

## 213. Plant-Microbe Interfaces: Comparative Genomics of Populus endosphere microbiomes.

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**Project Goals:** The goal of the PMI SFA is to 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 the 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 focus on 1) characterizing host and environmental drivers for diversity and function in the Populus microbiome, 2) utilizing microbial model system studies to elucidate Populus-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the Populus-microbial interface.

Populus is a widely studied model woody plant species and a potential cellulosic feedstock for biofuels. These trees are also host to a wide variety of microbial associations within their roots and rhizosphere and thus serve as a model to study interactions between plants and microorganisms. The Populus microbiome contains perhaps a thousand different bacterial species, although most are in low abundance. Over the past several years, the PMI SFA has isolated >3000 bacterial strains from Populus roots representing >425 distinct OTUs. The genomes for >100 of these strains were sequenced in collaboration with the DOE Joint Genome Institute. Here we compare three different genera for which we have genomes for >15 strains each. These include Rhizobium strains, Pseudomonas strains, and Chryseobacterium strains. Members of these genera are commonly found in the rhizosphere and endosphere compartments of Populus roots. Comparative genomics of these endophytes are done, within the broader context of all known sequenced genomes from the same genera. We describe a set of 31 Rhizobium strains that we isolated from the endosphere and rhizosphere compartments of Populus roots. We compare 162 genomes, from 18 different names species within the Rhizobium genus, as well as a set of 45 genomes without a species designation (e.g., Rhizobium sp. CF142). For the Pseudomonas genus, we compared all publicly available Pseudomonas genomes (65 complete and 1008 draft genomes) including 21 strains sequenced as part of the PMI SFA. For the Chryseobacterium genus, we compare 18 PMI strains with 36 publically available strains. Additionally, phenotypic differences in plant root architecture during co-cultivation, phosphate solubilizing activity and carbon utilization indicate functional diversity among the isolates. For comparative genomics-based systematics, we clustered genomes based on genomic relatedness based on average amino acid identity (AAI). The local relationship of pairwise genomic relatedness combined with global relationship of genomic clusters on a whole proteome tree resolves species (e.g., Pseudomonas fuscovaginae, Pseudomonas nitroreducens) not settled by 16S rRNA gene sequence analysis. Here we will present results from “core” and “pan” genome analyses. The core genomes of genomic clusters showed very similar functional distributions, which suggests that specific genes to genomic clusters may explain the influence of microorganisms’ ecology on their functional change. Furthermore, we examined the differences of strains by pathway profiles, carbohydrate-active enzyme profiles, and other specific genes. In addition, metabolic models were generated for specific strains and experiments performed, and

their results were compared with predictions based on the genome sequences. This analysis provides insight into the genotype/phenotype relationship and identification of species-specific gene families, and in some cases, it is possible to predict unique functions/ecological niches for a given species.

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