

Biomolecular Characterization of Microbial Communities in Systems Treating Acid Mine Drainage.

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Abstract. Acid mine drainage (AMD) is a critical environmental problem. It is formed by the oxidation of sulfide minerals which release acidity, sulfates, and metals that contaminate the water.

Sulfate-reducing permeable reactive zones (SR-PRZs) are an attractive means of passively treating AMD. Although SR-PRZs are microbially driven, little is known about their microbiology. Denaturing gradient gel electrophoresis (DGGE), quantitative real time PCR (QPCR), and cloning of 16S rRNA and *apsA* genes were used to study the influence of microbial inocula in the remediation of AMD and to characterize the microbial communities of two sulfate-reducing field bioreactors (Luttrell (LUTR) and Peerless Jenny King (PJK), near Helena, MT).

In a batch study, five inocula were compared in terms of their ability to remove sulfate and zinc and neutralize pH. Performance was dependent on the type of inoculum. The microbial communities in the inocula with better performance were more diverse and contained a variety of polysaccharides degraders, fermenters, and sulfate reducers. In a field study, the PJK and LUTR bioreactors were sampled at different locations. Based on the 16S rRNA gene sequences there was no statistically significant difference between the bacterial communities of the two sites. However, the sulfate-reducing bacterial communities were found to be significantly different between the two sites based on *apsA* gene analysis. In both studies, sulfate reducers were a small proportion of the microbial community.

The molecular tools utilized demonstrated to be well suited for the evaluation of microbial communities in the field and for guidance in the construction of ideal inocula.

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