

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

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Disease-suppressive soils are exceptional ecosystems in which beneficial microorganisms guard plants from infections by soil-borne pathogens. For most suppressive soils, the microorganisms and mechanisms involved in disease suppression are not known to date. Here, PhyloChip-based metagenomics of the rhizosphere microbiome was coupled with culture-dependent functional analyses to identify bacterial taxa and mechanisms involved in soil suppressiveness to the fungal root pathogen *Rhizoctonia solani*. The metagenomic analyses led to the identification of diverse bacterial and archaeal taxa and specifically pointed to the Proteobacteria, Firmicutes and Actinobacteria as the most dynamic groups associated with disease suppression. Targeted isolation and functional analyses led to the identification of specific members of the  $\gamma$ -Proteobacteria that produce chlorinated antifungal peptides that inhibit hyphal growth of *R. solani*. 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. Preliminary analysis indicated that several of these bacterial taxa are more abundant in the rhizosphere of sugar beet plants grown in the conducive soil than in suppressive soil. The interplay between the good, the bad and the ugly in the rhizosphere microbiome will be presented.