

Correlated cryogenic STXM and Microprobe study of biofilms from a Sulfide Contaminated Groundwater Spring

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Sulfide in natural springs is an important electron donor for microbial metabolism as it causes accumulation of great biomasses at spring outflows and in the subsurface. It is also toxic to most life. We sampled biofilms from two cold springs (MS4 and MS11) at Alum Rock Park, near San Jose CA, to investigate the diversity and biogeochemical roles of microorganisms whose combined functions detoxify sulfide and enable the establishment of complex microbial communities. Using genome-resolved metagenomic methods, in combination with 16S rRNA analyses, we found the springs to be dominated by filamentous bacteria from the Epsilonproteobacteria and Gammaproteobacteria lineages, which are commonly associated with sulfide oxidation based communities. The main organisms from both springs fall within four groups: Beggiatoa, Thiobacillus, Xanthomonadales, and Chromatiales. Cryo-preserved biofilm samples from the MS4 spring are dominated by thin white streamers (~2-4") in the form of filamentous cells. Correlative cryogenic microprobe analysis at S K-edge and STXM-derived XANES at S L_{2,3}- and C K-edges showed these filaments primarily contain diffuse sulfates and elemental S globules (150-1000 nm) surrounded by a protein layer. By contrast, MS11, with higher sulfate level than MS4, was mostly composed of Epsilonproteobacteria, with filaments mainly composed of carbonates, diffuse sulfates, and generally lacking S globules. Overall these data suggest biogenic sulfide oxidation through a S⁰ intermediate, consistent with the presence of sulfide oxidizers detected by 16S-rRNA analyses at this site.