

**Metatranscriptomics of the rhizosphere microbiome; the quest for bacterial genera and traits involved in natural plant protection.**

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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, soil 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. 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 microorganisms and traits expressed during disease suppression, 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 more than 1,000 bacterial taxa. The overall structure of the bacterial community was in accordance with the previous metagenomic results, 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 more than 200,000 proteic features representing different subsystems categories, including motility, chemotaxis, membrane transport and secondary metabolism. Results of the taxon and function-targeted analyses will be presented.