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Microbial iron oxidation in metal-rich wetlands: an integrated kinetics and omics study

CLARA S CHAN[1], GRACE TOTHERO[1], OLUSHOLA AWOYEMI[1], RENE L HOOVER[1], DANIEL KAPLAN[2], EDWARD O'LOUGHLIN[3] AND PAMELA WEISENHORN[3]

[1]University of Delaware
[2]Savannah River National Laboratory
[3]Argonne National Laboratory
Presenting Author: cschan@udel.edu

Iron-oxidizing microbes can drive many elemental cycles via their energy and carbon metabolisms, as well as by precipitating reactive iron oxyhydroxides that sequester organics and metals. To determine Fe-oxidizer impacts on environmental geochemistry, we need to know the environmental rates of biotic and abiotic oxidation, and the controls on these rates. To evaluate this, we conducted field campaigns in metal-rich wetlands at the Savannah River Site in South Carolina. We performed iron oxidation kinetics experiments on these terrestrial freshwater iron mats, in conjunction with 16S rRNA gene sequencing and metagenomic analyses of mats to identify the major iron oxidizing bacteria (FeOB) and the flanking community. The iron mats were dominated by known FeOB, notably a diverse set of *Gallionella* OTUs. We compare biotic oxidation rates with abiotic azide-killed controls and show that mat iron oxidation was dominated by biotic oxidation while oxidation by killed mat was much slower. There was also relatively low oxidation in filtered controls in light and dark treatments. Scanning electron microscopy shows the major morphologies in the mats are FeOB biominerals, including twisted stalks and sheaths. We have enriched a stalk-forming *Gallionella* from the wetland iron mats, and are continuing to isolate for further metabolic and genomic analyses. We will present the results of metagenomic sequencing of the Fe mat communities used in the kinetics experiments, including the major physiological mechanisms of the dominant FeOB. The genomes will be compared more broadly to a Gallionellaceae pangenome. These results set the stage for integrated kinetics, 'omics, and metabolic modeling work, as we work towards our longer-term goal to link FeOB metabolic models and kinetics to biogeochemical models in order to predict Fe, C, nutrient and contaminant metal cycling.