

## 208. Plant-Microbe Interfaces: Carbon Utilization Reflects Nutritional Environment of Pseudomonas Isolates

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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.

Plant roots are a rich source of carbon in a carbon-poor soil environment and are host to a diverse microbiome. Root zones can be segregated into two distinct compartments: the endosphere, defined as the internal environment of the root, and the rhizosphere, the volume of soil directly influenced by the presence of the root. The rhizosphere is high in organic acids that are generated by active exudation from the root. Bacterial strains from the genus Pseudomonas were isolated from both the rhizosphere and endosphere compartments of Populus deltoides root samples. Analysis of shotgun whole genome sequencing results revealed that rhizosphere isolates have significantly smaller genomes ( $p < 0.05$ ) and have functions biased toward metabolic processes and chemotaxis. Metabolic reconstructions were built, utilizing KBase tools, for each genome and were used to predict substrate utilization bias that may reflect nutritional environment of isolate. Genome informed predictions were tested using substrate utilization data for growth on a panel of 190 carbon substrates (Biolog PM1 and PM2 plates). Among the carbon substrates tested, 43 were utilized by all strains, 78 showed differential utilization and 69 were not utilized by any strain. While single molecules were not predictive of isolation compartment, grouping the molecules into larger classes based on functional groups showed that endosphere isolates are biased in utilization of modified sugars and nucleosides, and rhizosphere isolates are biased towards utilization of carboxylic acids and amino acids. These compound groups reflect the environment of isolation for the strains. This work provides insight into the chemical makeup of the endosphere and rhizosphere compartments, and highlights the importance of metabolism in studies of microbiome structure and function.

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