Incorporation Of “Omics” Information into a Soil Biogeochemical Model: A Novel Model Scheme to Regulate Microbial Functions and Soil Carbon Dynamics in Response to Environmental Change

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BER Program: TES
Project: Early Career Research Program (Melanie Mayes)

Both observations and modeling studies show large uncertainties in feedback between soil carbon and climate change. This uncertainty mainly stems from our limited understanding of the soil microbial community, in terms of its diverse structure, function, and capacity to adapt to environmental change. The advent of “omics” technology is revolutionizing our ability to understand the microbial community. Metagenomics analysis of soil samples from both phosphorus (P)-deficient and P-fertilized sites in Panama demonstrated that community-level enzyme functions can adapt to maximize the acquisition of P and minimize energy demand for foraging. This optimization of foraging can mitigate the imbalance of the C/P ratio between soil substrates and the microbial community, thereby relieving nutrient limitations on microbial CO\textsubscript{2} emissions. Incorporation of microbial dynamics into biogeochemical models remains challenging due to the difficulty in quantitatively parameterizing omics-based information. This study introduces the concept of the soil “enzyme function group” to parameterize omics-informed functions of the microbial community in the Continuum Microbial Enzyme Decomposition model (CoMEND).

In the CoMEND model, the chemical composition of soil organic matter (SOM) pools was based on data generated using Fourier transform ion cyclotron resonance mass spectrometry (i.e. C-rich SOM, N-rich SOM and P-rich SOM) and the degree of depolymerization. The enzyme functional groups that catalyze the SOM pools are quantified by the relative composition of gene copy numbers. The responses of microbial activities and SOM decomposition to nutrient and water availability are simulated by optimizing the allocation of enzyme functional groups to maximize P acquisition and minimize energy demand. The model is able to reproduce lab- and field-scale observations, including higher microbial biomass in field samples of P-fertilized soils, higher CO\textsubscript{2} production in lab-scale incubation experiments using P-fertilized soils, and seasonal variability in microbial biomass with wet and dry season alternation in tropical soils. Therefore, the omics-informed dynamic enzyme allocation in the CoMEND model enables us to capture varying microbial activity and soil carbon dynamics in response to shifting nutrient and water constraints over time in Panama soils.