Protein components of the microbial mercury methylation pathway

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Abstract

Mercury (Hg) in the environment and the resulting methylmercury (CH_3Hg^+) produced by microorganisms has emerged as a global concern in the last 50 years after a series of high profile, large scale contamination events, increased burning of fossil fuels, and a more recent major escalation of widespread use of Hg in artisanal gold mining. The Hg cycle in the environment is complex and still not completely known. Among the many different forms of Hg present in the environment, Hg, mainly as Hg(II), has been known to be converted to the more toxic CH_3Hg^+ by microorganisms. CH_3Hg^+ accumulates in the aquatic food chain and humans are eventually exposed to the toxic CH_3Hg^+ through their diets. When exposed to elevated levels of CH_3Hg^+, symptoms include mainly neurological pathologies along with reduced kidney and liver function. However, until recently the biotic mechanism of the conversion of Hg(II) to CH_3Hg^+ was not known. It has now been shown that a pair of genes, *hgcA* and *hcgB*, present in a variety of microorganisms, are necessary for bacterial Hg methylation to occur. The structure and functions of the proteins encoded by these genes are still being explored, and here new data are shown for residues in these proteins that suggest key structural elements necessary for the Hg methylation reaction. Also presented are data from other possible proteins in the carbon flow and cobalamin assembly pathways leading up to Hg methylation by HgcA and HgcB. The new work described here is significant in that it not only adds to the expanding base of knowledge of microbial Hg methylation with the identification of *hgcA* and *hgcB*, but also shows specific catalytic residues of HgcA and HgcB that can be further studied in organisms that methylate Hg. These data and the mutants designed to facilitate its acquisition can be used in future efforts to identify other members of the Hg methylation pathway. These data and constructs will also aid in future attempts to determine if the two genes evolved for the sole purpose of methylating Hg(II) or to support the life cycle of the organism harboring these genes in another, yet to be determined capacity.