Plant-Microbe Interfaces: Linking host genotype fitness and soil conditions to microbiome community assembly in the *Populus* root – soil interface

Veach, A.,[1] M. Cregger,[1] Z. Yang,[1] D. Yip,[1] N. Engle,[1] T. Tschaplinski,[1] J. Labbé,[1] G. Tuskan,[1] and **C. Schadt**[1*] (schadtcw@ornl.gov)

[1]Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN

http://pmi.ornl.gov

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 commercially and ecologically important trees species as well as a potential biofuel feedstock source. *Populus* species commonly occur in riparian areas throughout most of North America where they are considered a keystone species. *Populus* have become an important model host system to study plant-microbe interactions due to their amenability to laboratory and greenhouse experimental manipulation, as well as molecular biology tools enabled from genome sequencing. We conducted a trap-plant experiment using 12 *Populus* genotype clones that vary in higher-order salicylate concentration and composition (e.g., salicortin, salicin, tremuloidin, populin) to better understand how genotype, chemotype and phenotype of the host plant might influence plant and soil microbiome assembly and composition. To assess the relative importance of host genotype vs. soil conditions and origin, we planted 5 replicate cuttings per genotype (N = 120) in 2 soil types (2:1 sterile sand:soil inoculum) collected from two Oregon locations (Corvallis and Clatskanie) and allowed plants to grow for 4 months. At the end of the experiment, leaf chlorophyll content, leaf growth (number of new leaves since transplant), and net photosynthetic rate differed across genotypes and soil type ($P < 0.01$). In addition, ectomycorrhizal colonization of root tips differs between genotypes measured thus far (ranges between 0 – 17%). Host chemotypes were confirmed for roots from experimental samples via GS-MS analysis, and showed host total salicylate concentrations varying from 1221 – 10610 µg/g fresh weight (FW), tremuloidin varying from 17 – 225 µg/g FW, and populin ranging from 0 – 8.9 µg/g FW, depending on plant genotype. Microbiome data collection is ongoing and will be investigating belowground (root endosphere and rhizosphere soils) bacterial and fungal community composition effects of host chemotype, genotype and soils via Illumina MiSeq targeted amplicon sequencing, population sizes as detected by qPCR of 16S and ITS2 rRNA genes, and mycorrhizal colonization rates.