

## **Crosstalk: Interkingdom interactions in the mycorrhizal hyphosphere and ramifications for soil C cycling**

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**Project Goals: Arbuscular mycorrhizal fungi (AMF) are ancient symbionts that form root associations with most plants. AMF play an important role in global nutrient and carbon cycles, and understanding their biology is crucial to predict how carbon is stored and released from soil. This Early Career research investigates the basic mechanisms that underpin synergistic interactions between AMF and microbes that drive nitrogen and carbon cycling, addressing DOE's mission to understand and predict the roles of microbes in Earth's nutrient cycles. By coupling isotope-enabled technologies with next generation DNA sequencing techniques, our project investigates soil microbial interactions *in situ* using natural levels of soil complexity. This work will provide a greater mechanistic understanding needed to determine how mycorrhizal fungi influence organic matter decomposition and will shed light on large-scale nutrient cycling processes in terrestrial ecosystems.**

The arbuscular mycorrhizal association between the Glomeromycota fungi and land plants is ancient and widespread; approximately 80% of all land plants form symbiotic associations with AMF. Recent work has shown that mycorrhizal fungal type is one of the key predictors of soil C storage in terrestrial ecosystems. However, studies have come to opposing conclusions about the direction and magnitude of soil C accumulation in relation to mycorrhizal colonization. A greater mechanistic understanding is needed to determine how mycorrhizal fungi alter decomposition to help predict large scale C cycling processes in terrestrial ecosystems.

While AMF are obligate symbionts that depend on their host plant for C and cannot decompose soil organic matter (SOM), AMF can stimulate the decomposition of SOM and dead plant material. Our prior research strongly suggests that AMF partner with their microbiome in the zone surrounding hyphae, or hyphosphere, to encourage decomposition. The molecular mechanisms underpinning synergistic interactions between AMF and the microbial community during N uptake from SOM is a key knowledge gap limiting our ability to model these interactions. To determine how AMF harness hyphosphere microbial communities to stimulate decomposition, we are first using <sup>13</sup>C-Stable Isotope Probing (SIP) to identify the genomes of organisms in the fungal hyphosphere. We have sequenced <sup>13</sup>C-SIP hyphosphere metagenomes collected from a <sup>13</sup>CO<sub>2</sub> labeling experiment using living soil. Additionally, we are developing sterile plant-mycorrhizal microcosms ("MycChips," based off the EcoFAB platform) that we can use to interrogate hyphal-microbial interactions *in-situ*. For notoriously heterogeneous environments such as soil, it is critical to develop and apply systems biology tools with the ability to interrogate soil microbial communities at their natural levels of complexity. Using this framework, our work aims to deconstruct complex interkingdom interactions in living soil.

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