Goldschmidt 2026 Abstract
https://doi.org/10.46427/gold2026.37543

Distribution of putative mercury methylators along environmental gradients in a redox-stratified brackish system

JÚLIA DORDAL-SORIANO[1], MEIFANG ZHONG[2], THIBAUT COSSART[2], ISABEL SANZ-SÁEZ[2], TOVE BRATTHÄLL[2], PANAGIOTA XANTHOPOULOU[3], CLARA RUIZ-GONZÁLEZ[1], ERIK BJÖRN[2], ERIC CAPO[2] AND ANDREA G. BRAVO[1]

[1]Institute of Marine Sciences (ICM-CSIC)
[2]Umeå University
[3]University of the Aegean

Neurotoxic methylmercury (MeHg) is formed from inorganic mercury (Hg^{2+}) by microorganisms carrying the *hgcAB* gene pair, particularly under oxygen-deficient conditions. Stratified fjords, although being naturally prone to oxygen deficiency due to restricted water circulation, low temperatures, and limited water exchange, remain understudied ecosystems regarding Hg methylation. Hence, we investigated the distribution of putative Hg-methylating microorganisms and their environmental associations in Rossfjordvatnet, a stratified brackish enclosed fjord-like system in northern Norway. Water samples were collected for Hg speciation, environmental, and metagenomic analyses at seven depths along the 40 m water column, characterized by oxic surface freshwaters and anoxic marine bottom waters with high H_2S accumulation. Our results showed that *hgcA* gene abundances were very low in oxic waters, increased along the redoxcline, and peaked in euxinic layers, where higher concentrations of dissolved Hg(II)-sulfide complexes were also detected. In contrast, total prokaryotic cell abundance was lowest in the euxinic waters, noting that the Hg-methylating community increased despite a decrease in overall prokaryotic biomass. Positive relationships were observed between *hgcA* gene abundances and H_2S, dissolved organic carbon, total dissolved nitrogen, humic-like dissolved organic matter, and nutrients (e.g., silicate and ammonia), whereas negative correlations were observed with dissolved oxygen and nitrate species. Contrary to the pattern observed from the *hgcA* gene abundance, MeHg concentrations peaked at 10 m depth, below the redox transition zone, and Hg methylation rates (K_m) peaked at 20 m, showing that MeHg formation and MeHg accumulation occur in distinct redox niches. HgcA amino acid sequence richness was also higher in sulfidic layers, and members of Desulfobacterota were identified as the dominant putative Hg methylators, followed by representatives of Myxococcota and the PVC superphylum. Altogether, our findings provide new insights into the chemical and environmental variables influencing the vertical structure of Hg-methylating communities in brackish euxinic systems, which is crucial to better understand how the possible expansion of oxygen deficient areas will affect Hg biogeochemical cycling under future global change scenarios.