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SLAC Groundwater Quality SFA: Biogeochemical Redox Responses of Soil Microbial Communities to Seasonal Hydrological Transitions at Riverton, WY

Bradley B. Tolar[1*], Kristin Boye[2], Callum Bobb[1], Laura E. Spielman[1], Emily Cardarelli[1], John R. Bargar[2], and Christopher A. Francis[1]

[1] Stanford University, School of Earth, Energy, and Environmental Sciences, Stanford, CA
[2] SLAC National Accelerator Laboratory, Menlo Park, CA

Contact: btolar1@stanford.edu

The subsurface capillary fringe is a hotspot for biogeochemical cycling and microbial metabolic activity in soils, particularly those in alluvial systems. At the DOE legacy uranium ore processing site in Riverton, WY, extensive seasonal and episodic wet-dry cycling produces intense water table fluctuations that trigger strong redox oscillations throughout the soil column and large variations in dissolved uranium concentrations. Coupling between subsurface hydrology and biogeochemistry is most complex at unsaturated-saturated interfaces, due to the many hydrologic processes at play (percolation, capillary rise, advection) and the biogeochemical reactions that can be triggered (redox reactions, mineral dissolution and precipitation, sorption and desorption, etc.). The intense, intermittent hydrologic transitions and their biogeochemical consequences are governed in large part by the microbial response, which is then responsible for ensuing impacts on groundwater quality, including contaminant release and transport. How exactly the various microbial and geochemical processes are connected in non-steady state, spatially-heterogeneous systems is not yet understood.

We aimed to address this knowledge gap by collecting both microbial and geochemical samples to capture key redox transitions at the Riverton site from April to September 2017. Our goal was to characterize the microbial community throughout the soil column and observe its response to wet-dry transitions across a complete season. Next-generation sequencing (Illumina) was employed to identify biogeochemically-relevant microbial taxa based on the 16S rRNA gene, and also facilitated the identification of key samples for metagenomic and metatranscriptomic sequencing. We found a broad diversity of microbial clades in our samples, including bacteria involved in sulfur oxidation or reduction, dissimilatory metal-reducing bacteria, and ammonia-oxidizing Archaea. Overall, microbial communities grouped by soil depth or type. These data were paired with measurements of major biogeochemical elements (C, N, Fe, S) and metal contaminants (U, Mo), as well as soil temperature and moisture. Together, these results provide insight into how microorganisms respond to hydrologic transitions, and whether they are present and active during both wet (reducing) and dry (oxidizing) periods or only when conditions are optimal for their metabolism. This information is crucial for our understanding of these environments and we will apply these data to enhance reactive transport models capable of testing sensitivity of alluvial systems to hydrologic perturbations.