

Interactive comment on “Microbial methane oxidation at the redoxcline of the Gotland Deep (Central Baltic Sea)” by O. Schmale et al.

Anonymous Referee #2

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Comments on 'Microbial methane oxidation at the redoxcline of the Gotland Basin (Central Baltic Sea)', ms bg-2012-274 submitted by Schmale et al.

Methane (CH₄) is one of best studied oceanic trace gases. However, some aspects of the oceanic CH₄ pathways are still unknown. The ms under review presents new results from one station in the central Gotland Basin which shed light on the CH₄ oxidation at suboxic/anoxic interfaces. Although the ms presents interesting results based on a multidisciplinary approach incl. various chemical, geochemical and molecular biological methods, I have a fundamental concern about the design of the study. I think that the main conclusion of the ms is not justified by the presented results, see detailed comment below. Therefore, unfortunately, I can recommend publication of the ms in BG only with major revisions (if this is possible at all).

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From the data presented in Fig 2 and correctly discussed in the text it is obvious that CH₄, produced in the deep layer, is consumed between 115 and 135 m water depth (see page 8791, lines 17-21). Moreover, it is correctly stated that a turbidity max. is visible in about 120 m and it is stated that it results from enhanced microbial activity (page 8791, line 4/5). So, I am wondering why the investigation of the methanotrophic microorganism has been performed with a sample from 100m (see page 8791, line 20). This water depth is clearly located outside the zone of the CH₄ gradient (i.e. zone of CH₄ oxidation). In other words I am not surprised by the finding of reduced diversity of methanotrophs, simply because of the fact that the water depth of 100m is not relevant for CH₄ oxidation. Is there any reason why a water sample from 100m should be representative for the zone with the CH₄ gradient (115-135 m), where the CH₄ oxidation takes place? I would not be too surprised to find a higher diversity of methanotrophs at the depth of the turbidity max. in 120m.

The other aspect ignored is related to the question how representative are the results for the rest of the Baltic Proper? (results from only one station are presented!)

Thus I think that the main conclusion ('...support the idea that biogeochemical cycles in the Central Baltic Sea redoxclines are mainly driven by only a few microbial key species.' see abstract and discussion on page 8794, lines 9-22) is not justified by the presented results at all.

Interactive comment on Biogeosciences Discuss., 9, 8783, 2012.

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