Two poplar-associated bacterial isolates induce additive favorable responses in a constructed plant-microbiome system

Contact: Collin Timm, timmcm@ornl.gov

Dave Weston (865) 241-8323, westonda@ornl.gov

Funding Source: DOE Office of Biological and Environmental Research, Genomic Science Program and Plant Feedstock Genomics Project DE-SC001043

Background

- The Populus root microbiome is a diverse community that has a high abundance of β- and y-Proteobacteria, both classes include multiple plantgrowth promoting representatives.
- To understand the contribution of individual microbiome members in a community, we studied a simplified community consisting of Pseudomonas and Burkholderia bacterial strains and inoculated them on axenic Populus cuttings in controlled laboratory conditions.

Science

- Alone and in combination, Pseudomonas GM41 and Burkholderia BT03 increase root growth, photosynthetic potential, and activate unique pathways relative to un-inoculated controls.
- Complementary data, including photosynthetic efficiency, whole-transcriptome gene expression and GC-MS metabolite expression data, in individual and mixed inoculated treatments indicate that the molecular effects of these bacterial strains are unique and additive.

Significance

- First constructed community study to show that bacteria can have additive host effects.
- Microbiome function may be predicted from synergistic effects of individuals.





