

Genome-to-Watershed Predictive Understanding of Terrestrial Environments: Overview of the LBNL SBR SFA 2.0

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The LBNL ‘Genomes-to-Watershed’ SFA 2.0 project is developing predictive capabilities to quantify how the terrestrial microbiome affects biogeochemical watershed functioning, how watershed-scale processes affect the microbial community, and how these interactions co-evolve with climate and land-use changes. Development of such predictive capabilities is critical for guiding the optimal management of water resources, contaminant remediation, carbon stabilization, and agricultural sustainability – now and with global change.

Two study sites in the Colorado River Basin are serving as platforms for developing new approaches, insights and models. The Colorado River Basin is already threatened by drought, diminished snowpack, wildfires, and pest outbreaks, which have largely unexplored impacts on water, energy and other ecosystem services provided by the river corridor. Extensive characterization, field experiments, natural perturbations, and model development activities have taken place at a uranium-contaminated floodplain located near Rifle CO. Over 1,000 mostly novel subsurface genomes have been sequenced from the Site, providing some of the first insights into the diversity of the subsurface microbiome and metabolic roles of organisms involved in subsurface nitrogen, sulfur and hydrogen and carbon cycling. Metatranscriptomics have revealed the inordinate role of chemolithoautotrophy at the site. Geophysical methods have been used to document the presence of hot spots and hot moments of activity in the floodplain. Novel instrumentation has been installed to track water, carbon and nitrogen through the soil, vadose zone, capillary fringe and groundwater, providing new insights about transport across compartments and seasons. New approaches and conceptual models are being developed to quantify organic matter dynamics at mineral interfaces, and to document the mechanisms by which mineral associations affect carbon transport. GEWASC, a first-ever Genome-Enabled Watershed Simulation Capability, is being developed and tested at Rifle. Progress Trait-based and multi-scale models have been developed to represent the diversity of microbial functional processes within a larger scale reactive transport framework. Importantly, simulations have already demonstrated how incorporation of genome-informed reaction networks significantly improve prediction of terrestrial environment behavior.

Research has also been initiated at the pristine East River watershed in the headwaters of the Upper Colorado River Basin. At this site, hyporheic zone flow through organic, carbon-rich sediments located between meanders may have a large impact on carbon cycling in the river basin. Hydrological and biogeochemical measurements are being collected to quantify the fine-scale gradients, and geophysical and other measurements are being used to identify watershed larger functional zones. Models are being developed to incorporate and link the fine and large scale processes: from genomes-to-watersheds - with an eye toward extending to water basins.