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Interactive comment on “Influence of niche differentiation on the abundance of methanogenic archaea and methane production potential in natural wetland ecosystems across China” by D. Liu et al.

Anonymous Referee #1

Received and published: 17 November 2010

This paper reports the abundance of methanogens and methane production potential in natural wetlands in China. Four sites from various climate conditions were selected across China. The abundance of methanogens was measured using qPCR and methane production potentials were measured under simulated conditions in the laboratory. The authors found variations in the abundance and methane production potentials both laterally (across the sites) and vertically. There is no correlation between the abundance and methane production potential.

Overall, the paper is exceptionally well-written and well-referenced. It is well organized

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and flows logically. I recommend publication after the authors address the following comments:

General comments:

1. In correlating the methane production potential with the abundance of methanogens, a RNA-based approach, i.e., mcrA transcript gene abundance (normalized to 16S rRNA gene) should be more meaningful. It is kind of expected that the DNA approach does not show any correlation with the methane production rates. I realize that it's too late to redo the experiments using the reverse transcription qPCR (RT-qPCR), but at least the authors should discuss possible pitfalls of the DNA approach and offer alternative explanations for the lack of any correlation. 2. qPCR: I think qPCR of the functional gene of methanogens (for example, mcrA) would be more appropriate to link the gene abundance to methane production potential. I wonder why the authors did not consider the mcrA gene. Usually considering DNA extraction efficiency etc., a gene ratio, such as mcrA gene/16s RNA gene, should be used to correlate with methane production potential. 3. When correlating methane production potential with environmental parameters, temperature may be one parameter, but there are other important ones. So it may not be surprising to see a scatter plot (Fig. 3). The authors should try a multiple-regression analysis to include pH, SOC, TN, DOC simultaneously etc. Specific comments:

Page 7640: Line 5-10: this is repeat of the results.

Page 7643: line 3-4: I think it's premature to conclude that the abundance of methanogens is not an effective index for predicting the CH₄ production potential. This sentence should be qualified by stating that DNA-based, total methanogen abundance is not a good indicator, but if the authors measure active methanogen abundance, it may be a good indicator. Figure 6: Can the authors also plot methane production potential vs. environmental factors such as substrate availability (DOC etc)?

Fig. 7: Are there any error bars associated with this graph?

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Despite these issues, I thought overall the paper is of high quality and it should be published.

Interactive comment on Biogeosciences Discuss., 7, 7629, 2010.

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