

ANAEROBIC METHANE OXIDATION IN EUROPEAN CONTINENTAL SHELF SETTINGS

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Whereas processes and micro-organisms responsible for the consumption of methane in gas-rich sediments on continental slopes and in the deep sea are well known, few studies have investigated such processes in sedimentary settings characterised by low-methane fluxes. To better understand the role of anaerobic oxidation of methane (AOM) as a sink for methane in such settings, and to investigate the microbial ecology of these environments, we conducted geochemical studies on sediments from the Aarhus Bay in the South Eastern Kattegat and the Arkona Basin in the Baltic Sea. For each site, we determined pore water concentrations of methane, sulphate and sulphide and rates of AOM and sulphate reduction (SR). We also investigated the distributions of various lipid biomarkers and applied them as proxies for AOM. To evaluate the impact of AOM on the mineralogy, we measured solid-phase concentrations of redox-sensitive metals such as iron and manganese and investigated the mineralogy using X-ray diffraction and scanning electron microscopy.

There exists in both the Aarhus Bay and the Arkona Basin a sulphate-methane transition zone (SMTZ) that is characterised by maximum AOM rates and intense SR. Biomarkers in the sediments are diverse and include compounds deriving from higher plants (*n*-alkanes and *n*-alkanols), phytoplankton (e.g. long-chain alkenones and alkyl diols) and microbes (isoprenoidal and non-isoprenoidal diethers, isoprenoidal hydrocarbons, hopanes and fatty acids). Here, we place emphasis on the distributions of specific archaeal and bacterial biomarkers, namely archaeol and the structurally similar C₃₃ dialkylglycerol diethers (DGDs; putative SRB biomarkers), *sn*-2- and *sn*-3- hydroxyarchaeol, 2,6,10,15,19-pentamethylcosane (PMI), and branched C₁₅ and C₁₇ fatty acids. The co-occurrence of archaeol, *sn*-2- and *sn*-3- hydroxyarchaeol and PMI is characteristic of methane-rich sedimentary basins and has been reported for numerous cold seep sites (Niemann et al., 2006; Pancost et al., 2001b) and a variety of DGDs and structurally-related fatty acids are useful biomarkers for SRB involved in AOM (Blumenberg et al., 2004; Pancost et al., 2001a).

In the Aarhus Bay sediments, the abundance of *sn*-2-hydroxyarchaeol and PMI varies significantly with depth. At the SMTZ, the concentration of *sn*-2-hydroxyarchaeol increases

dramatically from below detection limit to $> 900 \text{ ng g}^{-1}$ and PMI abundances increase by more than one order of magnitude to 50 ng g^{-1} . Although archaeol is present throughout the sedimentary column and no significant changes in concentration with depth occurs, phospholipid-bound archaeol was detected only in sediments at and below the SMTZ. Thus, the relatively recalcitrant archaeol is probably not a useful biomarker for active AOM, but its phosphorylated (or glycolated) equivalent and the labile hydroxyarchaeol isomers likely are. Bacterial C_{33} DGD abundances also vary significantly with depth, and an increase in concentrations occurs in sediments from just above the SMTZ. In the Arkona Basin sediments, a similar suite of biomarkers was present (with the exception that neither *sn*-2- nor *sn*-3- hydroxyarchaeol were detected in any of the samples), and similar changes occur in the abundances of specific archaeal and bacterial biomarkers in the vicinity of the SMTZ.

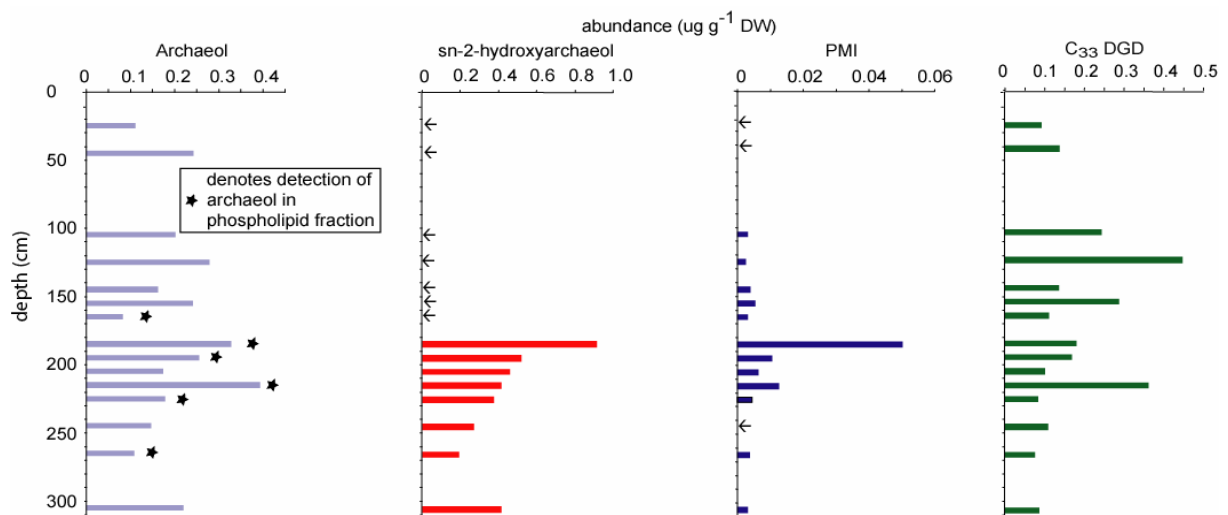


Figure 1. Abundance profiles for specific archaeal and bacterial biomarkers in Aarhus Bay sediments.

These biomarker distributions suggest that microbial communities similar to those found in cold seeps exist at the SMTZ of these low-methane flux settings. Furthermore, the lower abundances of lipid biomarkers at the low-methane flux settings – up to more than one order of magnitude lower – are indicative of smaller/less active communities mediating AOM.

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