Enhanced plant resistance towards phytopathogenic fungi depends on the rhizosphere microbial community composition

Nina Bziuk[1], Desirée Lauterbach[1], Søren J. Sørensen[2], Adam Schikora[1] and Kornelia Smalla[1]
[1] Julius Kühn Institute, Institute for Epidemiology and Pathogen Diagnostics, Braunschweig
[2] University of Copenhagen, Department of Biology, Section of Microbiology, Copenhagen
E-mail of corresponding author: nina.bziuk@julius-kuehn.de

The plant's resistance towards phytopathogenic fungi is assumed to be enhanced by interactions with its rhizomicrobiota. It is known that beneficial bacteria in the rhizosphere can trigger a faster and stronger immune response of the plant towards pathogens or abiotic stresses, which can also be called priming. Furthermore, the prokaryotic community compositions of agricultural soils differ depending on the applied management practice. We hypothesize that prokaryotic communities from different agricultural legacy might also influence the ability of the rhizomicrobiota of barley cultivar 'Golden Promise' to enhance the resistance against powdery mildew *Blumeria graminis* f. sp. *hordei*. Therefore, an experimental approach was developed suitable to test the priming ability of the rhizomicrobiota under greenhouse conditions. Detached barley rhizomicrobiota from plants grown in field soil was inoculated to a substrate/sand mixture, which was planted with barley seedlings. Control plants were treated in the same way but with saline solution. At growth stage 13, barley plants were infected with *B. graminis*, control plants were left untreated. The prokaryotic community composition was analyzed by sequencing of 16S rRNA genes amplified from total community DNA directly extracted from rhizosphere soils sampled nine days after infection. The priming efficiency was examined by a detached leaf assay and expression pattern of defense-related genes analyzed by qPCR. Although the resistance against *B. graminis* was not found to be improved, plants treated with the rhizosphere microbiota showed a stronger defense response after the fungal infection. Furthermore, an influence of the rhizosphere inoculant, as well as the presence of the fungal pathogen on the prokaryotic rhizosphere community with several differentially abundant taxa was observed.

Our results suggest a stronger priming ability of the rhizomicrobiota from field soil compared to the substrate community. The developed approach proved to be suitable for testing the abilities of prokaryotic communities originating from soils with different agricultural history to enhance the resistance of barley towards fungal phytopathogens.