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TITLE: Mercury Adaptation among Bacteria from a Deep-Sea Hydrothermal Vent

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ABSTRACT:

ABSTRACT Since deep-sea hydrothermal vent fluids are enriched with toxic metals, it was hypothesized that (i) the biota in the vicinity of a vent is adapted to life in the presence of toxic metals and (ii) metal toxicity is modulated by the steep physical-chemical gradients that occur when anoxic, hot fluids are mixed with cold oxygenated seawater. We collected bacterial biomass at different distances from a diffuse flow vent at 9°N on the East Pacific Rise and tested these hypotheses by examining the effect of mercuric mercury [Hg(II)] on vent bacteria. Four of six moderate thermophiles, most of which were vent isolates belonging to the genus *Alcanivorax*, and six of eight mesophiles from the vent plume were resistant to 10^{-10} M Hg(II) and reduced it to elemental mercury [Hg(0)]. However, four psychrophiles that were isolated from a nearby inactive sulfide structure were Hg(II) sensitive. A neighbor-joining tree constructed from the deduced amino acids of a PCR-amplified fragment of *merA*, the gene encoding the mercuric reductase (MR), showed that sequences obtained from the vent moderate thermophiles formed a unique cluster (bootstrap value, 100) in the MR phylogenetic tree, which expanded the known diversity of this locus. The temperature optimum for Hg(II) reduction by resting cells and MR activity in crude cell extracts of a vent moderate thermophile corresponded to its optimal growth temperature, 45°C. However, the optimal temperature for activity of the MR encoded by transposon Tn 501 was found to be 55 to 65°C, suggesting that, in spite of its original isolation from a mesophile, this MR is a thermophilic enzyme that may represent a relic of early evolution in high-temperature environments. Results showing that there is enrichment of Hg(II) resistance among vent bacteria suggest that these bacteria have an ecological role in mercury detoxification in the vent environment and, together with the thermophilicity of MR, point to geothermal environments as a likely niche for the evolution of bacterial mercury resistance.

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