

This manuscript describes the methanotrophic activity along the profile of sediments in an eutrophic and a mesotrophic lake. Hydrogenotrophic and acetoclastic methanogenesis was measured in lab incubation. Molecular analyses were also carried out, in order to quantify and describe the diversity of Archaea and methanogens. It is the second time I review this paper, and this version is significantly better than the previous one. But I still find the discussion part a bit weak. I would like more connections between the incubation and the molecular analyses. For instance, are there any correlations between the activity measurements and the concentration in the sediment of methanogens, or one clade of methanogens. This is missing and this piece of information could be valuable.

Below are some specific comments:

- 25: "ecosystems" instead of "ecosystem"
- 25: "layer depth-related" is unclear to me. Why not replace it by "depth-related"? Please replace "layer-depth", by "depth" or by "profile" throughout the whole document.
- 29-30: Rephrase: "in two freshwater lakes at different trophic status on the Yunnan Plateau (China), Dianchi Lake (eutrophic) and Erhai Lake (mesotrophic)."
- 34-36: Remove: "The layer depth-related changes of methanogenesis potential, and the abundance and community structure of methanogens were observed in either Dianchi Lake or Erhai Lake."
- 36-37: Rephrase: "...mcrA and archaeal 16S rRNA genes displayed a similar abundance change..."
- 42: Only genus and species names should be italicized (<http://blog.vancouvereditor.com/2011/03/science-writing-and-editing-scientific.html>)
- 44: Which trophic status? Please introduce it in the abstract, for instance in the sentence of l. 29-30.
- 45: You did not describe the vertical change in methanogenic activity in this abstract. Please add these results in the abstract.
- 48-49: It is not necessary to use keywords that are already present in the abstract (such as mcrA).
- 84: remove a space here: "acetoclastic pathway:hydrogenotrophic pathway"
- 85: Typo: "similar forms of organic matter"
- 89: Please rephrase: "To identify the methanogens and methanogenic pathways, both archaeal 16S rRNA..."
- 97: Remove "Many". You mention 1 or 2 studies per type of lake, which is not a lot.
- 100: Please clarify in the text what do you mean by "substrate".
- 102-103: "Methanogenesis ... might be different". What do you mean here? Different in activity, community structure...? Please clarify.
- 105: Correct this way: "... our attention: (1) How..."
- 122: Write "in situ" in italics
- 127-129: I know that it is quite obvious that D stands for Dianchi and E for Erhai, but you should state it explicitly somewhere.
- 146: We don't really care about the volume of your CH₃F solution you added to your incubation flasks. We want to know what is the final concentration. Please add this piece of information (2%).
- 154: Replace "quality" by "fragment size"
- 163: "literature" instead of "literatures".
- 166-167: Please specify in the text the coefficient of efficiency (E) and if inhibition tests were conducted.
- 168: For the ANOVA, were the data normally distributed between the 2 groups? Usually, we log-transform qPCR data for this kind of statistical test. Did you do it? More details are needed here.
- 175: You told me that this triplicate was a biological one. How is it possible, knowing the fact that you pooled together the 5 replicates you sampled, as stated in lines 131-132?
- 178-179: You have to deposit the 16S sequences to GenBank as well.
- 179-180: "After subsampling to the lowest number of sequences". This is not clear. Please rephrase.
- 184: "affiliation" instead of "identities"

- 184-185: More details about the taxonomic annotations are needed. How did you compare your sequences to the database, which similarity threshold did you choose?
- 187-189: You have to deposit the raw reads to SRA as well.
- 192-193: More details about the phylogenetic analysis are needed: which model? Bootstrap? Tree method?
- 207: Which statistical test did you use here? Please add it to the methods section.
- 212-213: Please rephrase "Dianchi Lake had the IMP of 47.0–182.8 nmol/gDW" to "IMP in Dianchi Lake ranges from... to..."
- 216-217: In which lake is the acetoclastic methanogenesis more important? Did you perform any statistical test to assess this (such as the one used in l. 207)? Please clarify in the text.
- 224-225: Please describe in the text the stats behind this p-value.
- 238: Please quickly define "library coverage" for the reader.
- 271-282: I strongly recommend to switch figure 3 with figure S1. Indeed, the content of figure S1 is directly related to the focus of the article, while figure 3 is not. Indeed, figure S1 is more relevant and meaningful to the research topic than figure 3. Same thing with figure S2, I think it deserves to be in the main text.
- 316: Please add here the clustering method (UPGMA)
- 333: "literature" instead of "literatures"
- 357-359: Use the present tense in this sentence.
- 369-370: I don't understand the link between the acetoclastic methanogenesis and the availability of organic matter. Both methanogenic pathways use as substrate fermented organic matter. Why the availability of organics would have a greater influence on the acetoclastic pathway? Could you please clarify it in the text?
- 370-373: Did you try to correlate acetoclastic methanogenesis with organic matter content?
- 390-391: Please add a link to a figure.
- 419-432: The high proportion of Methanomicrobiales (hydrogenotrophic) and the low proportion of Methanosarcinales (acetoclastic) is in agreement with your incubations, which highlighted a dominance of the hydrogenotrophic methanogenesis, over the acetoclastic one. You should write it somewhere in the main text.
- 425: Please add the description of Taihu Lake in the text (i.e. the third largest freshwater lake in China. It is a shallow eutrophic lake with an average depth of about 2 m.)
- 437-442: Do you have some geochemical data (maybe from other studies) that could explain these abrupt changes in the sediment profiles? If so, please add them to the discussion.
- 448-450: Please refer to figure S1 to show the data.
- 450-453: Please refer to figure S2 to show the data.
- 459-461: Please rephrase this way: "Methanoplasmatales-like methanogens are related to Thermoplasmatales archaeons. They are usually present in termite guts and high-salinity environments."
- 464-465: Please refer to figure S1.
- Figure 1: Please put the horizontal axis at the top.
- Figure 2: Specify in the caption and/or in the label axis the log scale of the gene abundance.
- Figure 2: Please inverse the vertical axis for a better readability. Put the horizontal axis at the top.
- Figure 4 caption: I think the bar represents 10% divergence.
- Figures S1 and S2 captions: "Samples D1–D6 and E1–E6 were from Dianchi Lake and Erhai Lake, respectively." was written 2 times.
- Figure S3: I would set the depth as a descending vertical axis (just like in figure 1 and 2).

-Missing things in this article:

- OTU tables (16S and mcrA-based) should be available to the reader (should be published online).
- Are there any correlation between data from figure 1 and figure S1/S2. Can you explain the activity profiles with your molecular data?

- Why is there only a tree with the mcrA data. Did you try to build a tree with 16S data? Are both trees congruent?