Multi-talented microbes drive Fe, S, N, and C cycling in an intertidal coastal aquifer: a metagenomic study

E.K. FIELD^{1*}, K.L. HOPPES², K.H. KIM², H.A. MICHAEL², T.E. HANSON³, C.S. CHAN^{2,3^}

 ¹Department of Biology, East Carolina University, Greenville, NC, 27858, USA (fielde14@ecu.edu)
²Department of Geological Sciences, University of Delaware, Newark, DE, 19716, USA (^cschan@udel.edu)
³School of Marine Science and Policy, University of Delaware, Newark, DE, 19716, USA

Submarine groundwater discharge is a significant source of nutrients, metals, and other solutes to coastal environments and ultimately global oceans. Discharge occurs from coastal aquifers where terrestrial, anoxic iron-rich groundwater mixes with seawater rich in oxygen, sulfate, and organic matter. Previous microbial community analyses in a coastal aquifer (Cape Shores, DE) demonstrated uncultivated bacteria were prevalent and their specific metabolic capabilities remained unclear. Here, we aim to address what nutrient and metal cycling processes these novel microbes may contribute to in this geochemically dynamic environment. Metagenomes of one sediment and four porewater samples were analyzed in conjunction with extensive geochemical analyses across gradients of O2, S, Fe, N, C, and salinity. Annotation of metagenome contigs and subsequent genomic bins indicate that microbial groups have adapted to this geochemically dynamic environment by maintaining multiple pathways for energy conservation including sulfur oxidation, dentrification, nitrogen fixation, iron reduction, and carbon fixation. In particular, Gammaproteobacteria with diverse metabolic capabilities were found across the site and appear to play an important role in linking sulfur, carbon, and nitrogen cycling. Notably, one bin related to sulfur-oxidizing Sulfurifustis variabilis indicates they may also link sulfur and iron cycling at this site. Parcubacteria and other CPR members are prevalent in the seaward groundwater discharge region and their genomes contain minimal energy conservation pathways which is in contrast to microbes in other regions of this site. Geochemical data and relative functional gene abundances of this seaward sample indicate iron reduction and sulfur oxidation may be occurring by less abundant community members. Overall, these results shed light on the metabolic function of the novel microbes associated with intertidal coastal aquifers and suggest they contribute to Fe, S, N, and C cycling in coastal environments. Ongoing studies will further expand our understanding of how these microbial communities control the chemistry of submarine groundwater discharge.