Trait-based Modeling of Mineral-associated Soil Organic Matter Formation in Distinct Soil Habitats

Gianna Marschmann[1*](glmarschmann@lbl.gov), Jinyun Tang[1], and **Eoin Brodie**[1]

[1]Lawrence Berkeley National Laboratory, Berkeley, California

Project Goals: Microorganisms play key roles in soil carbon turnover and stabilization of persistent organic matter via their metabolic activities, cellular biochemistry, and extracellular products. Microbial residues are the primary ingredients in soil organic matter (SOM), a pool critical to Earth's soil health and climate. We hypothesize that microbial cellular-chemistry, functional potential, and ecophysiology fundamentally shape soil carbon persistence, and we will characterize this via stable isotope probing (SIP) of genome-resolved metagenomes and viromes. We focus on soil moisture as a 'master controller' of microbial activity and mortality, since altered precipitation regimes are predicted across the temperate U.S. The ultimate goal of our SFA "Microbes Persist: Systems Biology of the Soil Microbiome" is to determine how microbial soil ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.

Trait-based soil C models are a useful tool for exploring the interactions between genomic traits and environmental conditions that drive variation in ecological strategies of microorganisms. Here, we use Equilibrium Chemistry Approximation kinetics and Dynamic Energy Budget Theory to model relationships between consumer identity, substrate preference, and bacterial growth efficiency of microbial guilds specialized for different soil habitats (rhizosphere, bulk soil). We synthesize genome-informed trait data of soil isolates, literature-based allometric scaling relations, and biophysical modeling approaches to constrain the model parameter space for plant-derived carbohydrate depolymerization, low molecular weight carbon uptake, and cell metabolism. Scenario simulations are used to investigate the interaction between plant substrate identity and soil microbial density on the formation of mineral-associated soil organic matter with focus on model sensitivities to microbial carbon use efficiency and biomass stoichiometry. Our allometric framework allows quantification of the influence of cell morphology on resource-based niche parameters and relevant microbial functional traits across different environmental conditions, thus providing a model-based link between microbial phylogeny, specific genes, phenotypic traits and environmental preferences.

References

1. Tang, Jinyun, and William J. Riley. "A theory of effective microbial substrate affinity parameters in variably saturated soils and an example application to aerobic soil heterotrophic respiration." *Journal of Geophysical Research: Biogeosciences* 124.4 (2019): 918-940.

This research is based upon work supported by the LLNL 'Microbes Persist' Soil Microbiome SFA, funded by the U.S. Department of Energy Office of Science, Office of Biological and Environmental Research Genomic Science program under Award Number SCW1632 to the Lawrence Livermore National Laboratory for the "Microbes Persist: Systems Biology of the Soil Microbiome" SFA, and a subcontract to Lawrence Berkeley National Lab where work was performed under contract DE-AC02-05CH11231.