Microbial contributions to carbon cycling differ qualitatively and quantitatively in agricultural, forest and meadow soils

Samuel E. Barnett,[1]* (seb369@cornell.edu), Nicholas D. Youngblut,[1] and **Daniel H. Buckley**[1]

[1]School of Integrative Plant Science, Cornell University, Ithaca, NY

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.

Soil is one of the largest terrestrial carbon stocks on Earth containing thousands of peta grams of soil organic matter (SOM). Microbes are primarily agents of SOM flux, contributing significantly to the global carbon cycle. Microbial community composition significantly varies between soil habitats, but it remains unclear to what degree these differences affect the quality and rate of C-cycling. To explore this question, we conducted a high-resolution DNA-stable isotope probing experiment in which we applied five model SOM substrates (xylose, amino acids, vanillin, cellulose, and palmitic acid) to soils from forest, meadow and agricultural lands. The sites were spatially contiguous and edaphically similar, differing primarily by historical land management practices. Over a period of 30 days we measured substrate specific respiration (as $^{13}CO_2$) and identified bacterial operational taxonomic units (OTUs) that metabolized each substrate as a function of ^{13}C assimilation into DNA.

We found that mineralization rates differed among substrates and habitats. Soluble substrates such as xylose and amino acids were mineralized rapidly while insoluble substrates such as cellulose and palmitic acid were mineralized slowly in all habitats. Vanillin showed the most variability in mineralization rate across habitat type with the highest rate observed in the agricultural soil and the lowest in the meadow. Community composition differed significantly among habitats and changed over time in response to substrate addition. Temporal variability was greatest in the agricultural soil. The identities of bacteria that assimilated ^{13}C differed by habitat and substrate type. Out of 779 responder OTUs most were habitat specific (78.6%), while a smaller set (7.5%) responded in all three habitats. Responder taxa differed at higher phylogenetic ranks among habitats. For example, at peak respiration, *Planctomycetes* were prominent assimilators of palmitic acid in forest soil, yet no *Planctomycetes* were responders in agricultural or meadow soils. Determining the ecological basis for differences among active microbial groups and habitats will improve understanding of SOM turnover and carbon fate in soil.

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