

Microbial communities and their role in Fe(III) hydroxysulfate mineral transformations in a river affected by acid mine drainage

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Located in southeast China, the Hengshi River is continually contaminated by acid mine drainage (AMD) produced from upstream Dabaoshan Mine. AMD contamination gradually decreases throughout the Hengshi River, creating an AMD contamination gradient. Illumina MiSeq sequencing indicated that patterns of spatial and temporal variations in microbial community composition were closely correlated with changes in the physicochemical conditions in the river. pH appeared to be the definitive factor that structured the microbial communities. Acidophiles (*Acidithiobacillus*, *Acidiphilium*, and *Leptospirillum*) were explicitly predominant in extremely acidic environments, whereas the acid-tolerant bacteria (*Gallionella*, *Geobacter* and *Geothrix*) were abundant in the moderately acidic, iron- and sulfate-rich locations. Most of these acidophilic and acid-tolerant bacteria are capable of Fe and S cycling and thus play important roles in the formation and transformation of Fe(III) hydroxysulfate minerals. Mineralogical analyses showed that large amounts of Fe(III) hydroxysulfate minerals presented in the upstream of the Hengshi River. Fe(III) hydroxysulfate minerals are unstable. A microcosm study was conducted to investigate the role of indigenous microbial activity in Fe(III) hydroxysulfate mineral transformation in the AMD-contaminated Hengshi River. The results suggested that microbial activity played a major role in the mineralogical transformation of Fe(III) hydroxysulfate minerals in the Hengshi River. The microbial transformations of Fe(III) hydroxysulfate mineral were mediated by microbial reduction and Fe(III) hydroxysulfate minerals were used as electron acceptors by indigenous microbes. The functional groups that mediated the transformation of Fe(III) hydroxysulfate minerals were Fe(III)-reducing bacteria and/or sulfate-reducing bacteria, including *Geobacter*, *Desulfosporosinus*, *Geothrix*, *Desulfurispora*, *Desulfovibrio*, and *Anaeromyxobacter*.