Microbial Mediation of Litter Decomposition in Soil: The Role of Plant Roots

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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 component of the terrestrial C cycle, with fluxes through the C pool mediated by soil microorganisms and modulated by their interactions with plant roots and root exudates. We characterized the metabolic profiles of *Avena barbata* root exudates collected in sterile hydroponic systems using gas chromatography-mass spectrometry (GC-MS). A variety of compounds were detected in exudate samples, including carbohydrates (e.g. glucose, fructose, galactose), low molecular weight organic acids (e.g. oxalic, malic, maleic acids), amino acids and amides (e.g. lysine, serine, glycine), fatty acids (e.g. arachidic, lauric, oleic acids), sterols (e.g. cholesterol) and others (e.g. hydroxylamine, glycerol). We are using this library of identified exudate compounds to inform spatially explicit analysis of *A. barbata* root exudates patterns in soil. To do so, *A.barbata* seedlings grown in microcosms were pulse labeled with $^{13}CO_2$ and the exudates were sorbed to an initiator-treated silicon wafer. Organic compounds on the wafer were then analyzed by nanostructure-initiator mass spectrometry (NIMS). Using the hydroponically-generated library, we are currently identifying compounds detected using the NIMS approach.

A concurrent effort examines the effect of live *A. barbata* on the mineralization of ^{13}C-labeled root litter in soil over two growing seasons. The mineralization rates of labeled root litter in the presence of *A. barbata* were determined and compared with those in a no-plant treatment by measuring total CO_2 and $^{13}CO_2$ fluxes. $^{13}CO_2$ flux in the no-plant treatment was significantly higher than in the presence of live *A.barbata* in the early litter decomposition stage, suggesting

an initial negative priming effect of live roots on litter mineralization. However, the trend changed after 40 days; after 70 days, the $^{13}CO_2$ flux rates from decomposing root litter became higher in the presence of live *A.barbata* plants, suggesting a positive priming effect.

The metabolic data and mineralization rates measured in the presence and absence of live plant roots will guide future investigations of the microbial metabolic pathways responsible for rhizosphere C processing. This work will be extended to distinguish the C-cycling transcriptome of rhizosphere microbial communities utilizing ^{13}C-labeled exudates to provide a mechanistic basis for understanding organic matter priming in the rhizosphere.

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