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Breeding for microbiome-mediated disease resistance

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Abstract

Plant-associated microbial communities play a crucial role for the expression of various plant traits including disease resistance. Increasing evidence suggests that host genotype influences the composition and function of certain microbial key groups, which, in turn, effects how the plant reacts to environmental stresses. Several studies indicate that modern plant breeding may have selected against plant traits essential for hosting and supporting beneficial microbes. However, they also highlight the presence of an exploitable genetic base for the regulation of the rhizosphere microbiota.

We illustrate the concept of breeding for microbial symbioses with pea (*Pisum sativum* L.). Firstly, genotypic variation for the efficiency of a mycorrhizal symbiosis is shown, as measured by an estimation of the plant benefit per symbiotic unit. Secondly, we extend the view towards the wider fungal community using ITS amplicon sequencing. Two pea genotypes with contrasting resistance levels against pathogen complexes are investigated to provide information on the functional diversity of the rhizosphere microbiome in a naturally infested agricultural soil. In the near future, microbial hubs and diversity indices will be linked with root exudation in order to elucidate the plant's capacity to influence the microbial composition leading to disease susceptibility or resistance. Current and future research activities of our group aim to make use of plant-microbiome interactions to develop advanced screening tools for breeders for an improved expression and stability of important plant traits.