Plant-Microbe Interfaces: Exploring plant-microbe associations using Random Walk with Restart on multiplex networks

Piet Jones,[1,2] J. Izaak Miller[2]* (millerji@ornl.gov), David Kainer,[2] Anna Furches,[1,2] Manesh Shaw,[2] Wellington Muchero,[2] Jay Chen,[2] Doug Hyatt,[2] Mirko Pavicic,[2] Hari B. Chhetri,[2] Dan Jacobson,[1,2] and **Mitchel J. Doktycz**[1,2]

[1]University of Tennessee Bredesen Center for Interdisciplinary Research and Graduate Education, Knoxville, TN; and [2]Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN

http://pmiweb.ornl.gov/

Project Goals: The goal of the PMI SFA is to characterize and interpret the physical, molecular, and chemical interfaces between plants and microbes and determine their functional roles in biological and environmental systems. *Populus* and its associated microbial community serve as the experimental system for understanding the dynamic exchange of energy, information, and materials across this interface and its expression as functional properties at diverse spatial and temporal scales. To achieve this goal, we focus on 1) defining the bidirectional progression of molecular and cellular events involved in selecting and maintaining specific, mutualistic *Populus*-microbe interfaces, 2) defining the chemical environment and molecular signals that influence community structure and function, and 3) understanding the dynamic relationship and extrinsic stressors that shape microbiome composition and affect host performance.

'Omics data provide insights into specific aspects of an organism or population, while combining multi-omics data enables the holistic study of complex biological systems including plant-microbe symbioses. Here we use a multi-omics approach to identify genes that affect the relationship between host (*Populus trichocarpa*) and microbial taxa from the host microbiome. Samples of xylem tissue were taken from a *P. trichocarpa* GWAS population, arrayed in common gardens. First, RNA-Seq was performed on the samples. Then, reads that did not map to *P. trichocarpa* reference (V.3.0) were classified using Parakraken against all publicly available genomes. Reads that were classified as genera in the PMI culture collection and host genes that were significantly associated to these genera via a genome wide association study were selected for further investigation. We used a multi-omics approach, building eight gene-gene networks from experimental datasets and publicly available networks. Each network models a different type of biological relationship between genes or gene-products and forms a single layer in a multiplex network. We then used a Random Walk with Restart Lines of Evidence algorithm (RWR-LOE) to explore the multiplex network, starting from the set of genes of interest. In the RWR-LOE approach, we use the principle of network-topology-based-association to identify genes that fall below the initial significance threshold, but are nonetheless associated with the genes-of-interest. We then used a series of Monte Carlo simulations to identify the subset of genes from the initial genes of interest that are highly functionally related.

Oak Ridge National Laboratory is managed by UT-Battelle, LLC for the U.S. Department of Energy under contract no. DE-AC05-00OR22725. 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 under FWP ERKP730.