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When MerB Goes Solo: Alternative Pathway for Anaerobic Mercury Cycling

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Mercury is a globally distributed contaminant whose environmental and health impacts are driven by the formation and persistence of methylmercury, a potent neurotoxin that bioaccumulates in aquatic food webs. In anoxic environments, inorganic mercury is converted to methylmercury by anaerobes such as SRB, FeRB and archaea. Demethylation processes, across the oxygen concentration gradient, limit methylmercury accumulation but remain less well constrained especially in anaerobic conditions. Reductive demethylation in oxic conditions mediated by the mercury resistance (mer) operon is a well-established detoxification pathway. Two enzymes are involved in this process: organomercury lyase or MerB, a small and poorly conserved protein and mercuric reductase MerA, a large and high energy demanding protein. MerB cleaves the C-Hg bond and the mercuric reductase MerA reduces the resulting Hg(II) to volatile Hg(0) preventing Hg(II) accumulation and cytotoxicity.

Recent metagenomic surveys have revealed a broad and phylogenetically diverse distribution of merB genes that lack the canonical downstream merA. The physiological function of these orphaned merB genes, and the mechanisms that prevent intracellular Hg(II) accumulation following C-Hg bond cleavage, remain unresolved.

We will investigate MerB-mediated methylmercury demethylation in anaerobic fermentative bacteria using *Clostridium acetobutylicum*, a model anaerobe that lacks merA. By heterologous expression of canonical and orphaned merB variants and by combining isotope-tracer experiments with direct quantification of Hg species, we test whether MerB-generated Hg(II) is reduced through fermentation-linked electron transfer pathways. We expect this work to demonstrate that MerB can function independently of MerA in anoxic systems by coupling demethylation to non-canonical Hg(II) reduction, thereby expanding current models of microbial mercury detoxification. These findings are anticipated to inform both mercury biogeochemical cycling frameworks and the development of anaerobic bioremediation strategies.