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Mercury methylation genes are widespread and diverse across marine hydrothermal vents

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Mercury (Hg) and methylmercury (MeHg) are contaminants of worldwide concern that pose significant risks to human health, primarily through seafood consumption. In the marine environment, Hg is supplied by multiple sources, including submarine hydrothermal vents (HV). HV are unique geochemical environments exhibiting steep physicochemical conditions, high concentrations of dissolved metals and harbouring unique microbial communities. Despite their geochemical significance, HV remain poorly investigated in the context of Hg methylation, which is carried out by anaerobic microorganisms containing the *hgcA* gene used as a proxy for the formation of MeHg.

Aiming at describing the global distribution and environmental drivers of Hg-methylating microorganisms in marine HV systems, we analysed 1,114 metagenomes from 28 locations worldwide across different types of marine HV and associated habitats, including seawater, plume, vent fluid, chimney, biofilms, and sediments. We determined the prevalence of the *hgcA* gene, and we detected it in a total of 18 locations spanning the Pacific, Atlantic, Arctic, and Indian Oceans, across different HV geological types. *hgcA* gene was detected in chimney, biofilm, sediment, and vent fluid habitats, but not in plume or background seawater; being more abundant in carbonate serpentinite vents compared to other HV types. *hgcA* gene was mainly related to *Desulfobacterota* (38.2% of total *hgcA*-relative abundance), *Myxococcota* (26.6%), *Bacillota* (6.5%), and *Chloroflexota* (5.1%). HV geological types influence the composition of Hg-methylating microbial communities, as previously shown for total prokaryotes [1]. Notably, pH (ranging from 1.75 to 11) significantly correlated positively with *hgcA* gene relative abundance and appeared critical for Hg-methylating community.

Together, these findings demonstrate that MeHg formation may span acidic to alkaline HV systems worldwide, firmly establishing HV as habitats for Hg-methylating microorganisms and emphasizing their contribution to the oceanic Hg cycle at microbial level.

[1] Zhou, John, Anantharaman, Reysenbach (2022), *Microbiome*, vol. 10, no. 1, p. 241. *Global patterns of diversity and metabolism of microbial communities in deep-sea hydrothermal vent deposits*