

## ***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 authors addressed methane concentration profiles and community structures of methanotrophs from 27 soils in 13 glacier fore fields. They detected in most sites USCgamma pmoA genotypes as the dominant detectable genotype, in three sites Methylocystis was the dominant methanotroph. The authors categorized the observed methane distribution in 5 categories and identified at all calcareous sites a methane-producing layer below the surface. Nonetheless, up to 90% of this indigenous methane was oxidized on its way to the soil surface.

The authors concluded that USCgamma methanotrophs might be cold-adapted

C58

species that are involved in atmospheric methane-consumption.

The study has some experimental limitations:

- 1) pmoA-Analyses (cloning, TRFLP) were only done in the upper 10 cm not in deeper soil layers. From my perspective it would have been mandatory to analyse depth distribution if this sampling was taken.
- 2) Please, comment in a revised version on how many cores were analysed in each specific site to get methane concentration profiles.
- 3) The reader gets the impression that not all measured methane concentration profiles were shown in Figure 1. Please, present them all as Supplementary files.
- 4) The number of pmoA clones being sequenced is extremely low? Why? Please, coverage values at the species-level OTUs need to be documented for each library - Were they above 90%?
- 5) The TRFLP analysis has been replicated - but not the DNA-extraction which is the major source of Variance in that kind of analysis. Please, comment on that.
- 6) No mRNA, which would have reflected much better the active population was analysed. Why?

The conclusion that USCgamma might be a cold ecosystem-adapted methanotroph is interesting, but only a more comprehensive statistical comparison to previous studies would allow for this conclusion. Please, add a statistical comparison with soil methanotroph communities that are subjected to similar low and higher mean annual soil temperatures, and that are as well unsaturated soils.

comments to text: Abstract ln 18, Please write out 'operational taxonomic units' p. 1266, ln 7, please write out 'approximately' p. 1268, ln 27, correct 'OTU' p. 1277, ln 22-24, This statement is only true for methane oxidation at atmospheric concentration. Please, rephrase accordingly. p.1280, lns 3-5, This statement may also be a result of the extremely number of analysed genotypes in gene libraries. It may be that behind one TRF much more different genotypes may be hidden. Please, consider this in a revised ms version. p. 1280, ln 11, correct 'Henneberger et al., 2012'