

Phylogeny of prokaryotes involved in mercury speciation in free-living and particulate-attached fractions in Minamata Bay, Japan

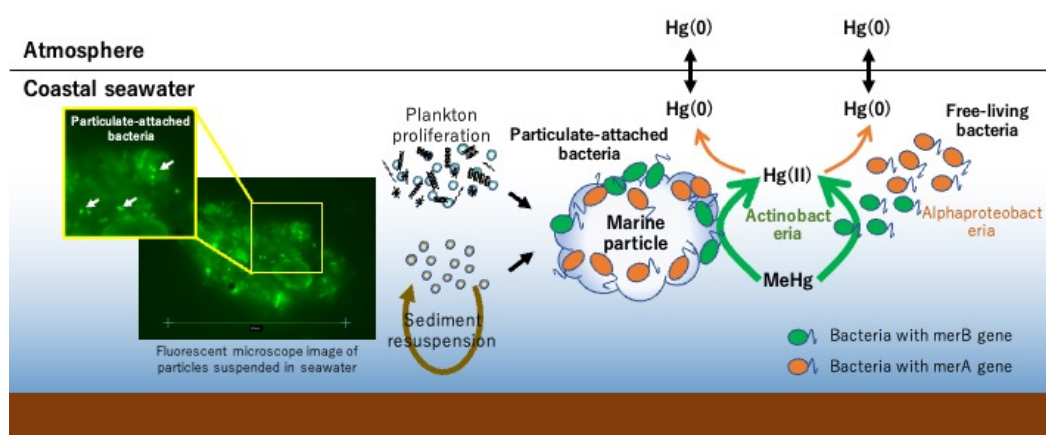
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Marine prokaryotes are involved in mercury (Hg) speciation in marine environments. However, information regarding the specific microbial lineages contributing to Hg speciation (namely, methylation, demethylation, and reduction) in seawater remains limited. In this study, we investigated the genes involved in methylmercury (MeHg) demethylation (*merB*), Hg reduction (*merA*), and Hg methylation (*hgcAB*) using a metagenome analysis encompassing free-living and particle-attached fractions in Minamata Bay, Japan. The Hg-related gene analyses have revealed that a high *merB* abundance rather than *merA* was observed when compared using all samples, suggesting that microbial MeHg demethylation could be prominent rather than Hg reduction in the seawater column. Phylogenetic analyses revealed that Alphaproteobacteria and Actinobacteria were dominant in the total *merA* and *merB*-like sequences, respectively. These results are important for understanding the role of microorganisms in mercury speciation (particularly in the removal process) in the marine environment.



The processes of methylmercury degradation and mercury reduction by free-living and particle-attached bacteria in coastal seawater