

Genome-resolved investigation of potential new mercury-methylating marine bacterial phyla

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Microbes that can transform aqueous mercury (Hg) into methylmercury (MeHg) require the gene pair *hgcAB*, previously associated only with anaerobic bacteria. Using genome-resolved metagenomic analyses, we found potential new Hg-methylating bacterial phyla in Antarctic seawater and Canadian coastal waters associated with variable degrees of oxygenation. Among these new phyla was a clade of *Marinimicrobia* with evidence to suggest acquisition of *hgcAB* through lateral gene transfer, as well as members of *Calditrichaeota*, SAR324 and *Nitrospina*. HgcAB-carrying *Marinimicrobia* and *Nitrospina* appear to be environmentally widespread across ocean sites, with major roles to play in marine biogeochemical cycling. Our findings suggest a broadened habitat range for Hg-methylating microorganisms than previously surmised. Under plausible climate change scenarios, these findings imply a need to assess possible negative ecosystem and human health impacts from increased mercury methylation potential.