

Microbiomics and Plant Health: An Interdisciplinary and International Workshop on the Plant Microbiome

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The microbiome refers to the collective genomes of all resident microorganisms of a particular organism, environment, or ecosystem. Plant surfaces and interior parts are populated by myriads of bacteria, fungi, and microbes from other kingdoms, which can have considerable effects on plant growth, disease resistance, abiotic stress tolerance, and nutrient uptake. Hence, deep insight into the mechanisms underlying plant microbiome evolution, composition, and function would provide new opportunities to improve crop health and yield and thus benefit global food security. To bolster the promise and potential of microbiome research in agriculture, Jianbing Yan from Huazhong Agricultural University (HZAU, China) and Marcel Bucher from University of Cologne (UoC, Germany) developed the idea to organize an interdisciplinary workshop on plant microbiome late in 2017. This idea turned into the First Sino-German Symposium on Plant Health and Microbiomics, which was sponsored by The Sino-German Center for Research Promotion, a joint center of the National Natural Science Foundation of China and the Deutsche Forschungsgemeinschaft (German Research Foundation) in Beijing. This bilateral symposium was held on September 24–28, 2018, at HZAU in Wuhan, China. A total of 40 scientists from China, Germany, Japan, and USA were invited to share their progress in the field and their thoughts and ideas on plant–microbiota interactions and soil and plant microbiomes.

This symposium included the following major themes: (1) current status and perspectives of plant microbiomics, (2) microbiome and plant disease resistance, (3) microbiome and plant nutrition, (4) emerging new methods to study plant microbiomes, and (5) microbiome and agriculture ecosystems. Due to space limitations, we can share only some of the presentations in more detail and summarize major points presented by symposium speakers.

The participants thoroughly shared recent progress on the metagenomics of maize, rice, and *Arabidopsis*-associated microbial communities. Considering the importance of maize as a crop for food and feed in both China and Germany, one-third of the talks were focused on maize in this bilateral symposium. Marcel Bucher summarized the scientific concept of the consortial research project RECONSTRUCT: unraveling the contribution of soil biodiversity

to maize growth and fitness through combined omics-based *in silico* modeling and reconstruction biology (<https://www.pflanzenforschung.de/de/plant-2030/fachinformationen/projekt-datenbank/aufdecken-des-beitrags-der-bodenbiodiversitaumlt-zu-wac-429>). This interdisciplinary project is funded by the German Federal Ministry of Education and Research and aims at the knowledge-based breeding of maize lines that can interact with functionally robust beneficial microbial assemblages, leading to high fitness and yield on agricultural soils with minimal external inputs. It is anticipated that the RECONSTRUCT project will in the long term lead to a thorough mechanistic understanding of the soil–rhizosphere–maize system in interaction with its microbiota. He also presented first results on how arbuscular mycorrhizal (AM) fungi modulate maize nutrient uptake and the root microbiome. On the other hand, Jianbing Yan introduced the progress of maize functional genomics in China and presented the design of maize CUBIC (complete-diallel design plus unbalanced breeding-like inter-cross) population resource, which was successfully applied to explore the genetic architecture of massive important agronomic traits. Along with metagenomics technologies, he is using the CUBIC lines to dissect the genetic basis of maize–microbiome interaction. Guotian Li (HZAU, China), Hui Li (University of Jinan, China), and Wanqi Liang (Shanghai Jiao Tong University, China) presented how they developed and used the genetic resources of maize and rice to dissect complex traits via forward and reverse genetic approaches. In addition, Yang Bai from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences (IGDB, CAS, China), presented an in-depth analysis of the *Arabidopsis* microbiome using metagenome sequencing and large-scale cultivation, providing a nice example of uncovering the establishment and functions of plant microbiota.

Plant health was an important topic in this symposium. Jian-Min Zhou (IGDB, CAS, China) introduced his long-term efforts to dissect the signaling pathways of plant innate immunity. He also talked about his recent work on the identification of

plant-produced compounds that specifically inhibit pathogenic bacterial virulence with less impact on the healthy microbiota. Bo Li (HZAU, China) presented how plants fine-tune the innate immunity signaling transduction via protein kinases and transcription factors. Gunther Doehlemann (UoC, Germany), Meng Yuan (HZAU, China), Alejandra Huerta (Colorado State University, USA), and Yan Wang (Nanjing Agricultural University, China) highlighted compelling examples of how crop immunity is modulated by different pathogen effector proteins. These findings pave the way to developing disease-resistant cultivars through traditional breeding approaches or the latest genome editing technologies.

In addition to improving crop resistance via genetic manipulations, the control of pathogens using microbes or viruses is an important complement for the long-term control of plant disease. A couple of interesting examples were presented in this symposium. Jiatao Xie (HZAU, China) presented a comprehensive study on fungus–virus interactions and recent promising results on fungal disease control using mycoviruses. Wenxing Xu (HZAU, China) reported the identification of a double-stranded RNA virus that is encased within filamentous particles from a pathogenic fungus of the tea plant (*Camellia sinensis*), which is the longest among known viral particles and might be used to control fungal disease in tea. Wende Liu (Institute of Plant Protection, Chinese Academy of Agricultural Sciences, China) identified a *Streptomyces* bacterium that conferred crop disease resistance by producing a small molecular compound. Zhonghua Ma (Zhejiang University, China) dwelled on how the bacterium *Pseudomonas piscium* isolated from wheat microbiota suppressed the pathogenic fungus *Fusarium graminearum* by manipulating fungal histone acetylation and epigenetic regulation. Chulong Zhang (Zhejiang University, China) identified a rice root fungal endophyte that could be used to protect rice from *Magnaporthe oryzae*. Jian Ye (Institute of Microbiology, CAS, China) talked about plant–virus–insect interactions and the potential role of the microbiome during these tritrophic interactions. These reports revealed the great potential of research on the plant microbiome including plant–microbe–virus interactions in crop disease control for sustainable agriculture.

