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Mercury Microbiology: Resistance Systems, Environmental Aspects, Methylation, and Human Health

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Abstract Mercury has no beneficial biological role, and is highly toxic to all forms of life. Bacteria are involved in the global environmental cycling of mercury, both by reducing Hg^{2+} to metallic Hg^0, which is less soluble in aqueous systems and therefore less bioavailable, and by oxidizing and methylating Hg species, and in the process making Hg more bioavailable and more highly toxic. The most thoroughly studied bacterial biotransformation of mercury is reduction by the widely distributed *mer* resistance operons found on plasmids and transposons in Gram-negative and -positive bacteria. The products of these resistance operons transport ionic Hg^{2+} from outside the cell to the cellular cytoplasm, where mercuric reductase reduces divalent Hg^{2+} to Hg^0, which is less toxic than Hg^{2+}. Metallic mercury vapor, Hg^0, is volatile under aerobic conditions, leaves the cell by passive diffusion, and is volatilized from the growth environment. Sometimes, additional gene(s) determine organomercurial lyase, the enzyme that cleaves organomercurial compounds to inorganic Hg^{2+}, which is then reduced to Hg^0. Two types of *mer* operons ("narrow spectrum" with inorganic Hg^{2+} resistance and "broad spectrum" with both organomercurial and inorganic mercury resistances) confer high levels of resistance on host bacteria. The expression of *mer* resistance genes is primarily regulated by the MerR protein, which is the prototype of an increasing family of metal and other effector-responsive transcriptional activators. Methylation of inorganic Hg^{2+} to CH_3Hg^+ is thought to occur nonenzymatically (perhaps even extracellularly) with microbially synthesized *S*-adenosylmethionine as methyl donor.

1 Introduction

Resistance to mercury and organomercurials was the first studied and is still the best understood of toxic metal resistance systems. Other than that for arsenic, it might be the most widely found toxic inorganic ion resistance system and occurs in all bacterial divisions where it has been sought. Mercury resistance genes are frequently found in new microbial total genome sequences. The current best overview of bacterial mercury resistance is found in Barkay et al. (2003). Mercury resistance occurs widely in Gram-negative and -positive bacteria and in environmental, clinical, and industrial isolates, and mercury resistance genes are frequently found on plasmids and encoded by transposons. The mercury resistance transposon Tn*21* occupies about 8 kb of the 94-kb plasmid R100 (NCBI accessions NC_002134; gi: 9507549), the first multidrug resistance plasmid found in Japan 50 years ago, together with several antibiotic resistance determinants. However, chromosomal mercury (organomercurial) resistance is also common, for example in *Bacillus* isolates (Narita et al. 2003).

The mechanism of Hg^{2+} resistance is specific and unlike those for other toxic metal ions. In the *mer* resistance mechanism, Hg^{2+} is bound in the periplasm of Gram-negative bacteria or outer surface of Gram-positive bacteria by MerP, imported into the cytoplasm of the cell by specific membrane-bound transporters (three types have been found: MerT, MerC, and MerF), and then reduced from Hg^{2+} to Hg^0 by the enzyme mercuric reductase, MerA.

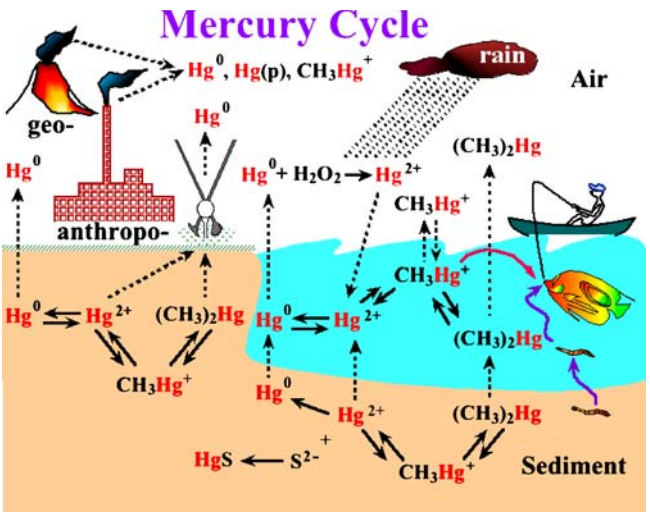

Fig. 1 The global mercury geocycle (modified from Barkay et al. 2003)