59. How do plant-microbial interactions regulate litter decomposition?

Mary Firestone[1,2*] (mkfstone@berkeley.edu), Shengjing Shi[1], Thea Whitman[1], Erin Nuccio1,[3], Donald Herman[1], Jason Shi[4], Zhili He,[4] Jennifer Pett-Ridge[3], Eoin Brodie[1,2], Jizhong Zhou[4], and Trent Northen[5]

[1] University of California, Berkeley; [2] Earth Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California; [3] Nuclear and Chemical Sciences Division, Lawrence Livermore National Laboratory, Livermore, California; [4] University of Oklahoma, Norman, Oklahoma; [5] Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California.

Project Goals: Our project (Mapping soil carbon from cradle to grave: drafting a molecular blueprint for C transformation from roots to stabilized soil organic C) works towards a fundamental understanding of C cycling in soil as mediated by soil microorganisms and their interactions with plants. How do the interactions between roots and soil microorganisms affect transformations of root derived C, decomposition and loss as CO2, as well as C sorption and stabilization in soil? We seek to gain a mechanistic understanding of the conversion of root-derived C to stabilized soil C, clarify the impacts of microbial activities on soil C sequestration, and substantially expand our understanding of molecular regulation of terrestrial C cycling.

Plants transfer atmospheric CO2 to belowground soil C pools, while microbes mediate C transformation and mineralization in the soil. However, the molecular mechanisms underlying soil-plant-microbial interactions are poorly understood. We have examined the effects of live Avena fatua roots (a common annual grass) on decomposition of 13C-labeled root litter in a California grassland soil over two growing seasons. The presence of live roots consistently suppressed rates of litter decomposition; however this effect disappeared with plant senescence. Presence of live roots significantly altered the abundance, composition and functional potential of microbial communities (assessed by qPCR, MiSeq 16S and ITS sequencing, and GeoChip 4, respectively). Two possible mechanisms – preferential substrate utilization and drying stress – are proposed as factors explaining the observed decrease in soil organic C decomposition in the presence of live roots. A simple model based on our recently collected data indicates that the decomposition of litter is primarily controlled by microbial functional potential. We are currently examining the molecular mechanisms underlying altered decomposition rates in the rhizosphere using metatranscriptomic analyses over the life of a root in the presence and absence of litter.

Meanwhile, we have developed a functional gene oriented pipeline for rapid processing and annotation of large metagenomic/metatranscriptomic reads with key functional gene information relevant to geochemical and ecological processes. The pipeline is being applied to investigate the functional gene composition and structure of soil microbial communities and will continue to be validated and benchmarked throughout our project. We are also profiling the spatial dynamics of enzymatic activity surrounding a plant root through the development of "Nimzyme" imaging technology. This approach uses nanostructure-initiator mass spectrometry (NIMS) technology to image in situ enzyme activity in intact systems. This type of spatial mapping of enzyme activities combined with transcriptome-based, genome-based, and proteome-based analyses of rhizosphere soil promises to reveal the bases of root-induced changes in microbial decomposition processes.

Funding for this research was provided by awards SA-DOE-29318 and DE-SC0010570 through the Genomic Sciences program of the Office of Biological and Environmental Research, U.S. Department of Energy to the University of California, Berkeley. Part of this work was performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under contract DE-AC52-07NA27344 and FWP SCW 1421 and at Lawrence Berkeley National Laboratory under the auspices of the University of California - contract DE- AC02-05CH11231.