Plant-Microbe Interfaces: Extending single plant-microbe co-expression and metabolic networks to community scales

David J. Weston[1] (westondj@ornl.gov), Dale A. Pelletier[1], Abhijit A. Karve[1]*, Jennifer L. Morrell-Falvey[1], Timothy J. Tschaplinski[1], Sara S. Jawdy[1], Lee E. Gunter[1], Nancy L. Engle[1], Jessy L. Labbé[1], Tse-Yuan S. Lu[1], Chris W. Schadt[1], **Gerald A. Tuskan**[1] and **Mitchel J. Doktycz**[1]

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

http://PMI.ornl.gov

Project Goal: 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 an initial 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 will focus on 1) characterizing the natural variation in *Populus* microbial communities within complex environments, 2) elucidating *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships, and 3) performing metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

Colonization of plants by nonpathogenic *Pseudomonas fluorescens* strains can confer enhanced defense capacity against a broad spectrum of pathogens. Few studies, however, have linked defense pathway regulation to primary metabolism and physiology. In this study, physiological data, metabolites and transcript profiles are integrated to elucidate how molecular networks initiated at the root – microbe interface influence shoot metabolism and whole-plant performance. Experiments with *Arabidopsis thaliana* were performed using the newly identified *Pseudomonas fluorescens* GM30 or *P. fluorescens* Pf-5 strains. Co-expression networks indicated that Pf-5 and GM30 induced a subnetwork specific to roots enriched for genes participating in RNA regulation, protein degradation and hormonal metabolism. In contrast, only GM30 induced a subnetwork enriched for calcium signaling, sugar and nutrient signaling and auxin metabolism, suggesting strain-dependence in network architecture. In addition, one subnetwork present in shoots was enriched for genes in secondary metabolism, photosynthetic light reactions and hormone metabolism. Metabolite analysis indicated that this network initiated changes in carbohydrate and amino acid metabolism. Consistent with this, we observed strain-specific responses in tryptophan and phenylalanine abundance. Both strains reduced host plant carbon gain as estimated by net photosynthesis, yet provided a clear fitness benefit when plants were challenged with the pathogen *Pseudomonas syringae* DC3000.

The trade-off between host carbon cost under optimal conditions and fitness benefit under pathogen attack brings to question how plant-microbe interactions are perceived and initiated within natural systems harboring complex microbial communities. Does the host, for example, favor carbon partitioning to microbial associates that in turn confer a fitness advantage? Alternatively, carbon acquisition from the host may simply be driven by the ability for the microbe to evade host plant defense. To begin to address these questions, we have developed a microcosm system providing axenic conditions in a realistic soil environment that is conducive to whole plant phenotype imaging and multi-omic sample collections. We are exploiting the use of whole-genome sequences from 43 microbial isolates collected from the *Populus* microbiome

(see Pelletier poster) to create synthetic communities. Within this system, we are currently testing whether host plant genotype and nutritional state feedback to influence microbial community structure. In addition, we are testing whether the selected microbial community confers a beneficial host phenotype through community decomposition studies.

The Plant Microbe Interfaces Scientific Focus Area is sponsored by the Genomic Science Program, U.S. Department of Energy, Office of Science, Biological and Environmental Research