Mercury Methylation: Genes and Communities

Environmental Remediation Sciences Program 4th Annual PI Meeting – April 20-23, 2009, Lansdowne, VA

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As part of the mercury Science Focus Area at Oak Ridge National Laboratory (Task 3) we have been examining the genes involved in mercury methylation and the microbial communities that may be involved in mercury methylation in streams contaminated with mercury as the result of past operations in Oak Ridge. We have used a comparative genomics approach and a comparative gene expression methodology to identify candidate mercury methylation genes in *Desulfovibrio*. We have identified a number of candidate genes using the comparative genomics approach and several of these have been tested to see if they confer mercury methylation abilities in *Desulfovibrio* unable to methylate mercury. To date none have proved to have this ability. The comparative gene expressions methods have indicated that the genes involved in methylation are likely constitutive as the addition of mercury at levels even beyond what would be expected in the environment does not induce notable changes in gene expression in either the methylators or non-methylators tested under sulfate respiring conditions. We are currently testing this response under other growth conditions. Using both a functional (functional gene array) and phylogenetic

(454 sequencing of 16S genes) approach we examined the community characteristics of streambed microbial communities across a range of mercury contamination. We hypothesized that there is a greater diversity of genes related to pollutants at the contaminated sites but a lower phylogenetic diversity. We also hypothesized that the number of deltaproteobacteria (the group involved in methylation) would be positively correlated with methyl mercury concentrations. In a preliminary analysis of the data we found pronounced phylogenetic and functional differences that appear to be related to seasonal trends. Also, we have found that representatives of the deltaproteobacteria are present at all sites though at relatively low levels. The predominant groups found in these aerobic surface sediments were cyanobacteria, betaproteobacter, and verrucomicrobia. More detailed analysis of the data will be done to test our specific hypotheses. Future research will focus on comparative genomics and transposon mutagenesis approaches for identifying the genes involved in mercury methylation in *Desulfovibrio* and *Geobacter* and in quantifying the presence of those genes in the environment.