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

Susan S. Hubbard, Deborah Agarwal, Jillian F. Banfield, Harry R. Beller, Eoin Brodie, 
Phillip Long, Peter Nico, Carl Steefel, Tetsu Tokunaga, Kenneth H. Williams (all 
Berkeley Lab) and the SFA 2.0 Team

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.