

4th Plant Microbiome Symposium

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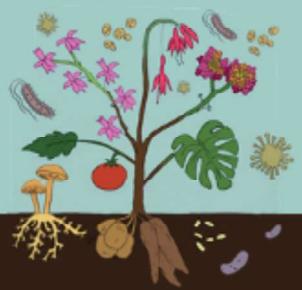


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SESSION 03 - SHORT TALK

3-C



Impact of *Bacillus subtilis* *eps* and *TasA* genes defective on rhizosphere microbiome assembly of tomato

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Bacillus subtilis holds significant agricultural and ecological importance as one of the most extensively studied plant growth promoters. To better understand *Bacillus* genetic traits associated with plant fitness, we used a mutant gene-defective model to analyze its impact on tomato development and on rhizosphere microbiome under a gradient of soil microbial diversity. We used *B. subtilis* strain UD1022 and its mutant (UD1022~~eps-TasA-~~) defective for biofilm formation. Control treatments and plants inoculated with wild or mutant *Bacillus* strains were used in the bioassay. Soil DNA isolation was followed by qPCR targeting *B. subtilis* *gyrB* gene, and 16S rRNA and ITS amplicon sequencing. Data analysis included comparisons of plant growth performance, *gyrB* quantification, and amplicon sequence variants processing using Dada2 pipeline, followed by exploratory, permutational variance, and covariance analysis. UD1022 strain significantly increased shoot and root dry masses when tomato was grown in soils with lower microbial diversity. UD1022 inoculation significantly changed soil bacterial and fungal communities' assembly in low microbial diverse soil (autoclaved soil), compared to UD1022~~eps-TasA~~ and control in the same soil. On the other hand, in high microbial diversity (natural soil) the rhizosphere microbiome is less affected by the inoculants. Bacterial network analysis showed that the UD1022 inoculation also impacted the relationship among bacteria phyla, by increasing the network's modularity and number of nodes, compared to control and UD1022~~eps-TasA-~~ treatments. For fungal network, the UD1022~~eps-TasA~~-inoculation caused higher changes on network's modularity, number of nodes and edges, compared to control and UD1022 treatments. In conclusion, knocking down genes associated with biofilm formation in *Bacillus*, impacts not only the ability of plant colonization, but also the assembly of the rhizosphere microbiome during plant development.