Organismal and Environmental Level Investigations of the Mercury Methylating Genes hgcAB

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The discovery and verification of the mercury metyhylation genes, hgcAB, has been a seminal discovery by the ORNL Hg SFA. Their discovery now opens up new avenues of research. A consequence of this discovery is verification of the prediction that the hgcAB genes can be used as a prediction of a cells capability to methylate mercury. Validation of this prediction has allowed for Hg-methylating organisms to now be identified in both the bacterial as well as archaeal branches of the tree of life and this activity now encompasses all anaerobic metabolisms from primary fermentors through to the methanogens. The latter is particularly relevant to agricultural environments as well as treatments plants. A recent question that has come to light as a result of this work is why are the rates and extents of methylation vastly different in methylating organisms when the same genes/proteins are involved, and we are working to address this question.

A scanning of all metagenomes to date reveals that while the hgcAB gene pair is relatively rare, there are environments where the genes appear to be more abundant than others. These more abundant environments include a variety of sediments and polluted marine areas as well as northern latitude permafrost while being almost absent from mammalian microbiomes and marine/ocean environments. However, differences in sequencing technologies, depth of coverage and other factors make direct comparisons difficult at best. From the apparently more abundant environments, identification of the organisms possessing the gene pair was overall successful except that there were no known organisms to correlate the hgcAB gene sequences to for the oxygen minimum zone of the North Pacific Ocean, permafrost in Bonanza Creek, AK or the hypersaline soda lakes. Further, several cases were found where these two genes appeared to be fused in Pyrococcus furiosis and uncultured members of the OP8 and OP9 candidate divisions. P. furiosis was not able to methylate Hg, suggesting that the gene fusion eliminated this activity. Further, our analyses suggest that the gene pair may have originated in the Archaea and calls into question whether the two separate genes or the fused genes are the ancestral form. Finally, co-occurrence analysis within the metagenomes suggests that particular pairings of organisms may be preferred and may have facilitated lateral gene transfer of hgcAB over time.