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Microbial methane oxidation in the water column of the central Baltic Sea under differing hydrographic conditions: Gotland Deep vs. Landsort Deep

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The pelagic turnover of methane is of crucial interest because it consumes – in most cases – very efficiently the methane that escapes from the sediment into the water column and thus hampers the transport into the atmosphere. Using a multidisciplinary approach that combines gas chemistry, methane oxidation rate measurements, and molecular biology we investigated the pelagic methane cycle in the deep central basins of the Baltic Sea (Gotland Deep (GD): 250 m water depth, Landsort Deep (LD): 460 m water depth). These two basins are characterized by a pronounced salinity gradient leading to a stable biogeochemical zonation from oxic conditions in the surface water to anoxic conditions in the deep water. In the GD the transition zone between the oxic and anoxic water body (redox-zone) is located between 81 and 127 m water depth; in the LD this zone is situated between 84 and 125 m. The stability of the redox-zone is different in both basins and depends mainly on the different intensities of lateral intrusions and interactions between the water body and the basin boundaries (e.g. boundary mixing). In the scope of our studies is the question: How do different water column stabilities influence the methane chemistry, the turnover of methane, and the composition of the microbial community that controls the methane flux within the redox-zone.

Our studies show, that in both basins the redox-zone is characterized by a strong methane concentration gradient (CH_4 conc. surface water: GD and LD about 10 nM; max. CH_4 conc. deep water: GD 1233 nM, LD 2935 nM) and a pronounced enrichment of ^{13}C CH_4 ($\delta^{13}C$ CH_4 deep water: GD -84 ‰ LD -71 ‰ $\delta^{13}C$ CH_4 redox-zone: GD -45 ‰ LD -4 ‰ $\delta^{13}C$ CH_4 values vs. VPDB) clearly indicates microbial methane consumption in that depth interval. Both basins show elevated methane oxidation rates within the redox-zone (GD: max. 0.20 nM d^{-1} and LD: max. 1.01 nM d^{-1}) with a 4 times higher turnover rate constant (k) in the LD compared to the GD (GD = 0.0022 d^{-1}; LD = 0.0079 d^{-1}). Expression analyses of the *pmoA* gene, a functional marker for aerobic methanotrophs, identified active type I methanotrophic bacteria in the redox-zone. At both sampling stations the diversity of active methanotrophs is restricted to one phylotyp named Uncultured GotDeep_pmoA1.

Our results demonstrate that the different hydrographic situation in the Gotland Deep and Landsort Deep is not influencing the microbial diversity of methanotrophs within the redox-zone. However, the turnover of methane within the redox-zones shows strong variations between the two basins. Based on the differing turnover rate constants detected in these basins we assume that the more stable redox-zone in the Landsort Deep is supporting the growth of methanotrophic organisms leading to a higher abundance of these microbes compared to the situation in the more unstable redox-zone of the Gotland Deep. However, in both basins the efficiency of methane consumption in the redox-zone is high enough to compensate the flux of methane from the deep water to the surface water.