

Tracking the distributions microbial communities and activities associated with acidic coal mine drainage in Appalachia, USA.

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Approximately 500,000 abandoned mines exist in the United States, many of which are coal mines of the Appalachian region. Intrusion of oxygenated water into these mine works leads to microbially mediated oxidation of coal seam-associated FeS phases (notably pyrite), yielding sulfate-rich, acidic (generally pH 2.5 – 4.5) fluids with high concentrations of Fe and other metal(loid)s that are referred to as acid mine drainage (AMD). Emergence of these fluids at the terrestrial surface and entrance into adjacent waterways has led to tens of thousands of kilometers of impaired streams. Differences have been reported among the microbial communities associated with AMD generation, but microbiological activities associated with the systems are generally viewed as dominated by Fe and S metabolism, with organic carbon production dependent on the lithoautotrophic activities of these organisms. We conducted a survey of pyrosequencing-derived 16S rRNA gene sequences to examine the composition of planktonic microbial communities associated with coal mine voids and corresponding AMD emergence points, where mine void fluids exhibited varying chemical characteristics (pH 3 to 6.6; Fe(II) 0.02 to 8 mM). Phylotypes attributable to lithotrophic lineages were prominent components of libraries recovered from mine void fluids. However, the most abundant phylotypes were attributable to organotrophic lineages within the Clostridia and Euryarchaeota in an acidic mine pool, and the most abundant phylotype detected in a circumneutral mine pool was attributable to Methylococcales. Sequence libraries recovered from AMD emerging at the terrestrial surface were dominated by phylotypes attributable to lithotrophic lineages (e.g. *Gallionella*, *Leptospirillum*) regardless of AMD chemistry. Our results indicate that organotrophic metabolism may play a more prominent role in modulating AMD chemistry than previously thought. Additionally, microbial communities associated with freshly emergent AMD are quite different from those of the mine works.