD expression increased steadily up to 1.5 fold change (FC) out to 12hpt. Interestingly, up to 6 hpt, even in the presence of extreme concentrations of SA (600 μ M, 800 μ M) a 2-fold increase in salD gene expression was observed, followed by a steady decrease in expression, while pchB gene activity increased from six up to twelve hours (1.5 FC).

Looking ahead, field evaluations of the efficacy of EaOp14 seed treatment are currently underway on spring oilseed rape (var. Ability, Lagonda, Contra, Lumen and Mirakel), while in vitro experiments have confirmed the ability of EaOp14 to inhibit the growth of the important wheat pathogen *Zymoseptoria tritici*. Supporting the through-to-practise application of this work be that for breeding/seed applications, future research will focus on the field efficacy of EaOp14 seed treatment, under different soil and stress conditions. Datasets generated will identify the potential role of EaOp14 in cropping regimes to support the yield potential of varieties, be that as a growth biostimulant and/or disease mitigation treatment.

Biologicals as seed treatments – benefits and (current) limitations

Nora Temme¹

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Biologicals are beneficial microorganisms or substances of natural origin such as plant extracts. As seed company, we develop biological seed treatments to strengthen and protect the seed and the seedling in a natural & sustainable way.

Biologicals as seed treatments have special challenges: Actives must survive applications & storage and must adapt to a given environment and establish quickly to compete with the natural soil microbiome.

At KWS SEED SE, we are working on solutions to overcome those challenges.

Bridging between academia and industry: a view from the seed industry sector

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Both academic and industry scientists strive to meet the demand for environmentally-friendly solutions to control pests and diseases as a replacement for synthetic pesticides. Breeding resistant varieties has been the usual path to address biotic challenges. In specific cases, protection of the emerging seedling is needed before genetic-mediated resistance is expressed.

Microbe-based pesticides applied on seeds are economically more attractive than spray application to plants in the field and require no action by growers. In this regard, academic research has been prolific in the discovery of beneficial plant-associated microorganisms that enhance resistance to biotic stresses. Yet, examples of commercial success are currently limited. In an effort to align academic research and industrial application, here we present the common research gaps and pitfalls the industry encounters in the attempt to make a “real-world” product from beneficial plant-associated microorganisms.

The current legal framework for registration of biocontrol microorganisms is a major burden as it is costly in time and cash. Economically-viable microbial production and consistent efficacy of beneficial plant-associated microorganisms across diverse (biotic) environments (both often neglected in academic studies) need to be demonstrated before registration can be considered. We also stress the need for more research on suitable formulations and product shelf-life to be able to capitalize on beneficial microorganisms.

Lastly, we discuss how recent findings on the impact of seed microbiome on plant health and productivity are followed with interest from the industry. For it to make an impact, we propose an applied approach addressing practical factors shaping the potential seed microbiota (e.g., the influence of production sites, extraction procedures and processing) rather than a sole focus on ecology.

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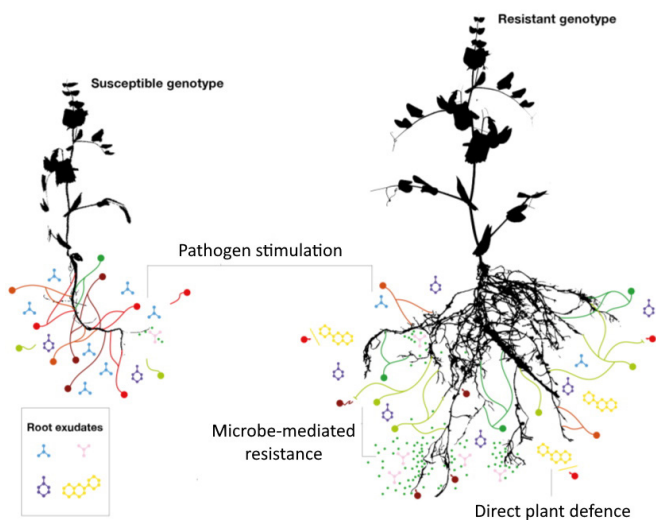
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3rd EUCARPIA WORKSHOP ON IMPLEMENTING PLANT-MICROBE INTERACTIONS IN PLANT BREEDING



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