Plant-Microbe Interfaces: Dynamics of bacterial microbiome of *Populus deltoides*

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Project Goal: Understand the genome-dependent molecular and cellular events involved in establishing and maintaining beneficial interactions between plants and microbes. *Populus* and its associated microbial community serves as an initial experimental system for understanding how these molecular events manifest themselves within the spatially, structurally, and temporally complex scales of natural systems. To achieve this goal, we will focus on 1) characterizing the natural variation in *Populus* microbial communities within complex environments, 2) elucidating *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships, and 3) performing metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

The root-rhizosphere interface of *Populus* is an ideal model to study the interaction between plants and microorganisms. In our recent paper (Gottel et al. 2011), we characterized microbial communities from root endophytic and rhizospheric habitats of *P. deltoides* in mature, natural trees. However the relative effects of drivers of community composition such as soil and environmental properties, seasonal variation, and host genotype that shape these communities remains unclear. To address these issues, we carried out 454 pyrosequencing using primers targeting V7-V9 region of 16S bacterial SSU rRNA from samples collected from the rhizosphere and endosphere of two-dozen sites distributed across watersheds in North Carolina and Tennessee over two seasons. From a total of 686,384 high-quality, denoised, non-chimeric sequences, we identified key bacterial taxa associated with the endosphere and rhizosphere. Proteobacteria consistently dominated both environments, while Actinobacteria were found across all samples and in some endosphere samples they replaced Proteobacteria as the dominant taxa. More than 24,000 unique bacterial OTUs were detected however 21,487 OTUs were exclusive to rhizosphere, while only 2,598 OTUs were found in endophyte samples. We did not observe a clear distinction in the community composition of samples collected over multiple seasons, but variations associated with location, soil properties, and plant genotypes were observed. Our data indicate that the endophyte associated bacterial community has low diversity, but is highly variable from tree to tree. While rhizosphere associated bacterial communities are highly diverse community makeup is very similar from tree to tree. This study is one of the more comprehensive analyses of bacterial communities in the endosphere and rhizosphere of *P. deltoides* to date and highlights the complexity of the bacterial diversity associated with mature trees in natural systems.

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