

**Poster #22-28****Modeling Microbial Controls on Biogeochemical Processes at the Savannah River Site**

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Project Website: [https://doesbr.org/documents/ANL\\_SFA\\_flyer.pdf](https://doesbr.org/documents/ANL_SFA_flyer.pdf)

<https://www.anl.gov/bio/project/subsurface-biogeochemical-research>

The Argonne Wetland Hydrobiogeochemistry SFA studies wetland hydrobiogeochemistry centered on a riparian wetland field site within Tims Branch at the Savannah River Site, focusing on hydrologically driven biogeochemical processes within three critical zones: sediment, rhizosphere, and stream. Microorganisms play a fundamental role as mediators of the biogeochemical processes happening in and across these compartments and their activity can result in the sequestration or release of contaminants such as U, as well as the movement of C through the ecosystem. Early 16S amplicon characterization of the microbial community shows that organisms within the *Proteobacteria*, *Nitrospirae*, and *Chloroflexi* phyla are abundant within the sediment compartment at this site, while highly abundant members of the flocc communities within the stream compartment include *Sideroxydans*, members of the *Methylococcaceae*, *Thiovirga*, *Desulfuromonadales*, and many *Betaproteobacteria*. These data were processed in KBase through a newly co-developed pipeline enabling the processing of amplicon data and the generation of microbe-microbe and microbe-metabolite interaction networks to identify common/widespread interactions, stable interactions, critical interactions, and putative keystone species from these samples. This utility of this approach is demonstrated with data collected from the Argonne Wetlands sites. Implications for the incorporation of microbial metabolic activity into reactive transport models will be discussed.