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ABSTRACT TITLE: Characterizing Metabolic Potential of the Subsurface for SFA 2.0

ABSTRACT: The role of the Metabolic Potential component of the LBNL Scientific Focus Area is to inform the overarching genome-enabled biogeochemical model (GEWaSC) and characterize prevalent metabolic pathways in subsurface microbial communities that mediate carbon and electron flux. The long-term objectives of Metabolic Potential are twofold: (1) Develop a concerted approach involving field and laboratory experiments and state-of-the-art informatics to characterize the metabolic diversity of subsurface microbial communities at the genome scale, integrating metagenomic, metatranscriptomic, metaproteomic, physiological, and geochemical/metabolite data to strengthen and validate models of carbon and electron flux, and (2) As inputs to the GEWaSC model, establish functional guilds that impact the carbon and coupled N, S, and Fe cycles in different subsurface regions. Major scientific objectives/questions to be addressed include the following: (1) Establish how aquifer microbial processes change in response to periodic or long-term geochemical changes and how responses to perturbation vary in biogeochemically distinct regions of the aquifer. Specifically, in what ways do the metabolic lifestyles/pathways of microorganisms modulate in response to seasonal changes in redox conditions as a function of water table fluctuation or organic matter loading? (2) To what extent can we establish the linkages between modes of degradation of organic matter (e.g., modification of specific compounds or functional groups) and the genetically encoded metabolic potential of microbial communities to which it is exposed? and (3) Establish under what conditions chemolithoautotrophy can play a significant role in subsurface carbon and electron flow.

The Metabolic Potential component will integrate multiple lines of investigation to address its key objectives and science questions: (1) state-of-the-art meta-omics analysis, (2) targeted physiological analysis (using high-throughput microplate assays with fluorophore-labeled substrates, as possible), (3) high-throughput microbial isolation, and (4) experimental systems consisting of field studies and laboratory studies (particularly flow-through columns). Meta-omics analysis will constitute the core of the Metabolic Potential component. Metagenome information will elucidate the phylogenetic membership of the community (e.g., using EMIRGE), and, after appropriate binning and genome reconstruction, can allow for highly detailed hypotheses to be developed about the metabolic lifestyles of individual community members (e.g., Wrighton et al. 2012; Handley et al. 2012). In conjunction with detailed, synchronous physicochemical data, metatranscriptome and metaproteomic data will provide information about which genes are most important to the organism under targeted sampling conditions and will be used to validate metabolic predictions. The Metabolic Potential component will take advantage of a JGI Community Sequencing Program (CSP) allocation as well as ggKBase, a product of DOE’s KBase program. Field (groundwater and aquifer sediment) samples will include background areas, critical zones (e.g., zones subject to water table fluctuations or naturally bioreduced zones containing high loadings of native organic matter), and samples from perturbation experiments. Planned laboratory column studies will include (1) experiments simulating water table fluctuations, in which formerly anoxic sediments are subjected to dissolved oxygen (in parallel with field perturbation experiments) and (2) detailed studies of microbial metabolism of native Rifle organic matter, involving in-depth meta-omics and organic matter characterization.

Some examples will be given of how prior LBNL SFA and Rifle IFRC genome-enabled studies will provide knowledge and expertise relevant to the proposed work for SFA 2.0.