

Microbiome Differences in Sugarcane and Metabolically Engineered Oilcane Accessions and Their Implications For Bioenergy Production

Background/Objective

- Oilcane is a metabolically engineered sugarcane that hyperaccumulates lipids in its vegetative biomass and may serve as an advanced feedstock for biofuel production.
- The potential impact of lipid hyperaccumulation on microbiomes — and the consequences of altered microbiomes on plant growth and lipid accumulation — are so far unexplored.
- This work probes the differences in microbiome structure of multiple oilcane accessions and non-modified sugarcane.

Approach

Four oilcane accessions (17T, 1565, 1566, 1569) and a non-modified sugarcane (WT) were greenhouse-grown in replicated experiments using soil derived from a sugarcane production field near Belle Glade, FL, USA. 16S rRNA and ITS rRNA amplicon sequencing were performed to compare characteristics of the microbiome structure from different plant compartments (leaf, stem, root, rhizosphere, bulk soil).

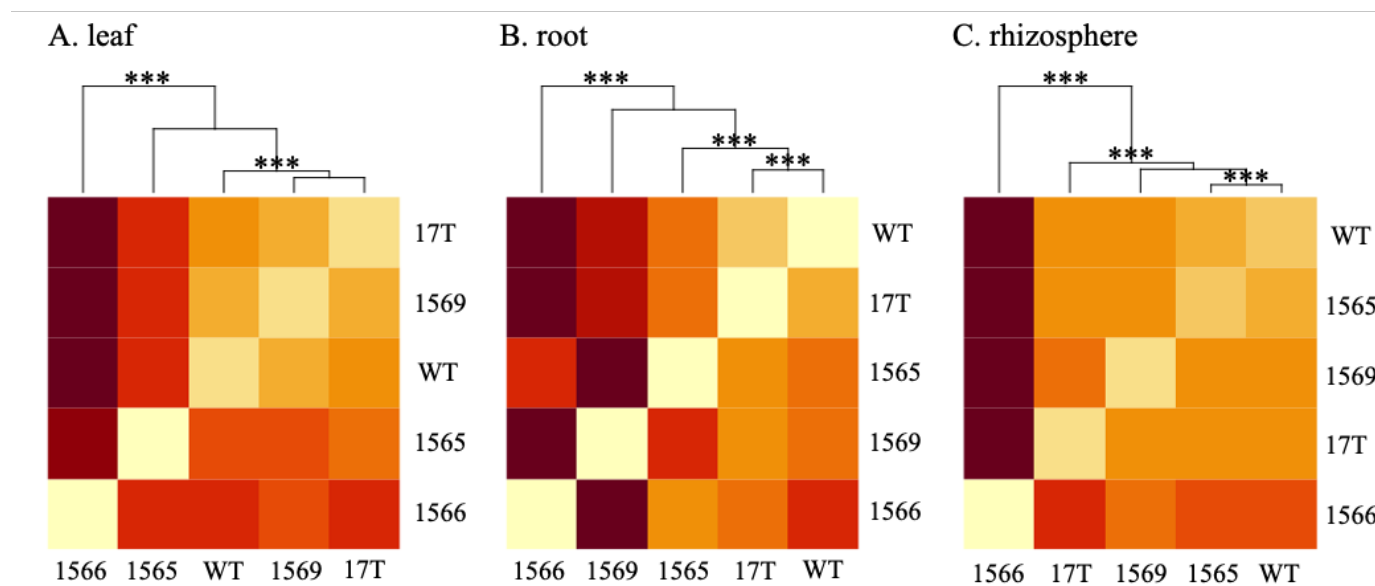
Results

All accessions were grown in similar soils but resulted in significant microbiome differences. Differences between wild type sugarcane and oilcane accessions and between oilcane accessions in the same plant compartments were also significant. These differences appear to be associated with taxa predicted to impact nutrient cycling and plant growth and development.

Significance/Impacts

This study reveals for the first time that genetically modified oilcanes are associated with distinct microbiomes and support a general bioenergy plant development strategy in which plant genotypes are selected by exploiting the advantages conferred by microbes.

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Hierarchical clustering heatmap of Bray-Curtis distance dissimilarity in the bacterial microbiomes. (A) leaf, (B) root, and (C) rhizosphere microbial community composition. The red color indicates a high dissimilarity. Symbols * denote significant differences at a p-value < 0.05.**