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Molecular and Genomic Insights into Nitrogen-Cycling Microbial Communities within the Terrestrial Subsurface at Riverton, WY

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Floodplains are hot spots for biological productivity that drive biogeochemical reactions and moderate ground and surface water quality, carbon turnover, and regional land-atmosphere interactions. Within the semi-arid upper Colorado River Basin (CRB) and intermountain west, a large fraction of shallow subsurface organic carbon (C) is believed to reside within fine-grained, organic-enriched sediments known as naturally-reduced zones (NRZs). NRZs, formed within the numerous contaminated DOE legacy site floodplains in the upper CRB, contain large inventories of nitrogen (N) and uranium (U). Microbial N-cycling has the capability to “unlock” the biogeochemical nutrient supply stored within NRZs, drive C cycling, and liberate U to the aquifers. Nitrification links organic matter decomposition to the production of nitrite and ultimately nitrate, an oxidant of U(IV) and the primary electron acceptor for denitrification. Nitrification and denitrification help mediate C turnover in NRZ sediments and are also the primary sources of the potent greenhouse gas, N₂O. Despite their biogeochemical importance, remarkably little is currently known regarding N-cycling microbial communities within terrestrial subsurface soils/sediments, let alone NRZs.

To address this critical knowledge gap, we are examining N-cycling communities at the DOE legacy U ore processing site in Riverton, WY, using a combination of molecular, meta-omic, biogeochemical, and modeling approaches. In addition to documenting the distribution and diversity of ammonia-oxidizing *Thaumarchaeota* using functional gene and high-throughput 16S rRNA amplicon analyses, we have recently obtained metagenome-assembled genomes (MAGs) from these biogeochemically-important *Archaea* from multiple depths within the Riverton subsurface. Ultimately, this multi-pronged approach will yield valuable genomic, ecophysiological, and biogeochemical insights into key microbial N-cycling guilds within the terrestrial subsurface.