

Interactive comment on “Methane emission and consumption at a North Sea gas seep (Tommeliten area)” by H. Niemann et al.

Anonymous Referee #2

Received and published: 12 September 2005

The manuscript describes the results of a well documented field campaign on the biogeochemistry, organic geochemistry and microbiology of a methane seep area in the North Sea. Methane release, microbial biomass and microbial activities were relatively low compared to previously studied seeps areas, thereby widening the range of studied systems. Results are mostly in agreement with other recent work. Interestingly, even the cell-specific methane oxidation rates are comparable to much more active areas. The subject fits well into Biogeosciences.

The results are mainly compared to other seep areas, which were much more active. A comparison to non-seep sediments where anaerobic methane oxidation was studied also seems interesting, especially the methane seep areas are rather small and were not directly sampled.

The methane-sulfate transition zones detected share a common feature namely that

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sulfate penetrates into the methane zone. This is unusual as acknowledged by the authors and is explained by a artifact of the coring technique used, which apparently caused a smearing of the sulfate profile. What is however not clear is why this didn't effect the methane and especially the sulfide profiles? Is there no other possible explanation for the deep sulfate profiles? For instance, the more-or-less solid marl may not support the growth of bacteria involved in anaerobic methane oxidation or subsurface porewater flows.

There is quite a variation in ratios between sulfate reduction and methane oxidations rates, and they tend to deviate from the expected 1:1 ratio. There is however very little discussion on this.

Discussion on fatty acid data suggests that the concentrations and compounds detected agreed with previous studies on ANME-I and -II dominated methane seeps. However, the relative contributions of the various compounds detected is very different from other observations. It was surprising to see major amounts of 18:2w6, which is a uncommon fatty acid in bacteria but is generally found in eukaryotes like certain algae, fungi and animals. This therefore indicates a major contribution of eukaryotic biomass, which is however not discussed and would be very surprising given the biogeochemistry of the system. Another unusual feature is the ratio between monounsaturated 16-carbon fatty acids. In subsurface samples, more 16:1w9c was detected than 16:1w7c, whereas this is highly uncommon in organisms. Although major efforts were made, the authors may want to have another look at the identification of these unsaturated fatty acids.

The reference to Blumenberg et al lacks page numbers.

Included the core number in Fig. 4.

Interactive comment on Biogeosciences Discussions, 2, 1197, 2005.

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