

4th Plant Microbiome Symposium

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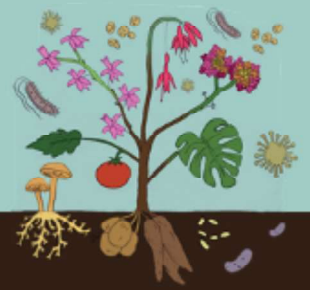
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SESSION 02 - SHORT TALK



2-C

Impact of the fungal pathogen *Fusarium oxysporum* on the taxonomic and functional diversity of the common bean root microbiome

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Plants rely on their root microbiome as the first line of defense against soil-borne fungal pathogens. The abundance and activities of beneficial root microbial taxa at the time prior to and during fungal infection are key to their protective success. If and how invading fungal root pathogens can disrupt microbiome assembly and gene expression is still largely unknown. Here, we investigated the impact of the fungal pathogen *Fusarium oxysporum* (*fox*) on the assembly of rhizosphere and endosphere microbiomes of a *fox*-susceptible and *fox*-resistant common bean cultivar. Integration of 16S-amplicon, shotgun metagenome as well as metatranscriptome sequencing with community ecology analysis showed that *fox* infections significantly changed the composition and gene expression of the root microbiome in a cultivar-dependent manner. More specifically, *fox* infection led to increased microbial diversity, network complexity, and a higher proportion of the genera *Flavobacterium*, *Bacillus*, and *Dyadobacter* in the rhizosphere of the *fox*-resistant cultivar compared to the *fox*-susceptible cultivar. In the endosphere, root infection also led to changes in community assembly, with a higher abundance of the genera *Sinorhizobium* and *Ensifer* in the *fox*-resistant cultivar. Metagenome and metatranscriptome analyses further revealed the enrichment of terpene biosynthesis genes with a potential role in pathogen suppression in the *fox*-resistant cultivar upon fungal pathogen invasion. Collectively, these results revealed a cultivar-dependent enrichment of specific bacterial genera and the activation of putative disease-suppressive functions in the rhizosphere and endosphere microbiome of common bean under siege.