Title: High Resolution DNA Stable Isotope Probing of Soil Indicates Changes in Microbial Community Metabolism Associated in Disturbance Due to Tillage

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Project Goals: Short statement of goals. (Limit to 1000 characters)

Project Goals: This research program will reveal fundamental aspects of soil C-cycling and provide ecological and metabolic insights on diverse non-cultivated soil microorganisms that play major roles in the global C-cycle. Specific goals include: 1) Map the C assimilation dynamics for thousands of non-cultivated microorganisms in soil by harnessing a full cycle microbial food web mapping approach that employs an array of ^{13}C-labeled molecules; 2) Map the C assimilation dynamics of soil microorganisms across soil systems as a function of soil characteristics; and 3) Evaluate ecological and seasonal patterns of activity and abundance for discrete microbial taxa across gradients of soil characteristics and as a function of their C-assimilation dynamics. These goals will be achieved by employing a newly developed microbial food web mapping approach, enabled by advances in ^{13}C-stable isotope probing of nucleic acids and next generation sequencing.

Bacteria are essential to the cycling and storage of carbon in the soil ecosystem. Tillage decreases soil organic matter content and changes the composition of soil microbial communities. Differences in microbial ecology between no-till vs tilled soils may contribute to differences in organic matter loss pathways, however mechanistic linkages between microbial community structure and function remain unclear in soils.

We employed high resolution DNA stable isotope probing (HR-SIP) to evaluate the temporal dynamics of microbial metabolism associated with the degradation of dissolved (^{13}C-xylose) and particulate (^{13}C-cellulose) forms of carbon in soils from a long-term tillage experiment. In addition, we used high throughput sequencing of 16S rRNA gene amplicons to assess seasonal variation in taxon relative abundance in relation to tillage history and pattern of isotope incorporation in HR-SIP experiments. Bacterial communities vary significantly with tillage as expected (PERMANOVA, $R2 = 0.14$, $p = 0.001$). No-till soils also had significantly higher rates of soil respiration and ^{13}C-xylose mineralization, but not ^{13}C-cellulose mineralization relative to tilled soil. The bacteria that incorporated ^{13}C xylose initially (days 1 and 3) differed in tilled vs. no-till soils, though similar taxa were ultimately enriched in both soil types over time. In contrast, the bacteria that incorporated ^{13}C cellulose remained similar between tilled and no-till soils throughout the experiment. The taxa participating in carbon transformations differed as a function of soil management history, with implications for carbon fate. These results suggest that changes in the structure of the microbial community, caused by tillage, affects xylose degradation dynamics but not cellulose degradation dynamics.

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