Latitudinal variations of Hg stable isotopes in seabirds document MeHg biogeochemitry in the Southern Ocean

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Mercury (Hg) biogeochemistry in the Southern Ocean ecosystems remains barely investigated and determining its fate and impact represents a major challenge. Since seabirds are exposed to large quantities of Hg via dietary input, mainly in the form of methylmercury (MeHg), they are effective bioindicators of Hg marine contamination. In this study, Hg isotopic composition was measured in blood of two ubiquist seabird models (penguins and skuas) breeding in the French Southern Ocean territories. A wide latitudinal gradient was covered from Adélie Land (66°39′S, Antarctic zone) to Crozet Islands (46°25′S, subantarctic zone) and Amsterdam Island (37°47'S, subtropical zone). Mass-dependent (MDF) and mass-independent (MIF) Hg isotopic values segregated populations geographically. Blood samples from Antarctic seabirds displayed lower MDF (δ^{202}Hg) values (-0.02 to 0.79 ‰) than subantarctic (0.88 to 2.12 ‰) and subtropical (1.44 to 2.37 ‰) species. However, mean odd-MIF values (Δ^{199}Hg) ranged slightly from Antarctic (1.31 to 1.73 ‰) to subtropical (1.69 to 2.04‰), thus exhibiting a total enrichment in the order of 0.3 ‰ between sites. This indicates that MeHg photodemethylation extrapolated from Hg odd-MIF values is limited, inferring that most of the bioaccumulated MeHg has a mesopelagic origin. The larger latitudinal variations of MDF suggests that greater biogenic transformation of Hg, such as net methylation, occurs in subtropical waters compared to Antarctic ones. This latitudinal-related biogenic effect reflects both regional mixed layer depth dynamics (vertical transport) and driven biological turnover (microbial activity). This study also demonstrates how complex interactions between marine Hg biogeochemistry and regional ocean dynamics drive specifically seabirds' exposure to Hg contamination.