

February 19th to 21st, 2018

Barbizon Palace Amsterdam • The Netherlands

2nd Plant Microbiome Symposium

Abstract Details

Title: **Wheat breeding influences root traits and selection of bacterial communities in the rhizosphere**

Authors: Vanessa Nessner Kavamura - *Rothamsted Research, United Kingdom**; Ian Clark - *Rothamsted Research, United Kingdom*; Penny Hirsch - *Rothamsted Research, United Kingdom*; John Caulfield - *Rothamsted Research, United Kingdom*; André Lúcio Franceschini Sarria - *Rothamsted Research, United Kingdom*; Maïke Rossmann - *Embrapa Environment, Brazil*; Mike Birkett - *Rothamsted Research, United Kingdom*; Itamar Soares de Melo - *Embrapa Environment, Brazil*; Rodrigo Mendes - *Embrapa Environment, Brazil*; Tim Mauchline - *Rothamsted Research, United Kingdom*

Session: C2. Rhizosphere - St Olof Chapel, 20/02/2018, 11:00 - 12:00

Time: 11:15 - 11:30

During the Green Revolution, wheat breeding developed high-yielding plants with dwarfing genes. This selection led to structural changes in wheat, which could have consequences for the associated microbial communities, however, to date, little is known about these. The main goal of this work was to study rhizosphere bacterial communities from eight hexaploid wheat cultivars grown under field conditions ranging in chronology from Chidham White Chaff, a tall cultivar from 1790, to Crusoe, a semi dwarf cultivar from 2012. Plants were harvested, DNA from rhizosphere soil was extracted and 16S rRNA gene subjected to Illumina amplicon sequencing. Root architecture information and exudate profiles were obtained. The breeding process appears to have influenced some root traits, especially root diameter and specific root length (SRL). A PCoA plot indicates rhizosphere bacterial communities from tall cultivars are distinct from those associated with semi dwarf cultivars and in general, tall plants show lower diversity and number of observed OTUs than semi dwarf plants. Some OTUs were found to be differentially abundant in the rhizosphere of tall and semi dwarf cultivars and we hypothesize that these differences might have some relation to differential root exudation. These data help in the development of agricultural models and we believe future plant breeding programs should include the selection of specific root traits and exudates that would affect the recruitment of a beneficial root microbiome. These could have positive impacts on plant health with increases in productivity in a sustainable way.