

10. Plant-Microbe Interfaces: Bacterial Community Effects on Host Plant Biomass Allocation through Experimentation and Modeling

Dave Weston^{1*} (westondj@ornl.gov), Jeremiah Henning,^{1,2} Collin Timm,¹ Nathan Cude,¹ **Gerald Tuskan**,¹ Dale Pelletier¹, and **Mitchel Doktycz**¹

¹Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN; ²Genome Science and Technology Program, University of Tennessee, Knoxville TN

<http://PMI.ornl.gov>

Project Goals: The Plant-Microbe Interfaces project's goals include understanding how bacterial strains and communities impact the growth of the host plant through direct interaction or modification of the environment. In this project we investigate the effects of specific bacterial isolates from the *Populus* endosphere on host plant traits. Our specific goal is to use genomic information and experimental observations to predict the effect of a defined microbial community on plant biomass generation and allocation.

Diverse microbial species and complex interactions make the prediction of function of a microbial community an arduous task. This is especially relevant in plant microbial communities, where hyper-diverse species pools exist in the rhizosphere: the immediate soil spaces around a plant root. Microbes in the rhizosphere can affect soil conditions by fixing atmospheric nitrogen, solubilizing inorganic phosphorous, and secreting hormones or other factors that directly influence the plant host. In turn, the plant host provides carbon sources and can harbor some of these microbes as endophytes. Deterministic factors that may influence endophytic colonization include: plant selection (avoiding innate immune response), host genotype, microbial competition, microbial niche differences, and environmental differences (pH, soil moisture, etc.) In natural ecosystems, it is exceedingly difficult to tease apart all interaction processes, which are undoubtedly occurring simultaneously. To address this complex network of interactions, we use a bottom-up approach to understand microbe-microbe, microbe-host, and microbe-environment relationships that influence collective community function. By choosing bacterial isolates with known host-effects and known interactions with complementary isolates, we reassemble simplified communities and predict community function using quantitative models.

Growth of *Populus deltoides* with single microbial strain inoculations demonstrate that microbial strains can have variable impacts on plant biomass allocation (root:shoot ratio), leaf number, root area, and stem length. But when grown with a three microbe consortia, we find a strong dominance hierarchy between microbes, which suggests niche separation or competition or plant selection. Surprisingly, the most dominant microbe in our mixes (*Burkholderia sp. BT03*, 97- 99% relative abundance), which displayed the most unique plant phenotype when grown alone with plant host (high root:shoot ratio, decrease stem length), contributed very little to plant phenotype in the mixed community. Thus, preliminary results show microbe-microbe interactions may be important in structuring endophytic communities, however community function may be driven by bacterial strains that exist at low abundances. Ongoing measurements of plant gene expression in response to microbial communities will help identify mechanisms of interaction.

Plant biomass generation is primarily limited by availability of nitrogen or phosphorous in the environment. Nitrogen and phosphorous availability can be increased by the presence of nitrogen fixing or phosphate solubilizing bacteria in the soil and/or endosphere. We are developing metabolic

models of nitrogen fixing endophytes isolated from *Populus deltoides* to examine how environmental conditions and the microbial genotype affects rate of atmospheric N₂ fixation when associated with the plant. Similarly, the amount of phosphorous solubilizing bacteria impacts the availability of phosphorous to the plant and other microbes in the system. Due to the difficulty in measuring these rates directly in root systems, we are generating quantitative models of fixation and solubilization rates in monoculture. The models are then combined using measured or predicted biomass fractions to simulate the community function in the natural environment. Ultimately, these models can be used to design microbial community structure and function to optimize plant biomass generation rate.

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