

## **Metagenomics and metatranscriptomics of the rhizosphere microbiome: understanding the interplay between the good, the bad and the ugly**

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In natural disease suppressive soils, plants are protected from fungal infections in spite of the presence of the pathogen. Disease suppressiveness is, in many cases, microbial in origin. For various fungal pathogens, suppressiveness develops in the field after several years of high disease incidence. Hence, the fungal pathogen appears to be required for activating specific antagonistic microorganisms. For most suppressive soils, however, the microorganisms and mechanisms involved in disease control are not known to date. PhyloChip-based metagenomics of a soil suppressive to *Rhizoctonia* damping-off disease uncovered the bacterial diversity of the rhizosphere microbiome. To get insight into the active bacteria and bacterial traits expressed during fungal attack of the plant roots, rhizospheric RNA from sugar beet plants growing in suppressive soil with or without the fungal pathogen was sequenced. Analyses of over 5 million sequencing reads revealed that the overall structure of the bacterial community was in accordance with the previous metagenomic analysis, with Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes and Planctomycetes as the dominant phyla. Bacterial taxa that were the most enriched in presence of the fungal pathogen belonged to the  $\alpha$ - and  $\beta$ -Proteobacteria, Actinomycetales and Sphingobacteria. mRNA sequence analyses revealed different subsystems categories, including regulation and signaling, motility, chemotaxis, membrane transport and secondary metabolism. Next to the beneficial rhizobacteria, metagenomic analysis also revealed the presence of several opportunistic and true human pathogenic bacteria in the rhizosphere microbiome, including *Staphylococcus*, *Salmonella*, *Clostridium* and *Vibrio* species. The potential mechanisms involved in the interplay between the good, the bad and the ugly in the rhizosphere microbiome will be discussed.