Title: **Influence of hyporheic exchange on coupled S-Fe-C biogeochemical cycling and microbial community function in riparian wetlands at the Savannah River Site**

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BER Program: ESS

Project: University Project

Project Abstract: Riparian wetland hyporheic zones(HZs), where oxic surface water and anoxic groundwater mix, drive steep redox gradients and promote hotspots and hot-moments of biogeochemical processes that are driven, in part, by microbiological activity. In freshwater wetland and stream sediments, carbon (C) turnover and fate is heavily influenced by the biogeochemical cycling of iron (Fe). "Hidden" or "cryptic" sulfur (S) redox processes may be further coupled to these Fe and C cycles. S biogeochemical cycling is not well constrained in freshwater systems but can include the production of reactive intermediate S species that promote further biotic and abiotic redox reactions (including those coupled with Fe reduction and methane oxidation), thus supporting higher rates of sulfur biogeochemical cycling than otherwise expected in these low sulfate environments. The overall goal of this project is to develop a mechanistic understanding of how hydrologic flow influences coupled abiotic-biotic Fe-S-methane cycles in riparian wetlands.

In the uncontaminated area of Tims Branch at the Savannah River Site, we have set up a number of subsites with continuous surface- and ground-water level and flux measurements. These sites vary in terms of flux direction and magnitude throughout the year, with visible cues of flux direction from the presence or absence of Fe-oxidize encrusted microbial mats in gaining or losing stream conditions, respectively. There is a high concentration of Fe in the sediment porewaters and sediments that varies seasonally and sulfide measurements were very low at all times of the year sampled. 16S rRNA gene sequencing was performed on sediment cores collected in January and August 2019 to characterize the spatial and temporal microbial community distribution. The overall microbial community was similar between the two seasons except for changes in the relative abundance of phyla with depth. Preliminary functional group analysis suggests a greater relative abundance of S cycling orders at gaining stream subsites relative to losing stream locations. Although it is unclear why, some subsites further downstream

that experience occasional flooding due to beaver damming had a much higher relative abundance of methanogenic orders than other sites. Correlations between geochemical parameters and microbial community, visualized through non-metric multidimensional scaling (NMDS) ordinations, revealed that the microbial community in losing stream sediments were most dissimilar to gaining stream sites, indicated that hyporheic fluxes impact microbial community structure. Metagenome analysis underway will help us further understand the spatial and temporal taxonomic and functional affiliations at these sites.