

LIPID BIOMOLECULES IN THE SUBSURFACE OF TIDAL FLATS: INDICATORS FOR MICROBIAL DIVERSITY

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Most of the global prokaryotic biomass is presumably harboured in the marine subsurface. So far, the investigation of marine sediments mainly focused on the ‘deep biosphere’ at open-ocean and continental-margin settings but less attention was paid to the deeper layers of coastal sediments. In the course of recent environmental studies, however, the community composition of subsurface tidal-flat sediments was analyzed using a cultivation-based approach (Köpke et al., 2005) or the phylogenetic characterisation of bacterial communities was targeted with molecular biological tools (Wilms et al., 2006).

Here, we present a multidisciplinary approach to analyze the vertical distribution of active microbial populations in the upper metres of a tidal flat sediment. A combination of complementary geochemical, molecular biological and microbiological methods was applied to investigate the activity and composition of microbial communities. One of our analytical approaches is the analysis of intact polar lipids (IPLs) using HPLC-ESI-MS. These diagnostic membrane lipids are rapidly degraded after cell lysis and thus are considered suitable biomarkers to trace viable microorganisms.

The sampling site Janssand is located in the backbarrier tidal flat area of the island of Spiekeroog in the Northwest German Wadden Sea. The sediment section at the sampling site was mainly sandy with interspersed mud-rich layers increasing in thickness towards the bottom of the core (Fig. 1A). The quantities of the IPLs decreased only slightly with depth and correlate well with the total cell counts obtained by DAPI staining. The major phospholipid types were phosphatidyl ethanolamine (PE), phosphatidyl glycerol (PG), phosphatidyl choline (PC), phosphatidyl inositol (PI), and small amounts of diphosphatidylglycerol (Fig. 1C). In surface sediments side chain diversity was higher than in deeper layers. Apparently, the microorganisms inhabiting deeper sediments incorporate more unsaturated or shorter acyl side chains in their phospholipids. Furthermore, phospholipids with alkyl diether and mixed alkyl-acyl side chains become dominant with increasing depth. In accordance with the molecular biological results this may indicate a substantial proportion

of sulphate-reducing bacteria (SRB) in the microbial community even in deeper sediment layers because these lipids were detected in mesophilic SRBs (Rütters et al., 2001). Whereas in the uppermost layers phospholipid-type diethers of archaeal origin were absent, archaeol-containing phospholipids were detected throughout the deeper part of the sediment column (Fig. 1C). Highly specialized consortia of sulphate reducers and members of the archaeal ANME groups presumably mediate the anaerobic oxidation of methane (AOM) within the sulphate-methane transition zones. In these layers with low contents of methane high numbers of ANME-2 and ANME-1 archaea were detected using molecular biological methods. The major IPLs detected in a deep sulphate-methane transition zone were PI and PG with archaeol and hydroxyarchaeol cores which support the identification of ANME-2 consortia. The isotopic composition of these diethers is currently being examined to show whether they are constituents of cell membranes from archaea mediating AOM.

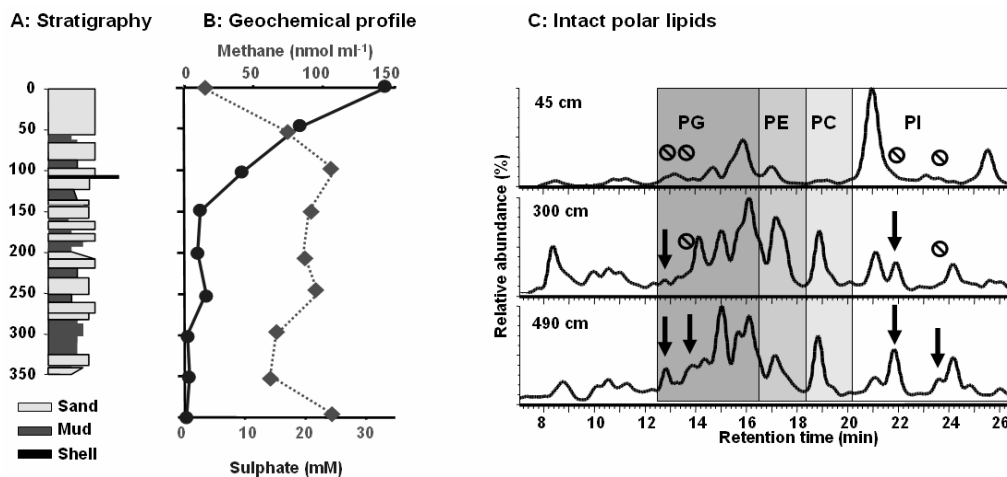


Figure 1. Vertical profile of a sediment core from the Janssand. A: simplified lithological profile; B: depth profile of methane (circles) and sulphate (diamonds) concentrations; C: base peak ion plots of IPLs from three different depths. At 45 cm depth phospholipid-type diethers of archaeal origin (arrows) were absent. At 300 cm PG and PI with archaeol-containing lipids were present and at 490 cm depth also hydroxy-archaeol core lipids were detected.

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