Title: Distribution and function of prokaryotes involved in mercury methylation, demethylation, and reduction in the western North Pacific Subtropical Gyre

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Journal: Frontiers in Microbiology (Impact factor 2025: 4.5)
DOI: https://doi.org/10.3389/fmicb.2025.1642479

Methylmercury (MeHg) is a neurotoxic compound that bioaccumulates, posing risks to ecosystems and human health. Microorganisms mediate Hg transformations via hgcAB gene (methylation), merB gene (demethylation), and merA gene (reduction), yet these pathways have rarely been assessed together in the open ocean. Here, we combined metagenomics with measurements of total mercury (THg) and MeHg across the western North Pacific subtropical gyre to assess the distribution of Hg-related microbes. THg showed no significant depth trend, whereas MeHg increased with depth. The hgcA was enriched in the mesopelagic zone (500–1,500 m), coinciding with elevated MeHg, and its greater abundance relative to merB, suggesting that MeHg production likely exceeded degradation. Phylogenetic and functional analyses revealed Nitrospina as the primary methylator, also showing a link to the nitrogen cycle. Furthermore, diverse microorganisms could potentially be responsible for both MeHg degradation and Hg(II) reduction. This study contributes to deepening our understanding of Hg cycling in the open ocean.

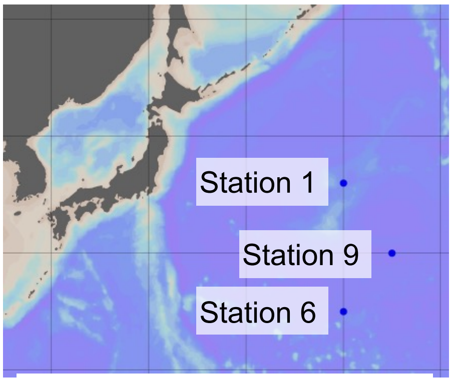

Fig. 1. Sampling stations

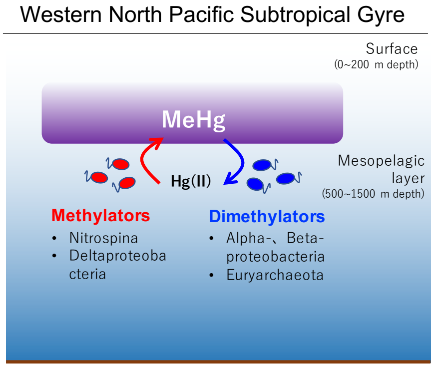

Fig. 2. Relationship between chemical transformation of Hg and microorganisms in the mesopelagic zone