

**Poster #21-53**

**SLAC Groundwater Quality SFA: Microbial Niche Partitioning at the Soil-Groundwater Interface in Transiently Reduced Floodplains**

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BER Program: SBR

Project: SLAC Groundwater Quality SFA

Project Website: <https://www-ssrl.slac.stanford.edu/sfa/>

The Intermountain West hosts a large number of uranium-contaminated legacy DOE ore processing sites. Our research at several sites have shown that they experience ‘hot moments’ driven by rainfall, inundation, and meter-scale seasonal water table rise/fall that notably impact subsurface biogeochemistry, particularly for C, N, S, and Fe species and alter redox conditions. Transitions between oxidizing and reducing conditions are accompanied by intense microbial activity, biogeochemical transformations, and increased nutrient and contaminant fluxes. Rewetting events make limiting labile substances newly accessible to primed microbial communities. Despite their importance, little is known about the structure and function of the microbial community at the soil-groundwater interface or the extent to which these communities are impacted by rapid changes in water saturation. Microbial biomass and diversity at the soil- groundwater interface exceeds bulk soil levels by orders of magnitude, however accessibility of these sediments have previously precluded their study beyond 30 cm depth. Furthermore, past studies have primarily examined bacterial and archaeal communities with 16S rRNA primer sets that separately target each domain, thereby limiting holistic interpretations of the overall microbial communities. Thus, depth-resolved knowledge of microbial community diversity and distribution within the subsurface is extremely limited, but is needed to understand biogeochemical perturbations initiated by the water cycle.

To address these knowledge gaps, we collected 82 soil samples from Riverton, WY, and 80 collectively from Naturita, CO, Grand Junction, CO, and Shiprock, NM that were retrieved from multiple cores extending to 6 m depth and represent variable connectivity with the adjacent rivers. We pair depth-resolved molecular characterization of the microbial communities with detailed geochemical measurements and present evidence that suggests niche partitioning in the subsurface is influenced by hydrologic transition regimes. We show that unsaturated and saturated zone sediment communities can be used as ‘endmembers’ to understand microbial community variability in the hydrologically- and redox-variable capillary fringe. This study also demonstrates that use of the modified V4-V5 primer set for 16S rRNA amplicon sequencing allows the simultaneous detection of diverse archaea and bacteria as well as rare groups in the subsurface. Forthcoming metagenomes from select depths will further elucidate the 16S trends described, provide insight into newly described taxa, and improve our spatial and temporal understanding of how microbial metabolisms adapt in response to hydrologic transitions. This work provides the foundation for more targeted studies of microbial function in the Riverton site capillary fringe during wet-dry transitions.