Anaerobic Mercury Methylation and Demethylation by Geobacter *bemidjiensis* Bem

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Microbial methylation and demethylation are two competing processes controlling the net production and bioaccumulation of neurotoxic methylmercury (MeHg) in natural aquatic ecosystems. Although mercury (Hg) methylation by anaerobic microorganisms and demethylation by aerobic Hg-resistant bacteria have both been extensively studied, little attention has been given to MeHg degradation by anaerobic bacteria, particularly the iron-reducing bacterium *Geobacter bemidjiensis* Bem. We report, for the first time, that the strain *G. bemidjiensis* Bem can both methylate inorganic Hg and degrade MeHg concurrently under anoxic conditions. Results suggest that *G. bemidjiensis* cells utilize a reductive demethylation pathway to degrade MeHg, with elemental Hg(0) as the major reaction product, possibly due to the presence of homologs encoding both organo-mercurial lyase (MerB) and mercuric reductase (MerA) in this organism. Similarly as observed with the *G. sulfurreducens* PCA strain, *G. bemidjiensis* Bem cells can mediate multiple reactions including Hg/MeHg sorption, Hg reduction and oxidation, resulting in both time and concentration dependent Hg species transformations. Moderate concentrations (10–500 μM) of Hg-binding ligands such as cysteine enhance Hg(II) methylation but inhibit MeHg degradation. These findings indicate a cycle of methylation and demethylation among anaerobic bacteria and suggest that *mer*-mediated demethylation may play an important role in the net balance of MeHg production in anoxic water and sediments.