

Poster #21-69**More than Meets the Eye: Microbial Communities and their Viral Predators Govern Carbon and Nitrogen Transformations in the Hyporheic Zone**

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Microorganisms are catalysts for carbon and nitrogen geochemical cycles in hyporheic regions of river sediments, yet the microbial metabolisms underlying these processes are largely unknown. Moreover, the viral ecology impacting these microbial nutrient cycles in river sediments is to a great extent unexplored. Here, we performed metagenomic and metaproteomic analyses on 6 sediment cores, with samples collected at 10 cm intervals from the surface down to 60 cm below the surface. We reconstructed 67 near-complete genomes from the 5 most abundant and active microbial lineages including members of Nitrospirae, Thaumarchaeota, Firmicutes, Proteobacteria, as well as members from 6 other phyla. Genome metabolic inferences indicated that ammonium is a central metabolite connecting all organisms in this system. Expression data confirmed that organic nitrogen degradation (e.g. peptides and amino acids) by Proteobacterial and Firmicutes members provides a source of ammonium to the system. One of the most dominant and active community members, the Thaumarchaeota (renamed to Crenarchaeota), oxidize ammonium into nitrite. Subsequent nitrite oxidation by members of the Nitrospiraceae could fuel denitrification by members of the Proteobacteria, ultimately yielding nitrogen gas production, including nitrous oxide. Evidence for heterotrophic carbon oxidation (e.g. phenolics) results in the generation of simple sugars and carbon dioxide, the latter of which can be consumed by autotrophic nitrifiers. Consistent with our proteomic data, chamber and porewater measurements demonstrated that nitrous oxide and carbon dioxide fluxes respond to river stage and the greatest nitrous oxide concentrations were near the sediment surface. Our viromic analyses recovered 412 unique viral populations, several of which may contribute to carbon and nitrogen cycling in this system. *In silico* predictions linked a 19 kb viral genome to 3 Thaumarchaeota genomes, suggesting viral predation of active nitrogen cycling microorganisms. Viruses also encoded carbohydrate and amino acid degradation auxiliary metabolic genes, indicating viral influence of carbon degradation and ammonium formation, respectively. Together these genome enabled predictions uncover microbial and viral roles contributing to interdependent carbon and nitrogen fluxes from river systems.