Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2018-184-RC1, 2018

Biogeosciences Discussions

Interactive comment on "Predominance of methanogens over methanotrophs contributes to high methane emissions in rewetted fens" *by* Xi Wen et al.

Anonymous Referee #1

Received and published: 14 May 2018

Review of the Biogeosciences Discuss. Paper "Predominance of methanogens over methanotrophs contributes to high methane emissions in rewetted fens by Wen et al. The authors present high throughput sequencing and qPCR data of microbial communities of two rewetted fens in northern Germany. Next to the microbial analyses the pore water chemistry, dissolved methane and the isotopic signal of the methane C was analyzed. The paper is well written but hampers in the experimental design and some missing analyses. First of all there are no datasets or samples available which connect the rewetting treatment to a control or a pre-disturbance measurement. With pre-disturbance we can argue the existence of the drained fen performance or even the performance of the fen before drainage. So to what can the results be compared?

I thought that the lateral scanning of the fens by different sampling points could explain this but actually the data is not discussed in this sense. At least at Huettelmoor the gradient goes away from the dam. The data is also not discussed to the methane fluxes of the different sampling points. For Huettelmoor they exist because there have been chamber measurements which should match quite close to the H1-4 cores if they are not exactly at the same spot. I also wonder why no potential activity measurement was performed to assess the activity of methane production and oxidation. Can this still be performed because it would give much information which is not told by the community analyses of gene copy numbers. Next I miss in the qPCR approach the measurement for Archaea. Why has this not be measured. In the MM section the authors should tell which depths have been sampled at each site. I can see the depths in the Figs BUT they need to be told in the MM. You have also to discuss in the Ms why the depth sampling was so different between fens and within the Huettelmoor fen. Probably the fens were never mentioned to be published together otherwise the sampling would be convergent. In the MM section I miss the sample n AND I want to point out that you have not replicated your study design. In my opinion this is a harsh critique. Taking two within replicates for DNA extraction is not the same you should have two to three adjacent lines. In the Intro and Discussion it is stressed that elevated methane emissions after rewetting is dangerous. I doubt that. First the dried peatland lost a lot of CO2 due to peat degradation and the onset of methane emission after restoration is a hint that peat formation starts to accelerate again and this process fixes more C than it loses. There is scientific literature around this and you may bring this into your discussion. In the MM I do not see if the rewetted Huettelmoor water table is 0.6 m above or below peat surface (line 126). In the Results of the MM statistical chapter I miss information of have many sequences were retrieved. How many OTUs were obtained and the bubble data is generated on and how many observations. In lines 201-202 is something I do not understand. Three PCR products of the same sample were combined. OK but why. But the next sentence says PCR products of different samples were pooled. . .???On lines 273-276 give the percentage of Methanotrophs

out of the total. You tell them in the discussion. This so, because you present for Methanogens this data on line 280. Looking at the Figs you have no real depth separation in your measured variables at Zarnekow. WHY? For the end; line 78-80 states wrong: there are more publications to the theme Reumer et al. 2018. Impact of peat mining, and restoration on methane turnover potentials and methane-cycling microorganisms in a northern bog. Applied and Environmental Microbiology 84, 3 e02218-17. https://doi.org/10.1128/AEM.02218-17. Putkinen et al. 2018. Recovery of methane turnover and the associated microbial communities in restored cut-away peatlands is strongly linked with increasing Sphagnum abundance. Soil Biology & Biochemistry 116: 110-119.

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