Sulfur isotope variability of DMS(P) production by antarctic sea ice microbial communities

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Antarctic sea ice microalgal communities are known to produce very large amounts of the organic sulfur metabolite dimethylsulfoniopropionate (DMSP), the biological precursor of the semi-volatile dimethylsulfide (DMS). In the remote atmosphere of polar oceans, DMS is a major precursor of non sea salt sulfate aerosols which directly influence cloud formation and albedo. Hence, it is essential to understand the processes controlling DMSP production by sea ice microalgae, and to assess how much of its degradation product, DMS, is effectively transferred to the atmosphere. Despite several field measurements of bulk ice DMS(P) concentrations, punctual measurements of sea ice-atmosphere DMS fluxes, and experiments with isotopically-labelled DMS(P) in brine, our knowledge of the sea ice DMS cycle remains very limited. In this study, we present a novel approach using sulfur natural isotope ratio ($\delta^{34}S$). We report the first profiles of the $\delta^{34}S$ of DMS(P) in natural sea ice cores from the Ross Sea and Weddell sea, by combining dry crushing extraction of DMS(P), and $\delta^{34}S$ determination at the picomole level with GC-MC-ICPMS. Depth-profiles of $\delta^{34}S$ of DMSP revealed considerable variability between regions, across seasons, and between sea ice horizons, with values ranging between 9.2 and 21.9‰. This variability is remarkable considering the relative sulfur isotopic homogeneity of DMSP in oceanic waters (18.9-20.3‰). The most ^{34}S depleted values, and highest spatial variability, were mainly observed in surface and interior ice in the winter and early spring, where adapted microalgae thrive in the extreme conditions (e.g. temperature and salinity) of brine microenvironments as shown by ancillary physical and biological data . This, combined with the remarkable consistency (~21‰) of the $\delta^{34}S$ of SO_4 in the same ice samples, suggests that the observed variability in DMSP probably originated from distinct metabolic pathways of DMSP synthesis.