

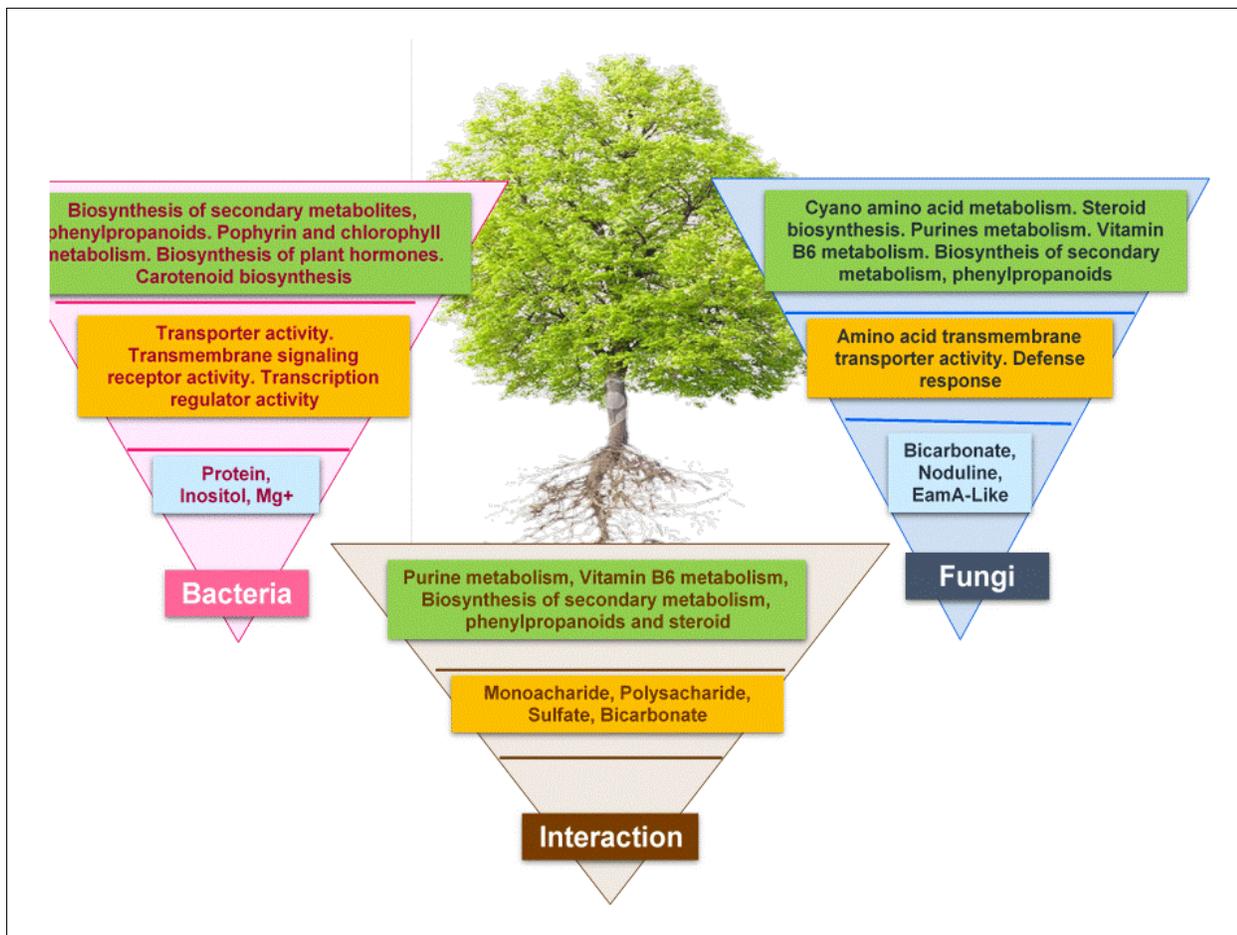
Molecular Mechanisms that Underlie the Beneficial Effects of a Plant-Fungus-Bacterial Community Interaction

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Symbiosis between soil bacteria, mycorrhizal fungi and roots of many ecologically and economically important tree species leads to coordinated resource exchange and enhanced productivity and resiliency in forest ecosystems. Although nutrient cycling and exchange of mineral nutrients are key features of this interaction, very little is known about the molecular mechanisms that underpin this process or the role of these processes in the formation of soil community structure. The Argonne “Environment Sensing and Response” Scientific Focus Area (ESR-SFA) program proposes fundamental research to elucidate the complex plant-microbial interactions between *Populus tremuloides* (Quaking aspen) and its fungal and bacterial symbionts that influence the capture, partitioning, and allocation of carbon (C) under nutrient limitation stresses. We have developed a unique tripartite system comprised of *Populus tremuloides* tree seedlings, *Laccaria bicolor* and *Paxillus involutus* ectomycorrhizal fungi, and *Pseudomonas fluorescens* mycorrhizal helper bacteria, which exhibits beneficial effects on plant biomass under nutrient limitation and is tractable to identify specific molecular mechanisms of community interaction.

A suite of experimental setups is utilized for assessment of phenotypic, biochemical, and physiological responses of plants in the context of transcriptomic, metabolomics and proteomic analyses. This integrated data set--from gene to protein to metabolite to phenotype – will support identification of the molecular mediators of acclimation to stress in a woody plant species and the metabolic networks influenced by rhizosphere communities. We have explored the molecular mechanisms underlying these interactions and have constructed models for the interaction of plants during association with the ectomycorrhizal fungi and/or mycorrhizal helper bacteria. Plant transporters related to inositol, protein and magnesium are up-regulated during bacterial colonization, which can be associated with changes in root growth and morphology and carbon-nutrient exchange at the interface. Plant transporters such as those associated with bicarbonate, auxin/amino acids and potassium are up-regulated during fungal colonization, which can be connected to root structural changes due to mycorrhizae formation and cation exchange capacity in the rhizosphere. This information will be essential to understanding the basis for occupancy of an ecological niche and to define the molecular interactions that occur in communities in changing environments.



The figure shows plants pathways, predicted transportome and secondary metabolites, which are differentially accumulated during bacterial, fungal or bacterial + fungal association. Each triangle represents plants response to bacteria (pink), ectomycorrhizal fungi (blue) and to both microbes (brown). Boxes represent the differentially expressed genes (green), transportome (yellow) and secondary metabolites (light blue). Transportome and secondary metabolites are predicted from omics data modeling as previously described (Larsen PE et al. PLoS One 2015 doi: 10.1371/journal.pone.0132837; see also associated poster).

The molecular function information derived from these studies will guide bacterial genome engineering and synthetic biology approaches aimed at modulating system response by manipulating components of transport or sensory systems. Overall, the capabilities and information derived from the experimental studies will support DOE mission applications in bioenergy, C management, climate change mitigation, and sustainability.