The Reduction, Oxidation, and Methylation of Mercury by Anaerobic Microorganisms

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Inorganic mercury [Hg(II)] can be methylated to methylmercury (MeHg) by certain strains of sulfate and iron reducing bacteria in anaerobic envirnments. However, this process is affected by the redox transformation and chemical speciation of Hg which can influnce Hg uptake and methylation by microorganisms. In this study, we investigated the reduction, oxidation, and methylation of mercury by three microorganisms within the *Deltaproteobacteria* under dark, anaerobic conditions in phosphate buffered saline (PBS) (pH=7.4). Two known methylators *(Geobacter sulfurreducens* PCA and *Desulfovibrio desulfuricans* ND132) and a nonmethylator (*Desulfovibrio alaskensis* G20) were used for comparative studies. Results show that interactions between mercury and these microorganisms differ greatly due to their phylogenetic and surface characteristics. *G. sulfurreducens* PCA is able to reduce Hg(II) to Hg(0), and reduction occurred upon direct contact of Hg(II) with cells. The reduction followed a pseudo-first order kinetics, with a half-life of < 2 h. The reduction was also found to depend on the cell density or cell/Hg ratio with a maximum of ~ 60% reduction of Hg(II) (50 nM) observed at a cell density of 10^{11} L^{-1}. However, neither *D. desulfuricans* ND132 nor *D. alaskensis* G20 was able to

reduce Hg(II) under the same experimental conditions. Both strains were instead found to oxidize Hg(0) to Hg(II), which was subsequently methylated by *D. desulfuricans* ND132 under anoxic conditions. Our results demonstrate the multi-functional roles of microcroorganisms in Hg species transformation and thus have important implications to the geochemical cycling and biological methylation of Hg in the environment.