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Microbial Ammonium Cycling is Critical to Nitrogen Transformations in Columbia River Sediments

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The hyporheic zone plays a major role in carbon and nitrogen fluxes in river systems, yet the microorganisms and their metabolic interactions mediating these processes are largely unknown. To address this knowledge gap, we performed metagenomic and metaproteomic analyses on sediment cores spanning depth and vegetative gradients adjacent to the Columbia River. To date we have reconstructed 20 near-complete genomes from the 6 most abundant and active lineages including members of *Nitrospira* (3 genomes), Thaumarchaeota (6 genomes), Actinobacteria (5 genomes), Aciduliprofundum, as well as novel members within the Deltaproteobacteria, Rokubacteria, and Armatimonadetes (3 genomes). Metabolic predictions from these genomes indicated that ammonium is central metabolite interconnecting nearly all the genomes. For instance, Deltaproteobacteria and Armatimonadetes genomes all encode the capacity to degrade amino acids providing a source of ammonium to system. This metabolite can then be oxidized by Thaumarchaeota to nitrite, which is subsequently oxidized to nitrate by *Nitrospira*, and regenerated to ammonium via dissimilatory nitrate reduction by Actinobacteria. Proteins involved in these predicted activities were detected in the metaproteomic data, confirming that active organic nitrogen fermentation, nitrification, and denitrification co-occur in the subsurface environment. Together our data indicate that nitrogen compounds are transformed by a network of specialists, cycling nitrogen in a modular fashion in the hyporheic zone.