

16. Mapping soil carbon from cradle to grave #1: drafting a molecular blueprint for C transformation from roots to stabilized soil organic C

Erin Nuccio,^{1,4} Rachel Neurath,¹ Shengjing Shi,^{1,2} Zhili He,² Donald Herman,^{1,3} Ulisses Nunes da Rocha,³ Peter Nico,³ Mary Lipton,⁵ Trent Northen,³ Jizhong Zhou,^{2,3} Eoin Brodie,^{1,3} Jennifer Pett-Ridge,⁴ Mary K. Firestone^{1,3*} (mkfstone@berkeley.edu)

¹University of California, Berkeley, ²University of Oklahoma, Norman, ³Lawrence Berkeley National Laboratory, Berkeley, ⁴Lawrence Livermore National Laboratory, and ⁵Pacific Northwest National Lab

Project Goals: The primary goal of this on-going project is to determine how organic C decomposition and stabilization processes in soil are impacted by the interactions of the soil microbial community with living roots. We are attacking this ambitious objective by testing three hypotheses:

- H1: The microbiomes of the rhizosphere and detritosphere undergo a functional succession driven by the molecular composition and quantity of root-derived C.
- H2: Elevated CO₂ impacts the function and succession of rhizosphere communities thus altering the fate of root-derived C.
- H3: Microbial metabolism of root-derived C is a critical controller of sorption and desorption of organic C to mineral surfaces in soil.

We will draft a molecular blueprint for C transformation from root to stabilized soil organic C by:

- 1) Tracking the functional succession of microbial communities during utilization of root exudates and decaying root litter under ambient and elevated CO₂. We are using genomic, transcriptomic, and proteomic approaches (stable isotope assisted when possible) to identify key metabolic pathways responsible for C transformation and mineralization during root in-growth and root death/decay; we will assess how these rates and pathways will change in response to elevated CO₂ (eCO₂).
- 2) Measuring how the composition and quantity of root C affects the enzymatic capacities of the root microbiome and ultimately impacts C sorption/desorption from mineral surfaces. By coupling stable isotopes with metabolomic, transcriptomic and proteomic techniques, NanoSIMS (isotopic imaging), and STXM (synchrotron molecular imaging), we are identifying critical root C components, resulting enzymatic capacities and ultimately, the microbial mechanisms that impact sorption and desorption processes. A hierarchical design, ranging from intact rhizospheres to simplified model rhizospheres, are providing experimental systems in which proteomics, metabolite profiling, and Nimzyme-based enzyme assays are tractable but in which development and application of these emerging techniques to soils will be furthered.
- 3) Using data generated in the above experiments, we will parameterize a trait-based model of the microbial community functions which underlie carbon stabilization and turnover in the rhizosphere. The new trait-based model will provide a critical framework for organization and resolution of the extensive molecular and environmental data that will result from this research. The research proposed builds on an extensive foundation of past work by the PIs exploring root-soil-microbe interactions.

Plant roots and associated soil microbiomes comprise the primary nexus of belowground carbon cycling in terrestrial systems. Roots provide the source of C for stabilized organic matter in soil and it is now understood that most plant C is utilized or transformed by soil microorganisms en route to stabilization. Microorganisms supply enzymes that catalyze the decomposition and transformation of plant C into cell materials and products that are stabilized by physical protection (e.g. sorption to mineral surfaces). The proposed project directly targets the DOE goals of understanding C sequestration through plant-

microbial interactions. The information gathered will also benefit biofuels research as well as plant-stimulated bioremediation. Because microscale interactions between roots and soil microbes determine transformation of root C, decomposition and loss as CO₂, as well as C sorption and stabilization, our work will begin to reveal how microbial genes provide a blueprint for defined components of C flow in soil.