Microbial methane consumption in the water column of the central Baltic Sea (Gotland Deep)

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Scientific Background

Compared to the number of studies on the microbial processes of methane oxidation in sediments, water column studies are scarce, and could to date just identify the turnover through oxygen and sulfate. Extensive water column investigations in the Baltic Sea identified the strongest methane enrichment within the stagnant anoxic water bodies of the deep basins. In contrast, surface water methane concentrations in these areas are only slightly enriched compared to the atmospheric equilibrium, indicating an effective mechanism that prevents the escape of methane from the deep water into the atmosphere (3).

Motivation

Little is as yet known about the processes that regulate the methane flux in the deep basins. In this work, we use a multidisciplinary approach that combines gas chemistry, molecular biology and lipid biomarker geochemistry and present data on a microbial methane sink within the pelagic redox zone of the Gotland Deep. Thus, this study aims to investigate whether aerobic methane oxidation also plays a role in the more dynamic and turbulent redox zone of the central Baltic Sea.

Gas-chemical, microbiological and biomarker evidences for aerobic methanotrophy

The methane gradient within the suboxic zone implied microbial methane consumption in the redox zone. The oxidation of methane within this zone was evident by the enrichment of ¹³C-CH₄ and elevated oxidation rates. Notably, methane monooxygenase gene expression analysis demonstrated that accordant methanotrophic activity was probably due to only one phylotype of the aerobic type I methanotrophic bacteria (2,4).

Pelagic microbial methane oxidation by alternative oxidants

Within the suboxic zone the concentration distribution of methane and nitrogen-species suggests microbial methane consumption by the use of nitrite and/or nitrate (Fig. 3). To study this process and to identify the involved microorganisms, we carried out an enrichment experiment. To detect the responsible organisms, the culture was incubated with ¹³C-CH₄ and ¹⁵NO₂⁻ and the cell-specific incorporation of these labels was analysed with NanoSIMS.

![Image](image-url)