

Microbially-mediated treatment of mining-influenced water (MIW) through the implementation of sulfate-reducing biochemical reactors (BCR) is an attractive option for passive, in situ remediation with low operating costs and reduced maintenance requirements. However, BCRs can be unpredictable in terms of how they recovery from environmental stresses such as oxygen exposure. Previous studies have demonstrated that the inoculum can impact performance positively, suggesting that engineered control of the microbial community structure could improve the resilience of BCRs to stress. The purpose of this study was to determine the effect of bioaugmentation and biostimulation on performance and recovery from oxygen stress. Twelve columns (six conditions in duplicate) were packed with a complex organic substrate (wood chips, etc.), inoculated with dairy manure, and fed simulated acid mine drainage containing Fe, Cd, and Zn at pH 5.5. The conditions tested were: 1) bioaugmentation with cellulose degraders (CD); 2) bioaugmentation with sulfate reducers (SRB); 3) biostimulation with ethanol (EtOH); 4) biostimulation with carboxymethyl cellulose (CMC); 5) dairy manure only control (DM); 6) un-inoculated control (CR). Once the columns reached steady state anaerobic performance, they were exposed to oxygen, allowed to reach steady state again, and then oxygen-exposed for a second, longer time. The results indicate that all columns performed well in terms of pH neutralization and removal of sulfate and heavy metals. However, the cellulose and ethanol biostimulated columns appeared to be the most resilient to oxygen exposure and performed best by the end of the experiment (171 days), while the bioaugmented columns performed similarly to the controls. The microbial communities were evaluated at each steady state using a suite of biomolecular tools, including active community profiling (ACP) and quantitative real-time PCR (Q-PCR) targeting key functional groups of sulfate-reducers, cellulose-degraders, fermenters, and methanogens. It was found that the active microbial community structure was distinct among the kinds and diversity of bacteria present following stress events. Functional gene analysis supported these observations, but provided finer resolution regarding the response of each functional group to stress.