Biogeosciences Discuss., 8, C4766–C4768, 2011
www.biogeosciences-discuss.net/8/C4766/2011/


Biogeosciences Discussions



# *Interactive comment on* "Methanotrophic activity and diversity in different Sphagnum magellanicum dominated habitats in the southernmost peat bogs of Patagonia" *by* N. Kip et al.

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Received and published: 8 December 2011

Rebuttal: Anonymous Referee #1 This is a nice paper that describes methanotroph diversity in Sphagnum dominated peatbogs in Patagonia. This has been achieved by studying 16S rRNA gene sequences and particulate methane monooxygenase sequences using a comprehensive pmoA microarray plus complementary pmoA clone library analysis. The work has been carefully done and the manuscript is clear and concise. The only problem I have with the work is that the authors perhaps play down the potential importance of facultative methanotrophs in this environment. There are

now primer sets specific for the facultative methanotroph Methylocella and if these have not been used, the possibility of their use in the future could be mentioned. Also, the fact that mmoX was not detected is surprising (again there are other mmoX primer sets that could be tried, including for Methylocella) given the abundance of Methylosinus and Methylocystis, many of which have a soluble methane monooxygenase. So do some Methylococcus and Methylomonas species. This is at least worth a comment.

REPLY: Many thanks for the interest in our work. To detect Methylocella spp and other methanotrophs, containing the mmoX gene, we performed a PCR using five different mmoX primer combinations derived from the literature (Miguez et al., 1997; McDonald et al., 1995; Auman et al., 2000) with DNA from the different peat ecosystems and the reference strain Methylocella palustris as a template. No PCR product was obtained from the environmental samples. The new primers for real-time quantitative PCR developed by Rahman et al. 2011 were not used, because we preferred more general mmoX primers, instead of species specific ones. Indeed besides Methylocella we would maybe expect to find mmoX genes of Methylosinus, Methylocystis and Methylomonas spp. which were detected with the pmoA methods, but it is not sure whether these detected species possess a mmoX gene. We already suggest it might be due to the primers that detection failed, but we will include a paragraph dealing with the mmoX topic in the Discussion section of the manuscript. Suggested text is as follows:

“No mmoX possessing methanotrophs were detected despite using different mmoX primer combinations (Miguez et al., 1997; McDonald et al., 1995; Auman et al., 2000). This might indicate a low abundance of Methylocella species. However, several Methylomonas and Methylocystis spp. also posses the mmoX gene but remained undetected. This might be caused by a limited detection range for the primers or because the methanotrophs present indeed do not possess a mmoX gene. For future studies it could be worthwhile to test the recently described more specific Methylocella spp. real time quantitative mmoX PCR primers (Rahman et al., 2011).”



BGD

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References:

McDonald et al., 1995 and Rahman et al., 2011 references were added to the list of references.

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Interactive comment on Biogeosciences Discuss., 8, 9357, 2011.