Linking Microbial Identity and Succession Patterns To Uptake Of Plant Derived Carbon In The Rhizosphere

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Project Goals: Our project (*Plant Stimulation of Soil Microbial Community Succession: How Sequential Expression Mediates Soil Carbon Stabilization and Turnover*) focuses on a fundamental understanding of C cycling in soil as mediated by soil microorganisms and their interactions with plants. Our work investigates how the interactions between roots and soil microorganisms affect transformations of root derived C, decomposition and loss as CO_2, as well as C sorption and stabilization in soil at ambient and elevated levels of atmospheric CO_2. Through our research we seek to provide a mechanistic understanding of the conversion of root C to stabilized soil C, clarify the impacts of increased concentration of CO_2 on soil C sequestration, and substantially expand our understanding of molecular regulation of terrestrial C cycling.

Soil organic C is the largest pool within the terrestrial C cycle and fluxes within this pool are regulated by complex interactions between edaphic factors, plants, soil microorganisms and minerals. Plant roots and their exudates exert control over the microorganisms mediating decomposition of complex C compounds. Over time, living roots become root debris and undergo decomposition by soil microorganisms, ultimately entering stabilized pools. Therefore, the change over time of the composition and function of the C degrading and transforming microbial communities associated with living and decomposing roots defines a central biological component of soil C stabilization.

In this research we are assessing structure and successional patterns within the microbial community mediating carbon transformations in the rhizosphere of *Avena barbata* (slender wild oat), by assessing community transcription and substrate (i.e., root exudates or root litter) use profiles along actively-growing roots (i.e., root tip to fully mature root) and through time as roots grow and eventually decompose. Initial results suggest that the rhizosphere microbial community differs along a root age gradient and we hypothesize that these differences will be reflected in resource use measured by stable isotope probing (SIP). We have constructed a suite of stable isotope labeling growth chambers and microcosms, which we are using to pulse label *A. barbata* plants and monitor the fate of added $^{13}CO_2$ as it moves into the soil C pool both as root exudates and decomposing root litter. We are specifically interested in the differential response of rhizosphere communities exposed to either independent or simultaneous additions of ^{13}C-live roots and ^{13}C root litter.

High throughput next generation sequencing is being used to measure rhizosphere microbial community diversity (16S rRNA) as well as being combined with community separation based upon uptake of added ^{13}C labels (SIP). 16S rRNA survey also forms the basis for development of probe sets for phylogentic microarray chips to be used for stable isotope probing via Chip-SIP, a new method that combines community identification with high density RNA microarrays and substrate use profiling by NanoSIMS isotopic analysis of the array spots. We are also trialing existing probes and using the acquired 16S rRNA data to develop probes for fluorescent in-situ hybridization (FISH) to spatially examine the rhizosphere microbial community. The FISH method will be combined with NanoSIMS isotopic analysis to simultaneously observe the fate of added ^{13}C label in intact soil/root samples.

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