Bioremediation Potentials of “Sheet-Flow” System Generated during Intrusion of Pristine Soil with Coal Mine-Derived AMD

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Coal mine-derived AMD is an environmental pollutant that is formed upon intrusion of oxygenated water into abandoned mine works and waste rock. This induces microbially mediated oxidation of FeS phases, and yields acidic fluids with high concentrations of Fe(II). When AMD enters circumneutral surface waters, dissolved Fe(II) oxidizes and precipitates as Fe(III) (hydr)oxides that smother stream substrate and destroy benthic communities. We have found cases where AMD emerges and mixes with formerly pristine soil while flowing as a fluid “sheet.” Mixing of AMD and soil in “sheet-“ systems give rise to microbial communities that efficiently oxidatively precipitate and remove Fe from AMD. Here, robust Fe(II) oxidizing bacterial (FeOB) communities develop upon mixing of AMD and soil, and without any human intervention; they arise from the combined influences of soil and AMD-associated microbial communities. Previous work in our lab, indicated that combined effects of initial AMD and soil-associated microbial community and geochemistry influence the efficiency of “sheet-flow” inspired system in oxidative removal of Fe from AMD. Also, the abundance of “uncommon-in-AMD” microorganisms in these systems exhibiting rapid Fe(II) oxidation, suggest that ability to oxidize under acidic conditions Fe(II) might be more widespread than expected.

To investigate, 1) how robust FeOB communities develop when AMD and soil interacts, 2) what major metabolic pathways are used by these mixed microbial communities?, 3) and if, efficiency of “sheet-flow” development is universal to geochemically variant AMD sites, we challenged pristine soil (VSG) with geochemically and microbiologically distinct AMD from two chemically distinct mines referred to as Powdermill (PM) and Wingfield Pines (WFP) in laboratory “sheet-flow” inspired incubations. AMD chemistry (pH and Fe (II)) and changes in the microbial communities (using integrated metagenomic and metatranscriptomic approach) were monitored throughout the incubation period (21days). We determined 1) abundance and distribution of functional genes during robust microbial Fe(II) oxidizing activities, 2) the relative contributions of soil vs. initial AMD to this development of microbial Fe(II) oxidation, 3) if Fe(II) oxidation activity is widespread among microorganisms, and 4) which organisms may be mediating or enhancing Fe(II) oxidation.

Preliminary results indicate development of robust microbial Fe(II) oxidizing activities in PM (low pH) AMD. However, WFP (high pH) AMD showed no significant difference between microbial and chemical Fe(II) oxidation rates. pH influences the kinetics of abiotic Fe(II) oxidation, which might impact in the metabolic capabilities and networks of Fe(II) oxidizing bacteria in these incubations. Therefore, we are currently analyzing molecular (DNA/RNA) data to understand contribution of AMD/soil microorganisms and changes in communities’ functions during increased Fe(II) removal. Findings from this work will be us to develop a predictive framework, upon which site-specific AMD treatment can be designed. Moreover, “sheet-flow” inspired systems may serve a model for development of inexpensive and sustainable AMD treatments.