Rhizosphere microbiome as possible inducer of enhanced resistance in barley

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The rhizosphere microbial community is known to harbor a multitude of diverse microbes. Therefore the plant microbiome is also called the second genome of the plant. The microbiome of a plant consists of beneficial, neutral and pathogenic bacteria. Beneficial bacteria may have strong influences on plants via mutualistic associations. The beneficial microbes play an important role in plant growth and health and provide protection against plant pathogens.

One of these protective mechanisms is priming for enhanced resistance. Priming through rhizosphere microorganisms can be achieved by specific compounds released by the microorganisms e.g. *N*-acyl homoserine lactones (AHLs) or other compounds. Defense responses to biotic and abiotic stresses of primed plants are faster and stronger, if compared to unprimed (naïve) plants.

Plant diseases are responsible for about 20 % yield loss worldwide. A better understanding of priming mechanisms would lead to the ability to develop breeding strategies for more resistant crops. Unfortunately, until now the mechanisms of priming are mainly investigated in the model plant *Arabidopsis thaliana.* Therefore, it is our aim to investigate priming in monocotyledonous crop plants.

This project aims to examine the ability of the rhizosphere microbial community of barley (*Hordeum vulgare*) to enhance the resistance against the powdery mildew-causing fungus *Blumeria graminis* f.sp. *hordei*. Cultivation-dependent and cultivation-independent methods are used to gain insights into the structure of the bacterial community in the barley rhizosphere. They also allow answering the question whether soil-specific members of the community are enriched in the barley rhizosphere. Future studies using next generation sequencing techniques will allow the identification of rhizosphere bacterial community members with high abundance.

To investigate the potential of rhizosphere microbial communities to prime barley, a standardized, greenhouse-based experiment was designed. The rhizosphere bacterial community of two barley cultivars grown in different soils was extracted. Subsequently, barley seedlings grown in a substrate/sand mixture were drenched with the extracted microbial fraction. The bacterial community composition associated with the barley roots was analyzed by Denaturating Gradient Gel Electrophoresis of 16S rRNA gene amplicons from total community DNA. The primed state of the barley plant was determined by monitoring the infection with *B. graminis* and analyzed by expression pattern of defense-related genes. The potential ability of different rhizosphere microbial communities to induce priming is assumed to offer great potential for new plant breeding strategies and should be the long-term achievement of this project.