Nutrient Cycling for Biomass: Interactive proteomic/transcriptomic networks for global carbon management processes within poplar-mycorrhizal interactions

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Project Goals: This project will facilitate the development of system-scale models of the symbiotic interaction between ectomycorrhizal fungi (such as *Laccaria bicolor*) and tree species (such as poplar) in response to environmental nutrient availability/biochemistry. The experimental plan will integrate multiple "omics" approaches to model ectomycorrhizal regulatory networks and metabolic pathways that are predictive of atmospheric carbon sequestration in the form of plant and/or subsurface fungal biomass. The project will test the hypothesis that essential regulatory and metabolic mechanisms can be inferred from transcriptomic and proteomic changes that occur at the mycorrhizal interface in response to environmental nutrient availability. Guided by abundant genome sequence and ongoing transcriptomic input, this hypothesis will be addressed using modern protein analytic approaches to fill the gap in our understanding of how mycorrhizal metabolic and regulatory processes at the transcript-level translate to nutrient uptake, carbon management and ultimate net primary productivity of plants in the environment. Specifically, we make use of targeted as well as discovery-based proteomics, biochemical assays and ChIP-seq characterization of carbon, nitrogen and phosphorous regulators to identify symbiosis-specific molecular mechanisms that control plant carbon management and allocation. These molecular mechanisms regulate nutrient cycling, accumulation of plant and fungal biomass, and ultimately are important to forest management and atmospheric carbon sequestration.