Bonar Hall | Dundee, Scotland, UK

3rd Plant Microbiome Symposium

24th - 26th May 2022



Abstracts

Number	S3.1
Authors	Costa, Lilian S A S (1,4); Faria, Mírian R de (1); Chiaramonte, Josiane B (1); Mendes, Lucas W (2); Sepo, Edis (3); Hollander, Mattias de (4); Fernandes, José M C (5); Carrion, Victor J (3); Bettiol, Wagner (1); Raaijmakers, Jos M (3,4); Mendes, Rodrigo (1).
Affiliations	 Embrapa Environment, Jaguariúna Brazil; (2) Center for Nuclear Energy in Agriculture, University of Sao Paulo, Piracicaba, Brazil; (3) Leiden University, Leiden, The Netherlands; (4) Netherlands Institute of Ecology NIOO-KNAW, Wageningen, The Netherlands; (5) Embrapa Wheat, Passo Fundo, Brazil.
Presenting author	Mendes, Rodrigo
Email address	rodrigo.mendes@embrapa.br
Presentation type	Oral
Session Name	Biotic and abiotic stress tolerance
Title	Repeated exposure of wheat to the fungal root pathogen <i>Bipolaris sorokiniana</i> affects rhizosphere microbiome assembly and disease suppressiveness
Abstract text	Soil-borne pathogens induce plant disease suppression by enriching members and activating functions in the rhizosphere microbiome. This is observed in disease suppressive soils, which show a remarkable ability to naturally suppress plant diseases caused by pathogens. Here, we selected two wheat genotypes, contrasting for <i>Bipolaris sorokiniana</i> resistance, to study how the pathogen affects the rhizosphere microbiome. As expected, the cultivation of the susceptible wheat led to a significant reduction in disease severity after five successive cultivation cycles. Conversely, the resistant genotype showed the opposite pattern, increasing disease severity over cycles. While bacterial families <i>Chitinophagaceae</i> , <i>Anaerolineaceae</i> and <i>Nitrosomonadaceae</i> are associated with disease suppression in the susceptible wheat (fourth cycle), <i>Chitinophagaceae</i> and <i>Comamonadaceae</i> are associated with disease resistance in the resistant plant genotype (first cycle). Metagenome analysis revealed that 604 BGCs, out of 2,571 identified by AntiSMASH analysis, were overrepresented during disease suppression in the rhizosphere of the susceptible plant genotype. These BGCs are associated with biosynthesis of terpenes, non-ribosomal peptides, polyketides, aryl polyenes and post-translationally modified peptides. The understanding of the rhizosphere microbiome dynamics during disease suppression allows the identification of key microbes and functions to be used in novel strategies to control soil-borne fungal pathogens. (Support FAPESP 2020/00469-2; 2019/12330-1; 2016/13754-1)

Number	S3.2
Authors	Pfeilmeier, Sebastian; Petti, Gabriella; Bortfeld-Miller, Miriam; Daniel, Benjamin; Field, Christopher; Sunagawa, Shinichi; Vorholt, Julia
Affiliations	ETH Zurich, Zurich, Switzerland
Presenting author	Pfeilmeier, Sebastian
Email address	spfeilme@ethz.ch
Presentation type	Either
Session Name	Biotic and abiotic stress tolerance
Title	The interplay between the leaf microbiota, plant immunity and opportunistic pathogens
Abstract text	The plant microbiota affects host health and fitness. However, it is unclear how the plant shapes its leaf microbiota and what role plant immunity plays in this process.