

Mapping the Metabolism of Nutrient and Carbon Exchange in the Plant-Microbe Symbiosis

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Abstract: This research will identify the molecular responses that enable circumvention of phosphorus (P) starvation response in symbiotic plant-microbe communities. Using JGI/EMSL capabilities to assess multiomic responses of plant root-microbe communities to P limitation, we will be able to develop and refine predictive models that link microbial community structure with carbon (C) capture and plant response to environmental stress. We will focus on P limitation because it is a major factor affecting C capture by plants and limiting biofuels feedstock productivity on nonagricultural soils. Plant-microbe symbioses play critical roles in enhancing the acquisition of P from soils for plant hosts, yet much of the research on plant C and nutrient capture and associated modeling efforts relies on studies lacking symbionts. Mycorrhizal fungi form mutually beneficial associations with over 90% of plant families, bacteria are ubiquitous in the rhizospheres of all plants, and both groups of microbes often affect host plant metabolism to increase nutrient acquisition and environmental stress resistance. These benefits have profound effects on ecosystem productivity, C sequestration by forests, and biofuels feedstock production.

Through this proposal, we will utilize aspen (*Populus tremuloides*) in symbiosis with ectomycorrhizal (ECM) fungi and plant growth promoting bacteria (PGPB) to pursue the following Specific Aims: (1) Assess ECM fungal and PGPB influence on the P starvation response in aspen; and (2) Integrate molecular information into systems models consistent with enhanced biomass production and P use efficiency in symbiotic aspen. By focusing on transcript, protein, and metabolite levels related to Pi uptake, C processing and exchange, and general stress responses in aspen roots and the microbial symbionts under P limitation, we will provide novel information regarding the tripartite associations in modulating transport processes, metabolic responses, and regulatory networks within plant root systems. Unique to this proposal is the development of engineered rhizosphere communities incorporating the ECM fungi *Laccaria bicolor* and *Paxillus involutus* and the PGPB *Pseudomonas fluorescens* and its focus membrane transport systems and processes involved in resource exchange in plant-microbe symbioses.

Specific institutional capabilities requested for the project include: (1) Transcriptomic profiling of plant-rhizospheric symbioses through JGI using libraries representing plant-microbe communities prepared at Argonne National Lab using ribo-depletion methods. (2) The development and application of proteomic methods with EMSL scientists to generate protein profiles that reflect plant-microbe symbioses with a focus on identification of integral membrane transporters. These protein profiles will be used to identify symbiosis-mediated translational patterns, refine the models generated using transcriptome data, and reconcile protein and expression patterns. (3) The utilization of next-generation metabolomic capabilities at EMSL to catalog metabolite profiles in aspen roots under P limitation and help to delineate strategies used by rhizospheric symbionts to acclimate the host plant and maintain C acquisition and processing under nutrient limitation.

The combined transcriptomic, proteomic, and metabolomic approaches, aligned with phenomic measures and integrated into predictive models, will inform strategies and approaches to enhance biofuel feedstock production and C sequestration on marginal soils, reducing the food-for-fuel trade-off currently plaguing these efforts.