The Biomolecular and Genetic Basis of Mercury Methylation

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Abstract:

Methylmercury is a potent neurotoxin produced from inorganic mercury by anaerobic microorganisms. However, until now the genes and proteins involved have remained unidentified despite more than four decades of work. By combining chemical reasoning, genomics, structural bioinformatics, and microbiology, we have discovered a two-gene cluster, *hgcAB*, required for mercury methylation by *Desulfovibrio desulfuricans* ND132 and *Geobacter sulfurreducens* PCA. In either bacterium, deletion of *hgcA*, *hgcB* or both genes abolishes mercury methylation. The genes encode a putative corrinoid protein, HgcA, and 2[4Fe-4S] ferredoxin, HgcB, consistent with roles as a methyl carrier and an electron donor required for corrinoid cofactor reduction, respectively. This two-gene cluster is present in all confirmed methylating bacteria and is absent in non-methylators. Homologs have been found in the genomes of more than 50 diverse microorganisms, suggesting a common mercury methylation pathway among bacteria and archaea with sequenced genomes. The identification *hgcA* and *hgcB* is a critical step toward identifying sources of microbial methylmercury production in the environment. Our focus on obtaining chemical and biological mechanistic insight will lead to improved models of global mercury cycling and earth systems modeling of mercury fate and transport.