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# The “Who” and “How” of Microbial Control over Soil Carbon Dynamics: a Multi-omics, Stable Isotope Probing, and Modeling Approach

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## Abstract

Soils are the largest repository of organic carbon (C) in the terrestrial biosphere and represent an important source of $CO_2$ to the atmosphere, releasing 60-75 Pg C annually through microbial decomposition of organic materials. Microbes are key drivers of C cycling, and exhibit a large range in C use efficiency (CUE). CUE is the substrate C incorporated into biomass per substrate assimilated. While small changes in CUE can have profound effects on soil $CO_2$ flux, our understanding of the intersection of genomic and abiotic factors driving soil CUE dynamics is still very limited.

Our long-term goal is to better predict the fate of soil C by developing mathematical and ecosystem models of SOM decomposition that incorporate a genetic and physiological understanding of CUE. The goal of this work was to define genes, metabolic pathways, and phylogenetic signals associated with microbial CUE for terrestrial microorganisms (bacteria and fungi). Our specific objectives are to: (1) Define genomic markers that indicate how terrestrial bacteria and fungi change CUE in response to environmental drivers of microbial activity; (2) Determine how well genomic markers identified predict CUE in soils; and (3) Improve predictions of soil C by incorporating genomics-informed CUE into ecosystem C models based on genomic features defined in and validated for soil in the course of this work.

We address these objectives by coupling multi-omics analyses (genomics, metatranscriptomics) with physiological assays (CUE, enzyme activities) across environmental drivers (substrate quantity/quality, temperature, moisture). We employ a hierarchical approach to incrementally scale from cells to ecosystems, starting with pure cultures of bacteria and fungi, then mock communities in artificial, organic matter-free soil, then finally field soil manipulated to elicit microbial communities differing in community composition and CUE. By focusing on microbial isolates and communities in a temperate forest (Harvard Forest), we leverage a rich context for validating data based on multiple ongoing field, lab and modeling studies of soil C cycling.

This research couples two culture collections of fungi and bacteria isolated from the Harvard Forest, along with over a decade of field measurements of CUE and C cycling, and microbial community analyses using metagenomics and metatranscriptomics. Because microbial feedbacks to the environment are regulated at the organismic level, the foundation of this research is the physiology and genomics of CUE among isolates that we have determined to be either dominant in our soil system, sensitive to climate change factors, or both. A series of three

experiments using artificial soil, lab incubation of field-collected soil, and a field manipulation is designed to validate potential omics-informed, novel genomic markers to be used as proxies for CUE in models. We test our new understanding of the genetic basis for CUE and its implications for soil C dynamics using the trait-based model DEMENT and the ecosystem models MIIMICS and SCAMPS. All models are modified to simulate SOM decomposition in mineral soils and validated with other temperate forest climate change manipulation studies. By developing mathematical and ecosystem models of SOM decomposition that incorporate a genetic and physiological understanding of CUE, we hope to facilitate more realistic models of SOM decomposition for C cycling in soils.

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