



## **Biosignatures indicate effective aerobic methane-consumption in the redoxcline of the central Baltic Sea (Gotland Deep)**

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Methane is an atmospheric trace gas influencing the global climate with a warming potential of about 25 to 40 times higher than that of CO<sub>2</sub> [1]. Among other sources, methane is produced under strictly anoxic conditions in limnic and marine sediments by microbial methanogenesis [2]. Most of the sedimentary methane is oxidized by phylogenetically and metabolically versatile prokaryotes before it reaches the atmosphere [3].

The brackish Baltic Sea is a semi-enclosed marginal sea in contact with the North Sea via Skagerrak and Kattegat. The bathymetry comprises a series of basins, such as the Gotland Deep and the Landsort Deep in the central Baltic, which are stagnant and anoxic due to the higher density of deeper waters compared to the waters above about 100 m water depth. The basins are only episodically ventilated during inflows of water from the North Sea. Thus, the stable redoxcline is only occasionally perturbed on a decade time scale by the saline inflows [4, 5].

A recent study in the central Baltic Sea revealed high concentrations of methane (up to 1086 nM) [6] in the anoxic water column of the deep basins. Although methane concentrations rapidly decrease in the redoxcline [7], surface waters remain methane-oversaturated [6]. Despite this fact, little is known about the temporal and spatial dynamics and the key-players in methane turnover in anoxic deep waters and at the redoxcline. Here we present biomarker data on abundances and compositions of methanotrophic bacteria in the water column of the Gotland Deep, the second deepest basin (241 m) in the central Baltic Sea. Analysis of particulate organic matter from different water depths for bacteriohopanepolyols (BHPs) revealed biosignatures for aerobic methanotrophs (i.e., 35-aminobacteriohopanetetrol) and, even more specific, for type I methanotrophic bacteria (35-aminobacteriohopanepentol)[8] in the oxic/anoxic transition zone. This finding is further supported by C16 monounsaturated phospholipid fatty acids such as 16:1 $\omega$ 8c and 16:1 $\omega$ 5t, also indicative for type I aerobic methanotrophs [9].  $\delta^{13}\text{C}$  analysis of the specific phospholipid fatty acids revealed only minor <sup>13</sup>C-depletions with  $\delta^{13}\text{C}$ -values of -37 to -41‰ vs. VPDB, indicating only a fraction of these phospholipid fatty acids to be sourced by methanotrophs. As in many other stratified marine water columns [10,11], total BHP concentrations are strongly increasing in the anoxic zone. Seemingly, however, the majority of these biomarkers is not sourced by aerobic methanotrophic bacteria, since phospholipid fatty acids specific for methanotrophs could not be identified. Specific markers for sulfate reducing bacteria such as 16:1 $\omega$ 5c already occurred in the oxic/anoxic transition zone but concentrations are strongly increasing in the anoxic zone.  $\delta^{13}\text{C}$ -analysis revealed no significant <sup>13</sup>C depletion of this compound, indicating that methane-dependent sulfate reduction is not prominent in the Gotland basin water body.

Our study clearly shows that aerobic methanotrophs effectively consume the upward-migrating methane at the redoxcline of the Gotland Deep. Anaerobic methanotrophy appears to be less important, but a more detailed study of this process will be the focus of forthcoming investigations.

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