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MICROBIAL COMMUNITY STRUCTURE AND FUNCTION RELATED TO GEOCHEMISTRY IN MERCURY CONTAMINATED STREAM SEDIMENTS

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

Streambed microbial communities were examined in Oak Ridge, TN across a mercury gradient using a functional gene array (FGA) and by phylogenetic characterization. The contaminated sites (e.g., mercury at 33.3 $\mu g/g$) exhibited elevated gene frequencies in general categories (sulfate reduction, denitrification, carbon utilization, and rubisco) and genes that could be associated with a response to contaminants (e.g., metal resistance and contaminant degradation) over the control site (e.g., mercury at 0.065 $\mu g/g$). The 16s clone libraries from the most highly contaminated had a higher proportion of cyanobacteria and lower diversity than the control. A synoptic snapshot of 6 sites (mercury range 0.071 $\mu g/g$ to 39.1 $\mu g/g$) shows a poor correlation between mercury in stream sediments and in the water (r = 0.71). This observation is 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 though further analysis (applying non-linear techniques such as artificial neural networks) of the data taken over a full year.