How Drought Modulates Formation and Persistence of Microbial-Derived Soil Carbon from Rhizosphere, Detritusphere, and Bulk Soil Microbial Communities

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Project Goals: Microorganisms play key roles in soil carbon turnover and stabilization of persistent organic matter via their metabolic activities, cellular biochemistry, and extracellular products. Microbial residues are dominant ingredients in soil organic matter (SOM), a pool critical to Earth's soil health and climate. We hypothesize that microbial cellular-chemistry, functional potential, and ecophysiology fundamentally shape soil carbon persistence, and we are characterizing this via stable isotope probing (SIP) of genome-resolved metagenomes and viromes. We focus on soil moisture as a 'master controller' of microbial activity and mortality, since altered precipitation regimes are predicted across the temperate U.S. *Our SFA's ultimate goal is to determine how microbial soil ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.*

Microbial residues are dominant ingredients of persistent soil organic matter (SOM). Via the 'microbial carbon pump,' plant carbon is processed by the microbial community *en route* to microbial-derived, mineral-associated pools of SOM—which are critically important to the Earth's carbon balance and soil health. Yet major uncertainty surrounds the microbial ecophysiological traits that regulate the microbial carbon pump, and how the relative importance of these traits varies in regions of the soil with distinct microbial communities (i.e. the rhizosphere, detritusphere, and bulk soil) and under different moisture conditions. Our SFA team is using stable-isotope labeling techniques to synthesize microbial ecology (via metagenome sequencing) with measurements of SOM formation and persistence under varying moisture regimes.

We conducted a 12-week ^{13}C tracer study to track the movement of two dominant sources of plant carbon – rhizodeposition and root detritus – into soil microbial communities and carbon pools under normal moisture vs drought conditions. Using a continuous $^{13}CO_2$-labeling system, we grew the Mediterranean annual grass *Avena barbata* in controlled growth chambers and measured the formation of organic matter from ^{13}C-enriched rhizodeposition. As the plants grew, we harvested rhizosphere and bulk soil at three time points (4, 8, and 12 weeks) to capture changes in soil carbon pools and microbial community dynamics. In a second set of microcosms, we tracked the formation of soil carbon derived from ^{13}C-enriched *A. barbata* root detritus during 12 weeks of decomposition; harvesting detritusphere and bulk soil at 4, 8, and 12 weeks. In a third set of microcosms, we studied the combined influence of rhizodeposition and root detritus, seperately tracking the contributions from each root C source using a reciprocal ^{13}C-labeling design.

Here, we present initial data from the greenhouse experiment and outline our broad experimental goals. In all microcosms, our soil moisture manipulations generated significant differences in drought (8 ± 2%) and 'normal moisture' (15 ± 4.2 %) treatments. The magnitude of this difference increased through time, and manifested as differences in soil respiration, as well as in aboveground plant biomass, plant height, root architecture. We have also extracted DNA from rhizosphere, detritusphere, rhizosphere + detritusphere, and bulk soil communities, and are measuring a range of microbial traits on these same communities, including carbon use efficiency, growth rate, and the production of extrapolymeric substances. The overarching aims of this project will be to determine how microbial community composition and microbial community assembly through time are influenced by soil moisture status, and to connect these community-level differences with the dominant microbial traits that may affect the formation, chemical composition, and long-term persistence of microbial-derived, mineral-associated SOM.

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