

The *Populus* holobiont: dissecting the effects of plant niches and genotype on the microbiome



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Background

- Microorganisms are ubiquitous across all environments, yet we are just beginning to understand the role they play within ecosystems and in association with host organisms.
- Individual plant-associated microorganisms are known to aid in key functions, like water and nutrient acquisition, stress response, suppression of pathogens, and reduced herbivory across the entire plant.

Science

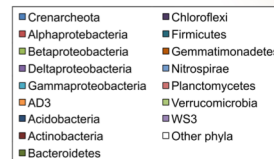
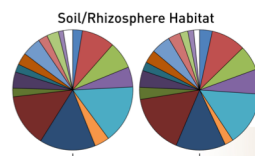
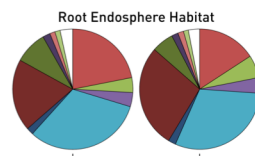
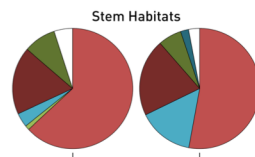
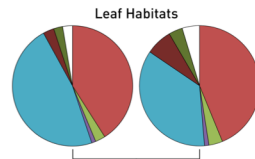
- Next generation amplicon sequencing of the 16S rRNA gene and ITS2 gene region were used to identify archaeal/bacterial and fungal communities across 30 different plant tissue types from *Populus deltoides* and *Populus trichocarpa x deltoides* hybrids grown in a common environment.
- Archaeal/bacterial and fungal microbiomes varied across broader plant habitat classes (leaves, stems, roots, soils). Contrary to archaea/bacteria, fungal microbiomes differed between genotypes more so than among fine-scale habitats within leaf niches.
- Differences in leaf fungal communities between the tree genotypes is evident in the elevated presence of two common fungal pathogens, *Marssonina brunnea* and *Septoria sp.*, on hybrid trees.

Significance

- This study provides a holistic understanding of microbiome structure within a bioenergy relevant plant host and to date is one of the most complete niche level analyses of any plant species.

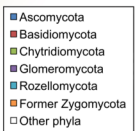
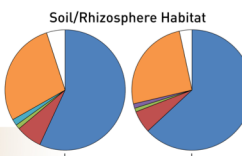
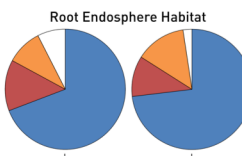
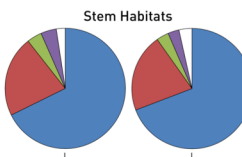
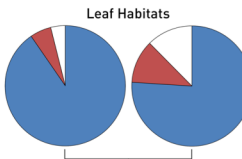
The Archaeal/Bacterial Phytobiome

P. trichocarpa x *deltoides* *P. deltoides*



The Fungal Phytobiome

P. trichocarpa x *deltoides* *P. deltoides*



Relative abundance of the dominant (>0.1%) archaeal/bacterial and fungal phyla averaged across niches within the broad tree habitats of *Populus deltoides* (DD) and *Populus trichocarpa x deltoides* (TD) hybrids.