Controls on the Composition of Microbial Derived Necromass in Soil

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Project Goals: The overall goal of this project is to test if plant-microbe interactions are limited to influencing the rate of C accrual, while mineralogy regulates the sink capacity of biofuel cropping systems. To accomplish this goal, we are (1) characterizing microbial necromass, (2) identifying the microbial pathways that contribute to necromass accumulation under controlled conditions, (3) characterizing microbial necromass accumulation in soil incubation experiments and (4) comparing long-term, cross-site microbial responses to cropping system inputs and edaphic factors.

Abstract text. Crop selection and soil texture influence the physicochemical attributes of the soil, which structure microbial communities and influence soil organic matter formation, cycling and long-term storage. At the molecular scale, microbial metabolites and necromass alter the soil environment, which creates feedbacks that influence ecosystem functions, including soil organic matter accumulation. Yet the generalizable mechanisms regulating the accrual and long-term stabilization of soil organic matter are still unclear. Using a long-term soil incubation and ^{13}C-labeling, we are testing the hypotheses that (1) microbial derived necromass is a significant component of soil organic matter and (2) soil texture and mineralogy significantly influence microbial derived organic matter composition and accumulation. By integrating lab to field studies, we aim to identify the molecules, organisms and metabolic pathways that control the formation of compounds that contribute to long-term organic matter stabilization in bioenergy soils.

As plant-derived inputs undergo microbial decomposition, some of the resulting organic residues are incorporated into microbial biomass, and a significant proportion of soil organic matter is attributed to the resulting microbial derived residues, or necromass. This includes biomass residues (lipids, proteins, amino sugars) and microbial exudates (enzymes, exopolysaccharides, lipids, glycoproteins). Yet little empirical evidence is available to support this conceptual model and inform management decisions that aim to amplify biological processes that enhance soil organic matter formation and persistence. To address this knowledge gap, we are conducting a long-term lab incubation and characterizing microbial residues using mirco-IRMS, GC-MS and ssNMR. Soil samples were collected from switchgrass (*Panicum virgatum*) plots from the DOE the Great Lakes Bioenergy Research Center (GLBRC) Intensive Biofuel Cropping System Experiments, including sandy loams of the Kellogg Biological Station (KBS) in MI, and silty loams from the Arlington Agricultural Research Station (AARS) in WI. These soils were amended with ^{13}C-labeled glucose, which was rapidly incorporated into microbial biomass. The sandy soils had a microbial community that was more active over the course of the two-month incubation, where 18.9 % of the added carbon (C) was respired in the first 24 hours for sandy

soils (MI) and 17.2% for silty (WI) soils. By tracking the remaining ^{13}C over time, we are determining the persistence and form of microbial derived molecules. To demonstrate the transformation of microbial necromass into soil organic pools, we waited for the initial ^{13}C labeled microbial community to turnover (2 months lab incubation) before sampling. We measured C pools and ^{13}C incorporation into microbially derived metabolite, protein and lipid pools as well as residuals that were unextractable and strongly associated with the soil. Despite respiring roughly 20% of the added glucose as CO_2 in the first 24 hours, approximately half of the added ^{13}C remained in the soil after 2 months. After extraction ~1/3 of the total soil C remained in the soil and contained ~20% of the soil ^{13}C. Although the metabolite, lipid and protein pools contained <0.2% of the samples on a mass basis, they contained 20-25% of the remaining label. Relative to proteins and lipids, the metabolites were the most highly enriched (>5000δ‰ $\delta^{13}C$), despite containing the lowest C concentration. Together these data reveal how C assimilated by microbes is transformed into pools of soil organic C. By using a cross-site approach this study demonstrates the influence of soil texture on the persistence of necromass pools. Incubations are on-going, and the final harvest will occur after the turnover of multiple generations of the soil microbiome to reveal the form and fate of microbial necromass in soil.

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