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Revelation of differently efficient methanotrophs in polar stratified water by a comparative application of methane oxidation methods

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Microbial oxidation in the oceans limits methane emissions to the atmosphere. This limitation depends on the efficiency of the present methanotrophic community. In the stratified water column of the arctic Storfjorden, East of Spitsbergen, we revealed differently efficient methanotrophic communities with a combination of biogeochemical and microbiological tools. Radioactive tracers ([3H]-CH4 and [14C]-CH4) in combination with the isotopic ratio of C-CH4 were used to estimate microbial methane oxidation and 16S rRNA DGGE-fingerprinting as well as functional marker gene analysis (pmoA, mxaF) were employed to characterize the associated microbial/methanotrophic communities. Our results indicate a quasi steady state established in surface and intermediate waters with methane plumes which are ongoing but not efficiently oxidized by methanotrophs, harboring a different methane oxidizing enzyme than methanotrophs in the deep basins. Oxidation rates derived from [14C]-CH4-incubations were lower than the rates derived from [3H]-CH4-incubations although 500 times more [14C]-CH4 was injected than [3H]-CH4 suggesting that the methanotrophs were at their maximum uptake velocity. The assumption was confirmed by the carbon isotope ratio of methane which did not show a strong enrichment in 13C. In contrast, in the deep basins (>80 m) sporadic methane inputs appear to be rapidly consumed by methanotrophic bacteria which seem to be more efficient in the oxidation of methane. Tracer incubations revealed that methanotrophs in the deep basins were not at their maximum uptake velocity. They could oxidize more CH4 than there was naturally available at the time resulting in higher rates derived by [14C]-CH4-tracer incubations. The potential of increased CH4 consumption in the deep basin was confirmed by the isotopic ratio showing 13C enriched CH4. All results indicate that low-affinity methanotrophic microbial communities live in the deep basins of the Storfjorden while high- affinity methanotrophs exist in the water above. The presence of different methanotrophic communities in the Storfjorden was confirmed by molecular microbiological results.