Synergistic effects of a chalkophore, methanobactin, on microbial methylation of mercury

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BER Program: Subsurface Biogeochemical Research

Project: Oak Ridge National Laboratory Critical Interfaces Scientific Focus Area

Project Website: https://www.esd.ornl.gov/programs/rsfa/

Project Abstract: Microbial production of the neurotoxin, methylmercury (MeHg), is a significant health and environmental concern as it can bioaccumulate and biomagnify in the food web. While the genetic basis of microbial mercury methylation is known, factors that control net methylmercury (MeHg) production in the environment are still poorly understood. A chalkophore or a copper-binding compound, termed methanobactin (MB), has been shown to form strong complexes with mercury [as Hg(II)] and also enables some methanotrophs to degrade MeHg. It is unknown, however, if Hg(II) binding with MB can also impede Hg(II) methylation by other microbes. Contrary to expectations, MB produced by the methanotroph *Methylosinus trichosporium* OB3b (OB3b-MB) enhanced the rate and efficiency of Hg(II) methylation more than that observed with thiol compounds (such as cysteine) by the mercury-methylating bacteria, *D. desulfuricans* ND132 and *G. sulfurreducens* PCA. Compared to no-MB controls, OB3b-MB decreased the rates of Hg(II) sorption and internalization, but increased methylation by 5–7 fold, suggesting that Hg(II) complexation with OB3b-MB facilitated exchange and internal transfer of Hg(II) to the HgcAB proteins required for methylation. Conversely, addition of excess amounts of OB3b-MB or a different form of MB from *Methylocystis* strain SB2 (SB2-MB) inhibited Hg(II) methylation, likely due to greater binding of Hg(II). Collectively our results underscore complex roles of exogenous metal-scavenging compounds produced by microbes and their interactions with others in controlling net production and bioaccumulation of MeHg in the environment.