

# Contribution of Microbial Inter-kingdom Balance to Plant Health

Soil-borne fungal and oomycetal pathogens cause devastating agricultural losses every year. The abundance and diversity of filamentous eukaryotes in the roots of healthy plants are influenced by root-associated bacteria that protect host plants from disease caused by fungi and oomycetes (Duran et al., 2018). This is the major conclusion published by Duran and her colleagues in the Max Planck Institute for Plant Breeding Research. The authors have systematically concluded the importance of microbial inter-kingdom interactions for healthy plant growth by metagenomic profilings and cultivation.

Plant roots interact with numerous microbes, including bacteria, fungi, and oomycetes from the soil environment, which is the main reservoir of the plant microbiota (Lundberg et al., 2012; Bulgarelli et al., 2013). The rhizosphere, a narrow zone of soil close to the roots, contain up to  $10^{11}$  microbial cells per gram (Egamberdieva et al., 2008). Some of these microbes are beneficial for plants, such as plant-growth-promoting rhizobacteria (PGPR) and fungi (PGPF) (Pieterse et al., 2012). For example, rhizobia fix atmospheric nitrogen in symbiosis with legumes; endophytic and mycorrhizal fungi facilitate phosphorus acquisition of their host plants (Hiruma et al., 2016). However, in many cases, fungi and oomycetes usually cause serious plant diseases (Dodds and Rathjen, 2010). Given the diversity of microbes that colonize plant roots, the dynamics of microbe–microbe interactions have recently received increasing attention (Agler et al., 2016), but how these microorganisms interact at the community level and the consequences on plant health is still poorly understood (Hassani et al., 2018).

To address these questions, Duran and her colleagues investigated the root microbiota of healthy *Arabidopsis* plants in three distant natural sites in Europe, by profiling simultaneously root-associated bacterial, fungal, and oomycetal communities. They found that geographically distant *Arabidopsis* populations host taxonomically similar root-associated bacterial communities but dissimilar and site-specific root fungal and oomycetal microbiota, indicating that potentially conserved beneficial traits exist in root-associated bacterial communities. In addition, they found negative correlation between bacteria and eukaryotic filamentous microbes, indicating cross-kingdom competition between bacteria and filamentous eukaryotes in plant roots.

To further study the interaction between bacteria, fungi, and oomycetes and their influence on plant health, Duran and her colleagues deconstructed the root microbiota by establishing bacterial (Bai et al., 2015), fungal, and oomycetal culture collections, providing opportunities for multi-kingdom reconstitution of the root microbiota under laboratory conditions. They inoculated different combinations of bacteria, fungi, and

oomycetes on germ-free *Arabidopsis* to investigate the impact of these microbial combination on plant growth. Notably, plant growth was severely impaired in the presence of fungi or oomycetes, but this growth inhibition was fully rescued by the synthetic bacterial community (Figure 1). Further, *ex situ* and *in planta* experiments showed that several individual bacteria from distinct taxa are sufficient to protect *Arabidopsis* from fungi or oomycetes, indicating that the bio-control activity is a redundant trait shared by phylogenetically unrelated root-associated bacteria.

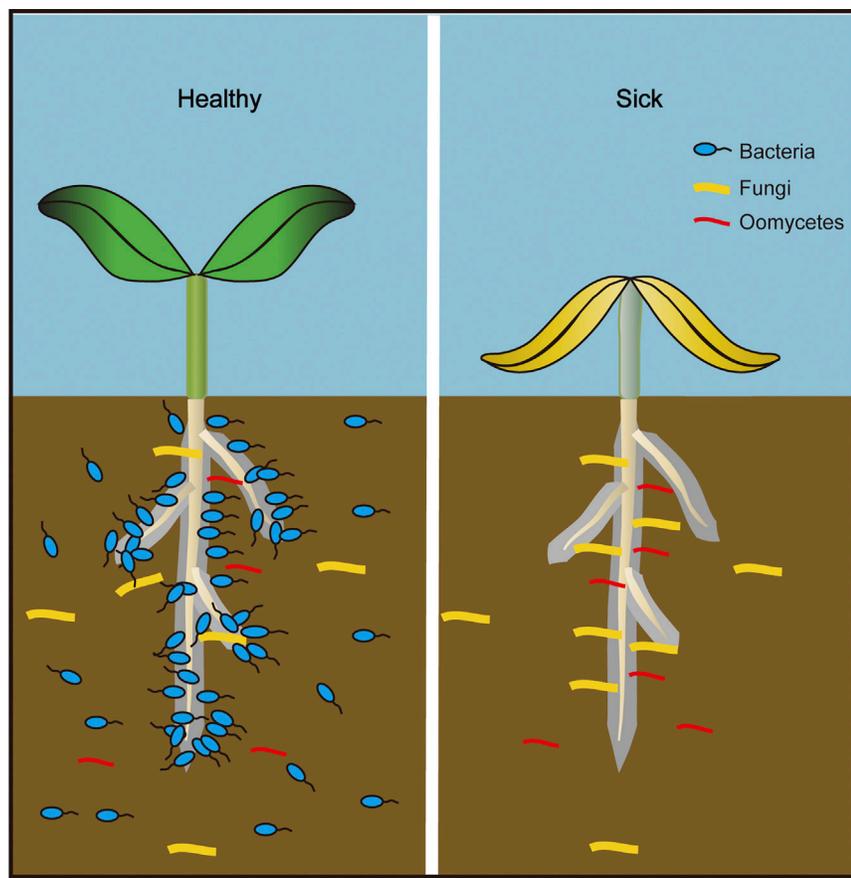
These results show that the root bacterial microbiota could complement the plant innate immune system and play pivotal roles for plant growth and survival in natural soils. Although plants have evolved a complex innate immune system, including PAMP triggered immunity and effector triggered immunity, to defend themselves against pathogens (Jones and Dangl, 2006), filamentous eukaryotic microbes can still infect plants in nature. Root bacteria with bio-control activities may form the first layer of a barrier for plants prior to the immune system. Given the fact that land plants have interacted with microbes for 450 million years (Hassani et al., 2018), it is tempting to speculate that plants with advantages of adaptation in natural environments may have evolved mechanisms to select bacteria with bio-control activities against filamentous eukaryotes to avoid growth retardation and energy costs resulting from immune responses. These bacteria may be attracted and regulated by plant root metabolites (Stringlis et al., 2018).

This work shows the strength of metagenomic technologies to dissect complex phenomena in nature by sequencing natural samples and validating corresponding results under laboratory conditions. It opens up unprecedented challenges and opportunities to investigate the complex interplay between bacteria, filamentous eukaryotic microbes, and plant hosts, and to dissect how microbial inter-kingdom balance can affect host fitness. Furthermore, as the current microbial profiling methods based on microbial relative abundance ignore the microbial load relative to host plants, it raises the need to develop new quantitative methods to measure the absolute abundance of bacteria and fungi in plant roots. Finally, it remains important to characterize bacterial genes and molecules that contribute to their protective functions and define host molecular components that regulate root microbiota assembly. All these together will help us to understand how plants coordinate selection of environmental microbes to survive in nature.

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**Figure 1. Bacterial Root Commensals Protect Plants from Soil-Borne Filamentous Eukaryotes.**

Bacteria efficiently inhibit fungi and oomycetes and make plants have healthy growth, while fungi and oomycetes cause serious disease in the absence of bacteria.

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