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Barbizon Palace Amsterdam • The Netherlands

2nd Plant Microbiome Symposium

Abstract Details

Title: **Mining of the endophytic microbiome for novel biosynthetic genes and antifungal metabolites**

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Session: E2. Endosphere - St Olof Chapel, 21/02/2018, 11:00 - 11:30

Time: 11:00 - 11:15

Endophytic microbes have been proposed to contribute to a range of plant support functions, including nutrient acquisition and disease protection. To date, the molecular mechanisms underlying disease protection in the endosphere have only been studied for individual culturable organisms. Here, we conducted a systematic microbiome-wide perspective on the taxonomic diversity and functional potential of the endophytic microbiome of plants grown in an agricultural soil that is naturally suppressive to damping-off disease caused by the fungal root pathogen *Rhizoctonia solani*. Metagenomic analyses showed an enrichment of Burkholderiaceae, Chitinophagaceae and Xanthomonadaceae in the endosphere of plants grown in disease-suppressive soil challenged with the fungal root pathogen. Binning of the metagenomic sequences allowed de novo assembly of 25 high quality genomes of different endophytic bacterial genera. Subsequent trait-based analyses revealed numerous biosynthetic gene clusters (BGCs) overrepresented in the endophytic bacterial families of plants under fungal pathogen attack, including BGCs involved in signal transduction and antimicrobial activities, in particular nonribosomal peptides and polyketides. Network analyses further indicated that the traits enriched in the endophytic microbiome are multifactorial involving several novel BGCs encoding metabolites with yet unknown activities.