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Polar microbes and their implications in the aquatic mercury cycle

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The methylmercury has the feature, in addition to its high toxicity for living organisms, to be easily incorporated, bioaccumulated and biomagnified through the food web in aquatic systems. Recently, the microorganisms implicated in the transformation of mercury to methylmercury have been found much more diverse than previously thought. Among them, 9 methanogenic Archaea strains are able to methylate the mercury in pure culture. However, few proofs exist *in situ* in polar aquatic systems. Antarctic polar regions receive atmospheric mercury through long-range transport of foreign emissions. In a context of increasing releases of heavy metals in aquatic environments and atmosphere, it is a crucial objective to elucidate the fate of mercury in Antarctic polar aquatic ecosystems and the role Archaea could play in mercury transformations. Hence, microbial diversity was investigated in pristine Antarctic lakes (South Shetland Islands, Antarctic, Chile) and continental sub-Antarctic beaver ponds (Tierra del Fuego, Chile) where benthic total mercury concentration was 14 ± 6.5 and 89 ± 13 ppm, respectively. Until 6.3% of the active community could be constituted by putative methylators and a positive significant correlation was found between total mercury concentration and putative methylator relative abundance (linear model, p -value=0.001). Putative methylator Archaea *Methanoregula* and *Methanosphaerula* have been detected but did not seem active in the studied ecosystems (RNA metabarcoding VS DNA metabarcoding).

Combined with these molecular data, mercury methylation and methylmercury demethylation activities were performed by addition of enriched stable isotopes of inorganic mercury and methylmercury, respectively and we expect to find highest methylation rates in the rich-organic matter ecosystems such as sub-Antarctic beaver ponds.