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Microbial community structure and function related to geochemistry in mercury contaminated stream sediments

Streambed microbial communities were examined in Oak Ridge, TN, along a mercury gradient using a functional gene array and by phylogenetic characterization. The contaminated sites (e.g., mercury at 33.3  $\mu\text{g/g}$ ) exhibited higher gene frequencies in several categories (sulfate reduction, denitrification, carbon utilization, and rubisco) and specific genes associated with a contaminant response (e.g., metal resistance and contaminant degradation) compared to the control site (e.g., mercury at 0.065  $\mu\text{g/g}$ ). The 16S clone libraries from the most highly contaminated site had a higher proportion of cyanobacteria and lower diversity than the control. A synoptic snapshot of six sites (mercury range 0.071  $\mu\text{g/g}$  to 39.1  $\mu\text{g/g}$ ) showed a poor correlation between mercury in stream sediments and in the water ( $r = 0.71$ ). This observation was consistent with the complex relationship between stream sediment and stream water concentration that is likely influenced by geochemical factors and mercury speciation. The relationships among community structure, methyl mercury, total mercury, and other geochemical factors will be examined through further analysis of the data taken over a full year (application of non-linear techniques such as artificial neural networks).