System-scale Modeling of Mycorrhizal Symbiosis

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Project Goals: The Argonne "Environment Sensing and Response" Scientific Focus Area (ESR-SFA) program addresses the hypothesis that cellular behavior can be modeled through an understanding of the biological interface with the environment and the cellular responses that originate from the cell/environment interaction. The overall objective of the ESR-SFA program is to identify the molecular basis of cellular transport and sensory pathways that mediate the response to environmental nutrients. This project furthers the objectives of this ESR-SFA by developing approaches that evaluate plant/fungal symbiosis by inferring molecular mechanisms from transcriptomic analysis of a laboratory *Laccaria bicolor*:aspen mycorrhizal system. Our approach generates testable biological hypotheses for the specific molecular mechanisms that drive nutrient exchange in ectomycorrhizal symbiosis. Increased understanding of how partners in plant/fungal symbiosis sense and respond to environmental parameters will identify the specific molecular metabolic and environmental response pathways for eukaryotic organisms in soil ecosystems.

The roots of many plant species have the ability to form symbiotic relationships with the community of soil fungi. In these relationships, mycorrhizal fungi provide mobilized nutrients from the soil, and plants provide photosynthetically-derived sugars. The plant:fungal symbiosis can provide growth and survival benefits, but the many details of the molecular exchanges are not completely understood. Deep RNA sequence analysis has revolutionized our access to the molecular activity of these communities, providing a system-scale perspective of symbiotic interactions at unprecedented resolution. However, no single method of transcriptomic analysis alone is sufficient to enable the inference of metabolite-space from transcriptomic-space. Identification of significantly expressed genes and mapping those genes onto known metabolic pathways generates a scaffold on which analysis of differential expression and predicted metabolic turnover can be accomplished. The results of this analysis are predictions of specific metabolic compounds and expressed protein activities that can be used to generate hypothesis-driven molecular biological experiments.

We generated a model of mycorrhizal metabolome that confirms prior biological knowledge and provides insight into the nutrient exchange process associated with mycorrhizal interaction. When *L. bicolor*:aspen mycorrhizae are cultured on media with inorganic nitrogen sources, *L. bicolor* is predicted to take up inorganic nitrogen from the media and synthesize complex nitrogenous compounds for its symbiotic plant partner. These predictions indicate *L. bicolor* is

an active metabolic partner in mycorrhizal interactions in addition to passively extending the absorptive surface of aspen roots. Proposed transcriptomic experiments, examining mycorrhizal systems in the context of different nutrient environments, will uncover additional mechanisms of mycorrhizal metabolic interactions. Application of further transcriptomic analysis methods such as identifying gene splice variants expressed during different stages of mycorrhizal interaction, have the ability to provide even greater richness to the transcriptomic-generated models of the mycorrhizal metabalome. The approach applied to this ectomycorrhizal system can be generalized to other interacting systems in the rhizosphere.

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