Biogeosciences Discuss., 11, C7740–C7743, 2015
www.biogeosciences-discuss.net/11/C7740/2015/

Biogeosciences
Discussions
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Interactive comment on "Seasonal methane accumulation and release from a gas emission site in the central North Sea" *by* S. Mau et al.

Anonymous Referee #1

Received and published: 2 January 2015

Mau et al "Seasonal methane accumulation and release from a gas emission site in the central North Sea" (manuscript # bg-2014-506), provides a welcome analysis of the dynamics of methane flux in a seepage-influenced coastal shelf site. This analysis includes summer and winter measurements of methane concentrations and oxidation rates, in the context of thermal stratification and horizontal and vertical transport processes. The data and analysis contributes nicely to modeling the contribution of coastal marine sources to global methane inventories.

General comments:

The analysis was well-supported across various metrics. Incorporation of new data into the existing literature was also generally good, and the data fit well with past estimates of methane flux. The main conclusions are sound. I have several questions for the

authors.

Specific comments:

First, is it possible to determine if in situ methane production is occurring and biasing rate measurements? See e.g. Tang et al 2014, Limnology and Oceanography. This and other sources suggest that methane production in relatively shallow oxygenated waters can occur – possibly arising from methanogenic organisms tightly coupled to photosynthizers. Methane production and consumption may be likewise tightly coupled between microorganisms, and tracers may not compete well as a substrate in such a scenario (Furthermore – particularly when considering a low 'on rate'/'enzymatic uptake' as speculated in this paper, the added mass of heavy isotopes may introduce significant bias in rate estimates).

Second, the Michaelis Menten averaging may not be appropriate or valid. In Baani et al, two isoforms of pMMO are shown to have different kinetics of methane oxidation. On an environmental scale one expects widely disparate Km's from different isoforms, or homologs, of the same enzyme. Indeed, from a biochemical view, determination of Km is most appropriate from purified enzymes - and not necessarily reliably determined otherwise, yes? Is it possible to provide an indication of error in your averaged Km? Or, perhaps bin the pre-averaged Km measurements according to methane concentration to generate confidence levels that you are not averaging across different biochemical processes. There is more scatter in Figure 7 than I would have expected from the text.

Lastly, it is not clear if you are posing that there is, or isn't, a microbial methane oxidizing community. What seems likely is that microbial methanotrophs are present in such low numbers and/or are such poor matches to your PCR primers that they are below detection. The latter of these possibilities has been directly demonstrated for marine planktonic methanotrophs (Hansman, 2008). Additional research using not only PCR but also methods with intrinsically less bias (e.g. SIP, metatranscriptomics) has demonstrated global cosmopolitan presence of canonical as well as unusual methanotrophs

in bottom waters. These published findings pertain directly to the problem of primer bias in PCR (e.g. Li et al 2014, Env. Micr.) Shallower marine waters (<∼200m) in the Pacific, Atlantic, and the Gulf of Mexico are almost invariably devoid of detectable canonical methanotrophs - but can host unusual pmo variants including those from unusual phylogenies. Your results from a relatively shallow marine source relate directly to these published trends (e.g. Tavormina 2013 and references therein).

Technical comments:

Twice the word 'ascend' should more properly be 'ascent,' on page 18006 line 9 and page 18019 line 12 (Please also remove the comma following 'vent sites' on line 12).

Page 18009 line 16: The word 'gaschromatograph' is two words in the English language.

Page 18018, line 13: Please change 'but showed also' to 'but also showed' to correct the grammar. Can you provide some interpretation of these results? Do you believe that so few bands were clearly resolved because the original product was phylogenetically diverse, or was the quality of the original product poor? I would be curious to see the non-denaturing gel, to have a sense of the efficiency of the initial amplification reaction.

Page 18019 line 25 through page 18020 line 5: It may be appropriate to add Narvenkar et al 2013 to these references.

Page 18027 line 20: The Kessler estimates, which are environmentally based from a marine system, are more relevant than estimates from terrestrial organisms grown in culture. It may be appropriate to mention that few if any planktonic marine methanantotrophs are currently available in culture thus doubling times are challenging to estimate.

Table 2. Crespo-Medina (Nature Geoscience 2014) recently reported Mox rates surpassing those included in this table. Consider inclusion.

Interactive comment on Biogeosciences Discuss., 11, 18003, 2014.