

Drought Stress Alters Plant-Microbe Interactions but is Contingent on Host Genetic Background

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Project Goals: The Center for Bioenergy Innovation (CBI) vision is to *accelerate domestication of bioenergy-relevant, non-model plants and microbes to enable high-impact innovations at multiple points in the bioenergy supply chain*. CBI addresses strategic barriers to the current bioeconomy in the areas of 1) high-yielding, robust feedstocks, 2) lower capital and processing costs via consolidated bioprocessing (CBP) to specialty biofuels, and 3) methods to create valuable byproducts from the lignin. CBI will identify and utilize key plant genes for growth, composition, and sustainability phenotypes as a means of achieving lower feedstock costs, focusing on poplar and switchgrass. We will convert these feedstocks to biofuels using CBP with cotreatment at high rates, titers and yield in combination with catalytic upgrading into drop-in hydrocarbon fuel blendstocks.

To avoid competition with food crops, biofeedstocks should be grown on marginal lands, such as those at risk for drought. Mitigation of drought stress on biofeedstocks therefore plays an important role in increasing the sustainability of biofuels production. Plant-microbial interactions have been shown to alleviate abiotic stress on plants, however the impact of drought stress and host genotype on plant-microbe interactions in the biofeedstock *Populus trichocarpa* remain underexplored. To understand how plant-microbe interactions in *Populus* are impacted by host genotype and drought, we grew drought-tolerant and drought-susceptible genotypes of *Populus trichocarpa* under drought and control conditions in a greenhouse. Following four weeks of growth under varied water conditions, we measured plant growth and characterized the root-associated microbial communities through 16S rRNA and ITS amplicon sequencing. Our results revealed that root biomass was significantly higher in drought-tolerant genotypes, suggesting a potential drought-stress mitigation strategy. Root-associated microbial communities were also significantly impacted by drought condition and host genotype. Bacterial/archaeal and fungal alpha diversity was significantly lower under drought conditions, and drought-tolerant *Populus* genotypes had lower fungal alpha diversity than drought-susceptible hosts. Furthermore, drought condition and host genotype significantly impacted the compositions of the bacterial/archaeal and fungal communities. Drought condition was the most important explanatory variable shaping the bacterial/archaeal community composition, while host genotype accounted for the most variation in the composition of the fungal community. These results suggest that *Populus* genotype exerts control over the selection of root-associated microbial communities and that drought stress alters these communities. The selection of specific microbial communities by *Populus trichocarpa* may confer benefits to the plant. Our results point to exciting future research avenues, such as understanding the mechanisms by which *Populus* selects for beneficial microbial communities.

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