

***Interactive comment on “The role of endophytic methane oxidizing bacteria in submerged *Sphagnum* in determining methane emissions of Northeastern Siberian tundra” by F. J. W. Parmentier et al.***

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First of all we like to thank the commenter for his contribution to this paper. The commenter notes that maybe more mechanisms should have been studied to attribute the difference between the vegetation types to oxidation alone. We like to respond to this and point out that the reviewer has overlooked key aspects of our work and, importantly, that the field experiment we executed in Far East Siberia is not quite compatible, neither in detail of the processes studied, nor in level of execution of the experiment, with a controlled laboratory experiment.

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First, the commenter notes that water level and active layer differences between sites may explain production differences since differences are observed between the two vegetation types, as is apparent from Figure 3. We like to point out that to exclude differences occurring due to water level, we only studied inundated vegetation types, (this is emphasized several times in the paper). Since the soil is flooded, changes in water level do thus not relate to changes of oxidation zones in the soil profile.

While a larger active layer could potentially provide a larger reservoir for methane production, most production usually occurs in the topsoil where temperatures are higher. Soil temperatures in the topsoil are almost completely similar (as shown in Figure 3), while the difference in active layer depth was rather small. Active layer depth therefore is unlikely to explain the large differences observed.

As in the paper, we must conclude that the different water levels and active layer depth are unlikely to lead to the large difference in the observed fluxes.

Second, the commenter notes that methane oxidation should have also been studied in the soil profile of the vegetation type without *Sphagnum*. We are aware that differences in soil conditions (pH, organic matter, redox potential etc) can lead to differences in production and oxidation of methane. Ideally this would have been studied here also. However, the study site is located in a pristine and remote tundra area. While this is an ideal location to study mechanisms occurring in undisturbed tundra, the logistics are very difficult. This makes any microbiological analysis difficult, not to say impossible as travel and legislation issues prohibit fast transport and analysis of soil microbial features. It was thus not feasible to perform analysis of vertical profiles of methane oxidation at this site. However, the fast export of *Sphagnum* samples was possible and executed, making a microbiological analysis possible. This analysis showed that methane oxidation rates in the *Sphagnum* samples from our site were extremely high compared to other samples from around the world. The authors of this publication suggested that this was due to a unique microbiological community at our

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site (Kip et al., 2010). Therefore, we focused in this paper on the issue of whether these processes could be detected under in-situ conditions.

So, while we wish to study the uniqueness, our site does not allow us to explore all mechanisms and processes in great detail. However, to assess the likelihood that the other parameters, which the commenter suggested to be investigated, could provide an alternative explanation to the observed differences, we modeled methane fluxes from this site with a well-established process model. This model showed that, while oxidation is likely to occur in the non-*Sphagnum* site, it had to be 50% higher in the *Sphagnum* dominated site to explain the observed differences. This is in line with the microbiological analysis and these two methods combined make it very likely that methane oxidation in *Sphagnum* is one of the key processes.

Within the limitations posed by this site, our model analysis, in combination with the high methane oxidation potential in *Sphagnum*, makes it thus very likely that the observed differences are in fact much more strongly related to these methanotrophic bacteria in *Sphagnum* than to other environmental parameters.

References:

Kip, N., van Winden, J. F., Pan, Y., Bodrossy, L., Reichart, G.-J., Smolders, A. J. P., Jetten, M. S. M., Damste, J. S. S., and den Camp, H. J. M. O.: Global prevalence of methane oxidation by symbiotic bacteria in peat-moss ecosystems, *Nature Geoscience*, 3, 617–621, 2010.

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