A comparison of Hg(II) uptake and accumulation between mercury methylating and non-methylating bacteria

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Hg(II) uptake is a key first step in the methylation of Hg(II) by anaerobic bacteria and thus, conditions affecting its transport greatly influence the amount of methylmercury which accumulates. Experiments with mercury methylating and non-methylating bacteria support a common active Hg(II) uptake mechanism inhibited by Zn(II) and Cd(II) but not other divalent metals. Thus, Hg uptake appears to be a result of accidental import during the acquisition of essential trace metals, such as Zn(II). While the mechanism of uptake is similar in methylating and non-methylating bacteria, the fate of the Hg(II) following its uptake is quite different. In the Hg methylating strains, Geobacter sulfurreducens and Desulfovibrio sp. ND132, methylmercury is produced in the cytosol and rapidly exported out of the cell. Thus the accumulation of Hg(II) in methylating organisms is offset by the export of methylmercury. In contrast, Shewanella oneidensis does not produce methylmercury, and this is reflected in higher Hg(II) accumulation rates and yields as compared to other methylating strains. Despite the lack of methylation, however, cells of S. oneidensis appear to export Hg(II) possibly as a complex with a thiol such as glutathione. The export of Hg(II) or methylmercury in these different bacteria may represent metal homeostasis mechanisms to deal with the accidental uptake of toxic heavy metals such as Hg(II) at sub-toxic concentrations, where the mer-mediated Hg resistance pathway is not necessary.