# 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(II) uptake appears to be a result of accidental import during the acquisition of essential trace metals, such as Zn(II). While the mechanism and rate of uptake is remarkably similar in methylating and non-methylating bacteria, differences have been observed in Hg bioavailability to organisms living at different redox zones. For instance, a fermentative firmicute, *Ethanoligenes harbiense*, had low affinity for Hg(II) and exhibited the lowest accumulation rates relative to other organisms tested. The iron-reducing bacteria, *Shewanella oneidensis* and *Geobacter sulfurreducens* both showed similar initial uptake rates and specificities for Hg-thiol complexes with some thiol ligands, such as cysteine, enhancing uptake and other thiols such as penicillamine or glutathione inhibiting uptake. In contrast, the sulfate-reducing bacterium, *Desulfovibrio* sp. ND132, isolated from highly sulfidic estuarine waters, had the highest affinity for Hg thiol complexes and was able to take up Hg bound to a variety of thiols, including both penicillamine and glutathione, neither of which support Hg uptake in iron-reducing bacteria. These results demonstrate differences in Hg bioavailability across taxa and respiratory guild. Data obtained from this study is critical for understanding how different populations respond to changing Hg speciation in order to better predict methylmercury accumulation in the environment.