

ABSTRACT BOOK

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POSTERS**ENVIRONMENT, BIODIVERSITY, PLANT & FOOD***No. 1***Changes in microbiome composition predict variation in plant traits**Antonino Malacrinò, Alison E. Bennett

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Quantifying the effects of variation in microbiome composition on host traits is still an outstanding challenge in holobiont biology. Plants, for example, assemble most of their microbiome from soil, which composition is influenced by both biotic and abiotic factors, driving variation in plant-associated microbial communities (e.g., roots, leaves). The impact of this variation in plant microbiome composition on host traits and function is still little understood. We set out to address this question in a greenhouse experiment using tomato as a model. We extracted a diverse microbial community from restored prairie soil, manipulated it to have incremental changes in microbiome composition, and added the manipulated communities to tomatoes growing in sterile soil. We then characterized microbial community composition in soil, roots, and leaves, and measured a suite of plant traits to determine whether changes in soil microbiome composition influenced them. We found clear signatures of changes in microbial community composition on host traits, and interestingly we found that incremental changes in microbiomes composition altered plant fitness traits more than morphological traits, with variations across plant development and compartments (soil, roots, leaves). Under the global changes we are witnessing, our results are relevant to predict the impact of shifts in microbial communities on plants traits, or to help us to manipulate microbiomes to alter plant traits and function, which is key towards a more sustainable agriculture.

*No. 2***Exploring the impact of intercropping on the rhizosphere microbial communities of cultivated lettuce**Kristina Michl, Simone Bosco, Verena Gschiel, Gabriele Berg, Tomislav Cernava

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The influence of microbial diversity on plant growth and health is well described as microorganisms contribute to enhanced nutrient uptake and increased resilience against various stressors. Integrating this perspective into agricultural practices has the potential to result in improved crop productivity and resistance. Intercropping, the simultaneous cultivation of multiple crops in the same field, has been explored as an alternative to monoculture, revealing benefits such as heightened microbial diversity and improved plant growth in various cropping combinations. In this study, we aimed to assess the effect of

intercropping on the microbial composition of the rhizosphere of *Lactuca sativa* var. capitata L. Rhizosphere samples were collected at three time points during the growing season from fields with different cultivation methods, including monoculture with and without mulching, and intercropping with narrow or wide. High-throughput sequencing of the 16S rRNA gene fragment and ITS region was done to analyze the taxonomic structure of bacterial and fungal communities, respectively. The relative abundance of both bacterial and fungal communities was primarily influenced by the sampling time point, followed by the cultivation method. Moreover, the Shannon diversity index revealed significantly higher diversity in both intercropping treatments at the first time point compared to the monoculture. PERMANOVA analysis indicated that both sampling time and cultivation system contributed similarly to the observed variance. Non-metric multidimensional scaling (NMDS) plots revealed distinct clustering of samples based on cultivation systems, illustrating a shift in bacterial and fungal communities due to different treatments. In summary, while intercropping had a pronounced effect on microbial diversity early in the cultivation season, mulching also exhibited an increase in diversity over time, although determining distinct communities compared to intercropping.

No. 3

Halophytes vs. crop plants: Unraveling Microbiome Structure and core taxa

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Climate change and anthropogenic activities are intensifying salinity stress that significantly reduces plant productivity and biodiversity in many agroecosystems. Nonetheless, there are salt-tolerant plants (halophytes) that are adapted to under extreme salty conditions. Over years these plants along with their associated microbiome evolved various mechanisms to alleviate salt stress. Exploring the microbiome composition of different halophytic plants is an opportunity to discover a halophyte specific microbiome. Studies comparing the microbiome structure between halophytic and non-halophytic plants, such as conventional crops, are still rare. Therefore, we performed a comprehensive meta-analysis study using published bacterial 16S rRNA gene sequencing datasets to reveal microbiome structure and identify core taxa in various halophytic and non-halophytic plant hosts. Fifteen studies met our quality selection criteria to retrieve microbiome datasets, covering 40 plants, representing 10 different halophyte species and 4 different non-halophyte species from around the world. Microbiome structure analysis revealed distinct compositions for halophyte plants that face high salinity concentrations in their rhizosphere from halophytes grown at low salinity or from crop plants. Furthermore, 17 bacterial genera exclusively detected in all halophytes grown at high salt concentrations. These findings demonstrated that salinity is one of the environmental factors controlling the structure of the rhizosphere microbiome. Additionally, this advances our understanding and reinforces the "cry-for-help" theory of how stressed plant possibly assemble special microbiome to mitigate stresses. In silico identifying shared core taxa