

## **An Evaluation of Microbial Community Structure and Function in Mercury Contaminated Stream Sediments**

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Although, there has been extensive work on the presence of mercury resistance genes in mercury contaminated environments, there is a relative lack of information on the total bacterial community in highly contaminated mercury sediments. Streams draining DOE facilities in Oak Ridge, TN, have been exposed to discharges of mercury and we are examining the response of streambed microbial communities to this exposure across a Hg contamination gradient using a functional gene array (FGA) and by phylogenetic characterization (a 16S rDNA approach). The version of the FGA used for this study contains 23,864 probes covering 14,000 known microbial functional genes. We hypothesized that there would be a greater diversity of genes related to pollutants at the contaminated sites. In repeated sampling at two to six sites, there was a notable response in the FGA results that appears to be related to seasonal changes. We observed low numbers of genes in all categories at all sites during the winter months. Results from warmer months indicate greater differences among sites. In general, during the warmer months the contaminated sites (e.g., mercury at 33.3 µg/g and numerous other contaminants) exhibited elevated gene frequencies in all general categories compared to the control site (e.g., mercury at 0.065 µg/g). In addition to the genes that could be associated with a response to contaminants (e.g., metal resistance and contaminant degradation), genes involved in metabolism (sulfate reduction, denitrification, carbon utilization) were also elevated at the contaminated sites. We also observed an elevation in the number of different RuBisCO genes present with a much higher number at the most highly contaminated site compared to the control site. The only two currently completed 16S clone libraries are from these sites and interestingly the proportion of cyanobacteria is much higher in the clone library from the contaminated site. Also, the 16S

diversity evident in the contaminated site is lower than that at the control site. In November 2007 (when differences among sites were reduced), a synoptic snapshot of six sites where total mercury in sediments ranged from 0.071 to 39.1  $\mu\text{g/g}$  and where there were wide ranges in concentration of soluble reactive phosphate, nitrate, sulfate, uranium, and total organic carbon (TOC) shows that there was a poor correlation between mercury in stream sediments and mercury 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. During this sampling, concentrations of uranium and nitrate were correlated ( $r = 0.71$  to  $0.90$ ) with gene frequency for nitrogen cycling, sulfate cycling, metal resistance, and organic contaminant degradation. Aside from these relationships, the highest correlations ( $r = 0.65$  and  $0.66$ ) were between TOC and gene frequency for organic contaminant degradation and sulfate and gene frequency for organic contaminant degradation. Thus, for the samples analyzed to date, the FGA appears to be able to detect differences in the diversity of genes for specific functions that can be related to site geochemistry.