

## 60. Mapping soil carbon from cradle to grave: Identifying metabolic processes underlying patterns of rhizosphere microbial succession and organic matter priming

Kateryna Zhalnina<sup>1,2\*</sup>([kzhalnina@lbl.gov](mailto:kzhalnina@lbl.gov)), Heejung Cho<sup>1</sup>, Ulas Karaoz<sup>2</sup>, Stefan Jenkins<sup>2</sup>, Richard A. White III<sup>3</sup>, Mary S. Lipton<sup>3</sup>, Jizhong Zhou<sup>4</sup>, Jennifer Pett-Ridge<sup>5</sup>, Trent R. Northen<sup>2</sup>, Mary K. Firestone<sup>1,2</sup>, and Eoin L. Brodie<sup>1,2</sup>

<sup>1</sup>University of California, Berkeley, California; <sup>2</sup>Lawrence Berkeley National Laboratory, Berkeley, California; <sup>3</sup>Pacific Northwest National Laboratory, Richland, Washington; <sup>4</sup>University of Oklahoma, Norman, Oklahoma; <sup>5</sup>Lawrence Livermore National Laboratory, Livermore

**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 CO<sub>2</sub>, 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.

Interactions between plants, soil microorganisms and soil minerals underlie both the stabilization and decomposition of soil organic carbon (SOC). Plants increase the concentration of labile C in soil through exudation, providing readily assimilated substrates for rhizosphere microbiota and stimulation or repression of SOC mineralization may result (i.e. positive or negative priming). The soil microbiome displays strong patterns of succession in response to living plant roots and although both positive and negative rhizosphere priming have been widely observed, the metabolic processes underlying these successional patterns and SOC priming are not well defined. Using combined modeling and experimentation we are working to define key traits of soil microorganisms relevant to their fitness in the rhizosphere and transformation of carbon. From a library of approximately 300 bacterial isolates we sequenced 38 heterotrophic bacteria representative of the dominant organisms identified in metagenomes of this Mediterranean grassland soil. Analysis of genome properties and content allowed us to predict important physiological features of the isolates, such as minimum generation times (MGTs), optimum temperature and substrate utilization capabilities. MGTs inferred directly from genomic sequences agreed well with in vitro observations. All analyzed genomes revealed a repertoire of features relevant to life in the rhizosphere, such as high gene copy number of sugar and organic acid transporters and polymer degrading enzymes (glycoside hydrolases and polyphenoloxidases). Isolates from the Alphaproteobacteria and Actinobacteria had the highest occurrence of these features in their genomes. To test genomic predictions we have performed a number of functional analyses using enzymatic, exometabolomic and proteomic assays.

We have developed and curated draft genome-scale metabolic models of select isolates and have used exometabolomic data to perform gap filling. These metabolic models will be used to evaluate via simulation the metabolic response of soil heterotrophic bacteria to root exudates and their impact on rhizosphere succession and SOC mineralization. Explicit features of the genome-scale models (electron donors and acceptors, C use efficiency, metabolic feedbacks and trade-offs) together with experimental data (gene expression, protein secretion, metabolite uptake and release) will be used in future work to parameterize genome-informed trait-based models of the soil microbial community aimed at predicting succession and C transformation in the rhizosphere.

*Funding for this research was provided under contract FOA DE-PS02-09ER09-25 through 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 performed under the auspices of the U.S. Department of Energy by Lawrence Livermore National Laboratory under contract DE-AC52-07NA27344 and at Lawrence Berkeley National Laboratory under the auspices of the University of California - contract DE-AC02-05CH11231.*