SLAC Floodplain Hydro-Biogeochemistry SFA: Hydrological and microbiome dynamics drive shifts in subsurface geochemistry and oxic-anoxic interfaces in floodplain soils

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Project: SLAC Floodplain Hydro-Biogeochemistry SFA
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Project Abstract: Subsurface microbial communities in floodplain soils drive major biogeochemical cycles (e.g., C, N, S) and control the fate and transport of many metals and contaminants (e.g., Fe, Mn, Zn). Each year floodplains experience seasonal rise and decline of the water table that determines nutrient and other inputs to the subsurface, as well as the oxygen penetration depth. Within the soil column, the boundary depth between oxic and anoxic conditions is therefore controlled largely by floodplain hydrology. Snowmelt-induced flooding and other precipitation further contribute to shifts in the depth of this oxic-anoxic interface. Thus, it is critical to define connections between seasonal hydrology and changes in microbial community composition (and function), as these are not yet well understood.

In our study site along the Slate River, CO, we observe two types of interfaces, namely: (1) an oxic-anoxic interface within the fine-grained layer, as well as (2) a deeper physical interface where soils/sediments shift to a coarse cobble layer. This cobble layer is more directly connected to the river, with oxygenated groundwater moving through it, thus forming a secondary oxic-anoxic interface deeper in the soil column. Using these two interfaces as a guide, we investigated microbial community composition across multiple depths (~10-30 cm resolution) and time points from 2018-2021 at two Slate River floodplain sites. This spatiotemporal analysis consistently revealed phylogenetically- and metabolically-diverse populations of bacteria and archaea, including methanogens and methanotrophs, sulfur-oxidizing and -reducing taxa, ammonia-oxidizing archaea, and iron-cycling bacteria. These communities showed a striking depth distribution across oxic-anoxic boundaries; for example, within the *Archaea*, ammonia-oxidizing *Thaumarchaeota* were abundant in shallow oxic soils, whereas methanogens and *Bathyarchaeota* were found exclusively in deeper anoxic soils. We also investigated the impact of hydrologic perturbations on subsurface microbial communities and geochemistry, through field inundation experiments as well as the coincidental construction of a beaver dam at one site in 2019. The resultant flooding caused microbial community shifts that are reflected in observed geochemistry, as well as modeled oxygen penetration depth. Further analyses, including genome-resolved metagenomics and metatranscriptomics, will be employed to examine floodplain microbiome dynamics at an even finer scale and connect both hydrology and geochemistry to specific biogeochemical processes.