Another major focus of this workshop on plant microbiomics was on the mechanistic understanding of the interactions between plants and host-associated beneficial microbes. The symbiotic processes between plant hosts and fungal or bacterial (rhizobial) microbes have been investigated in detail in the AM and root nodule symbiosis. Here mutualistic microbes hold great potential to improve crop nutrient uptake. Ertao Wang from the Shanghai Institutes for Biological Sciences (CAS, China) gave an impressive talk with insight into AM fungal signal perception by the host and how the host plant feeds its fungal symbiont with fatty acids. Li Xue (UoC, Germany) demonstrated how a single transcription factor, *CBX1*, regulates the symbiotic exchange of the nutrients C and P in mycorrhizal *Lotus japonicus*. She also shared her recent results on how the AM symbiosis triggers changes in the composition of the root microbiome. Peng Yu (University of Bonn, Germany) explored the role of AM fungi on maize lateral root initiation and presented the *ERF* transcription factors playing important roles during this process. Yangrong Cao (HZAU, China) talked about signaling pathways operating in the legume–rhizobium symbiosis, and particularly emphasized the functions of immunity-related genes in the symbiosis. His data suggested

that rhizobial infection affects the plant innate immunity and is involved in the maintenance of the rhizobial endosymbiosis during nodulation. Izabela Fabianska (UoC, Germany) reported on the plant-mediated effects of soil phosphorus on the root-associated fungal microbiota in *Arabidopsis thaliana*. Lukas Schreiber (University of Bonn, Germany) stressed the importance of biosurfactants during the interaction between bacteria and plant cuticles, which may enhance the ecological fitness of epiphyllic bacteria. Another intriguing example of beneficial plant–microbe interactions was given by Kei Hiruma (Nara Institute of Science and Technology, Japan). He tracked the plant growth-promotion capacity of different strains of ascomycete fungi of the genus *Colletotrichum*, and further studied the genes involved in the transition between pathogenic and mutualistic lifestyles of these fungi.

Experimental approaches to elucidate the complex interaction between host genetics and the plant microbiome face many technological challenges. A number of innovative methods employed to study the plant microbiome were shared with the audience. Kenichi Tsuda from the Max Plank Institute for Plant Breeding Research (Germany) introduced a novel method for *in planta* bacterial transcriptome and proteome profiling. His group dissected interactions between *Arabidopsis* and *Pseudomonas syringae* using this method, which provided unprecedented insight into how plants control bacterial growth and behavior. Ben Niu (Northeast Forestry University, China) reported on the establishment of a simplified synthetic bacterial community of maize roots through host-mediated selection. Such synthetic bacterial communities could serve as a useful system to study maize–microbe interactions under controlled laboratory conditions. Lili Zhang (Institute of Microbiology, CAS, China) and Kabin Xie (HZAU, China) reported on improved methods to remove host contamination in rice 16S rRNA microbiome profiling. In addition, Kabin Xie and Nan Peng (HZAU, China) presented the CRISPR technologies for plant and bacterium genetic engineering, respectively. There is no doubt that rapid progress on the technologies such as third-generation DNA sequencing and CRISPR genome editing will greatly advance the plant microbiome research.

Microbiome studies often utilize large datasets obtained through marker gene sequencing, metagenome sequencing, proteomics, metabolomics, ionomics, and even high-throughput phenotyping (phenomics) assays. Therefore, sophisticated bioinformatics tools are required for mining biological information from such high-dimensional data. In this symposium, Ye Deng (Research Center for Eco-environmental Sciences, CAS, China) introduced a molecular ecological network analysis approach to construct species interaction networks based on 16S rRNA sequencing or microarray data. Georg Basler (Max Plank Institute for Molecular Plant Physiology, Germany) addressed recent progress in integrating metabolic, transcriptomic, and microbiomic data of maize to computationally model maize–microbiome interactions studied within the RECONSTRUCT project. As massive datasets are accumulating continuously in the plant microbiome research community, artificial intelligence and machine learning technologies will be in great demand to analyze such big data.

In addition to discussing plant–microbiome interactions at the micro-environment scale, experts on ecology were also invited to discuss the roles of plant microbiota in agroecosystems.

Meeting Report

Michael Bonkowski (UoC, Germany) talked about the importance of protists grazing in microbial communities, which were shown to be essential to shape the rhizosphere microbiome. Yongguan Zhu (Institute of Urban Environment, CAS, China) highlighted the role of plant–microbiome interactions in the biogeochemical cycle of antibiotic resistance genes underlying the potential of plant-associated microbes in the dissemination of antibiotic resistance via food consumption or direct contact. Yunfeng Yang (Tsinghua University, China) surveyed bacterial, fungal, and diazotrophic communities in paddy soils at local and regional scales. His study not only showed the biogeographical patterns of the soil microbiome but also identified potential driving forces of soil bacterial community turnover.

In sum, this symposium provided a comprehensive platform for academic exchange among Chinese, German, Japanese, and American scientists in the area of microbiomics and plant health. After one week of intensive learning and knowledge sharing, the importance of interdisciplinary and international collaborations toward harnessing the rich repertoire and variations of the microbiome for sustainable agriculture was highly rated.

Molecular Plant

Research co-operations on plant microbiome in agriculture will be encouraged by the documented success of the Earth Microbiome Project and the Human Microbiome Project, which highlight the importance of collaborative networks and open science for innovative and high-impact microbiome research that will deliver solutions to the challenges facing humanity in the future.

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