



Characterization of Fe(II) oxidizing bacterial communities in Appalachian coal mine drainage

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We characterized the microbiologically mediated oxidative precipitation of Fe(II) from coal mine-derived acidic mine drainage (AMD) at two sites in northern Pennsylvania. At the Gum Boot site, dissolved Fe(II) was efficiently removed from AMD whereas minimal Fe(II) removal occurred at the Fridays-2 site. Neither site received human intervention to treat the AMD. Culturable Fe(II) oxidizing bacteria were most abundant at sampling points along the AMD flow path corresponding to greatest Fe(II) removal and where overlying water contained abundant dissolved O₂. Rates of Fe(II) oxidation determined in laboratory-based sediment incubations were also greatest at these points. Ribosomal intergenic spacer analysis and sequencing of 16S rRNA genes recovered from sediment bacterial communities revealed similarities among populations at points receiving regular inputs of Fe(II)-rich AMD and provided evidence for the presence of bacterial lineages capable of Fe(II) oxidation. A notable difference between bacterial communities at the two sites was the abundance of Chloroflexi-affiliated 16S rRNA gene sequences in clone libraries derived from the Gum Boot sediments. Our results suggest that inexpensive and reliable AMD treatment strategies can be implemented by mimicking the conditions present at the Gum Boot field site.