Beneficial Partners: Mycorrhizal Resource Exchange in Bioenergy Cropping Systems

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Project Goals: The LLNL Bioenergy SFA seeks to support sustainable and predictable bioenergy crop production through a community systems biology understanding of microbial consortia that are closely associated with bioenergy-relevant crops. We focus on host-microbial interactions in algal ponds and perennial grasses, with the goal of understanding and predicting the system-scale consequences of these interactions for biomass productivity and robustness, the balance of resources, and the functionality of surrounding microbial communities. Our approach integrates 'omics measurements with quantitative isotope tracing, characterization of metabolites and biophysical factors, genome-enabled metabolic modeling, and trait-based representations of complex multi-trophic biological communities, to characterize the microscale impacts of single cells on system scale processes.

Mutualistic associations between plants and mycorrhizal fungi can enhance plant productivity, plant resilience to stress, and carbon (C) allocation belowground. A better understanding of plant-mycorrhizal relationships can inform more sustainable and productive management of cellulosic bioenergy crops, such as switchgrass (*Panicum virgatum* L.), a C4 perennial grass championed for its high biomass yields and tolerance to a broad spectrum of climatic conditions and soils otherwise unsuitable for agricultural production. We are investigating context-dependent resource exchange between *Panicum hallii*—a plant model species closely related to switchgrass—and two mycorrhizal fungi: the arbuscular mycorrhizal fungus (AMF) *Rhizophagus irregularis* and the ericoid mycorrhizal fungus *Serendipita bescii*. Both fungal species have been found growing in association with a wide range of plant species, including switchgrass and several other bioenergy crops. Due to differences in their genomic repertoires, we hypothesize that each fungal species confers plant benefits and ecosystem services through unique mechanisms.

We grew *P. hallii* with and without *R. irregularis* and *S. bescii* in microcosms containing 'live' marginal soil harvested from a pasture in Oklahoma. We imposed water limitation in half of the microcosms in order to assess plant and mycorrhizal response to drought. Additionally, half of the microcosms were grown in a $^{12}CO_2$ atmosphere and half in a $^{13}CO_2$ atmosphere. The microcosms were harvested destructively at three timepoints over the course of a growing season. Coupled with stable isotope probing (SIP), this design allows us to track plant- and mycorrhizal-derived ^{13}C into other microbial taxa, soil C pools, and C fluxes (CO_2, volatiles, dissolved C). Since each microcosm included root and hyphal exclusion chambers, we expect to be able to examine key biogeochemical fluxes, nutrient exchange, multipartite interactions, microbial community assembly, metabolite production, and gene expression in spatially distinct ecological niches. Our current results indicate that plant performance was slightly enhanced in the presence of mycorrhizal fungi under both drought and water-replete conditions. Isotopic analyses and NanoSIMS imaging suggest that a substantial quantity of the C that plants allocate to their mycorrhizal partners is further assimilated by other microorganisms. Although much of this C is retained below ground, some returns to the atmosphere as CO_2 and volatile organic compounds. These results shed light upon the complex and dynamic nature of plant-microbe-soil interactions and can be used to evaluate the potential role of mycorrhizal partnerships in bioenergy crop production.

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