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Biogeosciences Discussions

Interactive comment on "Activity and diversity of methane-oxidizing bacteria in glacier forefields on siliceous and calcareous bedrock" *by* P. A. Nauer et al.

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The present paper describes a comprehensive exploratory survey into methane cycling and microbial communities involved in glacier forefields. Methane profile measurements clearly indicate that glacier forefields can act as sink as well as source of atmospheric methane, depending on the nature of the bedrock supporting the glacier. The investigated methanotrophic community was surprisingly non-diverse. The paper is excellently written and the authors discuss their results in an appropriate way. This study is valuable contribution to the knowledge on these pioneer ecosystems.

Comments: 1: It is a pity that the authors did not assess methanogens in parallel, for

e.g. by looking at the mcrA gene. Maybe this was done? If yes, I would suggest adding this information to this paper. 2: I think the authors should give a more up to date and comprehensive overview of methanotrophs in the introduction. Mention anaerobic methane oxidation as well, as also Verrucomicrobial MOB, NC10 phylum and the filamentous MOB (Crenothrix). Also in the introduction a statement is made which I think is neither completely correct nor relevant (line 20/21). Aerobic MOB have also been isolated from low methane habitats after enrichment using high methane concentrations. The classical low affinity MOB are also present in low methane habitats. 3: Why did the authors not assess sMMO in these samples? Do the authors expect that sMMO or sMMO containing MOB will not play a major role in these habitats? 4: I think the authors should give an explanation why the amplification with the primers designed for the pmoA2 was so successful. As far as I know there are no MOB who contain the pmoA2 exclusively. Hence, the MOB amplified know should also contain the pmoA1. Hence, I am puzzled by the results obtained. I think this needs some more in depth explanation. 5: in the methods section the authors do not say anything about the method to assess quantity and quality of the DNA extracted. Also no information is given on amount of DNA put into the PCR as possible test for PCR inhibition. Please, provide these data. 6: Reviewing this paper I would suggest a different title. Considering the fact that the obtained soil methane profiles can not be linked directly to the MOB observed in combination with the fact that DNA based analyses has been used, I would refrain in this case from using activity in the title: Alternative: Soil methane cycling and microbes involved in glacier forefields on siliceous and calcareous bedrock.

Interactive comment on Biogeosciences Discuss., 9, 1259, 2012.