

Introduction

Methane concentrations in the backbarrier tidal flat of the island of Spiekeroog were found to be sixty times higher than in the open ocean (Grunwald et al. unpublished). However, sources and sinks of methane in tidal flats are completely unexplored. This study is the first step to a detailed analysis of the methane cycle within the Wadden Sea. Therefore, a more than five meter long sediment core was recovered during a sampling campaign in November 2004. Analyses included the measurement of methane concentrations (Fig. 4) and the quantification of prokaryotic cells by direct counts and quantitative PCR (Figs. 5 & 6). Numbers of key genes for methane production and oxidation (*mcrA*) and for sulfate reduction (*dsrA*) were additionally recorded along the sediment column (Fig. 7).

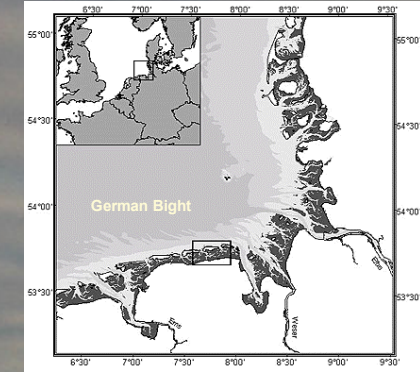


Fig. 1: Sampling area: East Frisian Wadden Sea near the island of Spiekeroog

Fig. 2: Sampling of long sediment cores requires a lot of technical equipment and manpower

Results

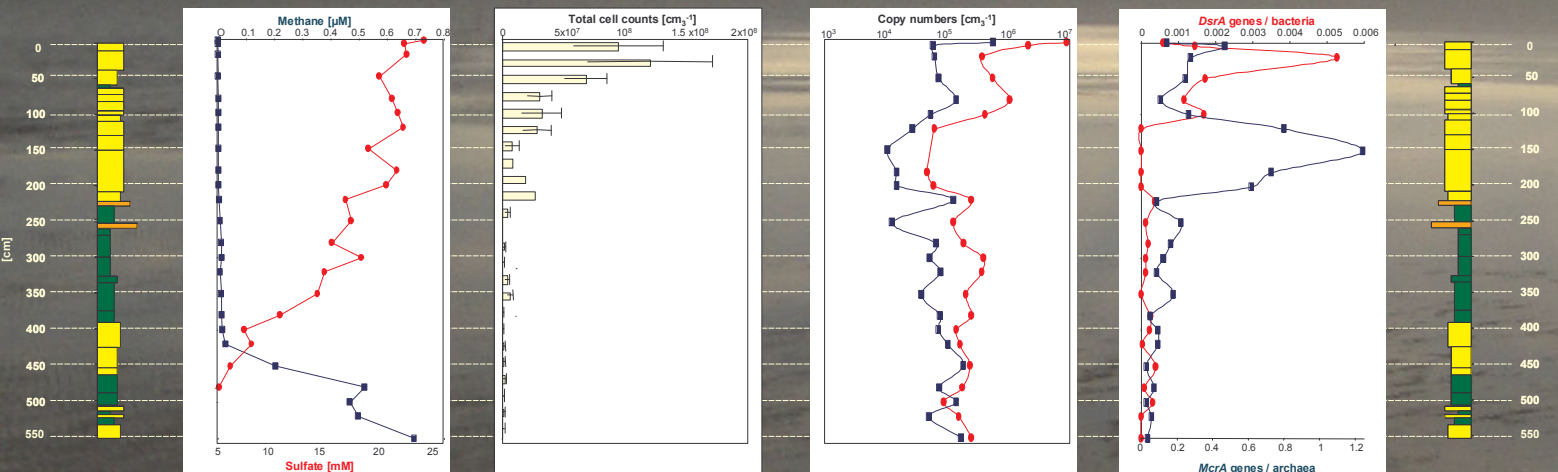


Fig 3: Stratigraphy
sand
mud
shell

Fig 4: Concentrations of sulfate in mM (red circles) and methane in μM (blue squares)

Between 220 cm and 400 cm methane increased from 0.003 to 0.015 μM within sulfate-rich layers. A sulfate-methane-transition-zone was located at about 400 cm. Below 480 cm sulfate concentrations dropped under the detection limit, while methane increased strongly.

Fig 5: Total cell counts obtained by staining with SybrGreen

The total cell numbers decreased with depth by two orders of magnitude. A slight increase was counted at a depth of 220 cm (a lithological boundary) and at 350 cm (above the sulfate-methane-transition-zone). The decrease of bacterial numbers within the first two meters was also detectable by quantitative PCR. The archaea to bacteria ratio was highest above the shell layer and in the transition-zone.

Fig 6: Distribution of archaea (blue squares) and bacteria (red circles) determined by quantitative PCR

Fig 7: Ratio of *dsrA* to bacteria (red circles) and *mcrA* to archaea (blue squares)

The number of *mcrA* gene copies per archaea was high over the entire sediment column showing two peaks below the surface and above the lithological boundary at 220 cm. High numbers of *dsrA* genes per bacteria were only detected within the sulfate-rich zone between 20 cm and 100 cm.

Fig 8: Stratigraphy
sand
mud
shell

Conclusions

- The profiles of methane and sulfate suggest a hot spot of anaerobic oxidation of methane (AOM) between 350 cm and 450 cm below the sediment surface.
- However, low methane concentrations and high abundances of the *mcrA* gene might indicate concomitant methanogenesis and AOM also in the shallower sulfate-containing layers.
- The profiles of microorganisms and key genes for physiological processes are correlated with the lithological stratification.

Outlook

- Methane emission and transport will be determined over a complete tidal cycle.
- Rate measurements of AOM are in progress, methane oxidation in oxic compartments will be investigated in the near future.
- The distribution of different physiological groups of methanogens along the sediment column will be studied by the analysis of specific enrichment cultures.

Acknowledgements

We thank the Senckenberg Institute, Department for Marine Research for borrowing the equipment and Tina Treude (MPI Bremen) for technical advice in methane and AOM measurements. This work was supported by a grant of the DFG.

For more details see also posters from A.Gittel, B.Engelen, J.Köster and the talk of M. Grunwald