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Interactive comment on “Exploring the response of West Siberian wetland methane emissions to future changes in climate, vegetation, and soil microbial communities” by T. J. Bohn and D. P. Lettenmaier

Anonymous Referee #1

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This paper addresses an important question in the assessment of climate warming effects on the methane emission from Boreal and Arctic wetlands: the potential effects of adaptation or change of bacterial communities. The approach of the authors is modeling of future methane emission from the West Siberian Lowlands. They apply the VIC land surface model, in combination with the Walter-Heimann wetland methane model, a model that is applied widely. They conclude that if microbial populations simply adapt to higher temperatures, the future increase of methane emission at the end of this century will rise with 6% only, while the emissions will more than double if also shifts in

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microbial communities occur, by migration of southern communities to higher latitudes.

Although the approach of using models for exploring and quantifying these effects is in itself a valid, the way in which the authors have implemented it in this article is highly questionable, as detailed below.

In the first place, the Walter-Heimann model is not the best model for this purpose, since it treats the methanogenic and methanotrophic communities as a 'black box', parametrized by a few bulk parameters describing the methane production and consumption rates and their temperature sensitivity. Second, the authors derive these parameters for northern and southern microbial communities by model optimization. However, the optimization procedure is not described adequately in the article. It apparently does not take into account the way in which the various model parameters may influence each other, and constraints by data on microbial population parameters are not made clear. The optimization results in unlikely high values for the temperature sensitivity (Q10) parameter of methanogens for southern microbial populations, which in turn has influenced their model results. Third, the authors hardly consider the effects of various wetland types, e.g. differences between oligotrophic and eutrophic wetlands, which may have influenced their supposed latitudinal differences between microbial populations, and might be more important than climate-related differences. Fourth, microbial activity being the key point of the paper, one might expect a better use of the growing body of literature on the characterization of methanogenic/methanotrophic microbial populations in wetland soils.

Because of these flaws, the conclusions of the paper on the effects of microbial population changes remain speculative. In the discussion paragraph several of the uncertainties in the model application are discussed, although not exhaustive. In particular the uncertainties resulting from estimating the model parameters by optimization are not discussed.

The authors could try to improve the paper by constraining their estimates of microbial

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population parameters using experimental data, and not only model optimization. However, I doubt whether this is possible given their study area. Alternatively the authors could experiment with a range of parameters for the microbial population behaviour, rather than relying on a single set of parameters derived from optimization. A new version of the paper should be based on a new set of model experiments, with microbial model parameters that reflect realistic scenarios of microbial population change rather than the optimization results that are used now. This is beyond 'major revision', so I suggest to reject this paper in its present form. Below more detailed comments are given.

Page 16333, lines 21-24 and 26-28. The fact that the eutrophic mires in the south emit more methane than the tundra wetlands, is not necessarily an effect of climate and vegetation alone, but likely also relates to trophic status. In eutrophic wetlands the availability of nutrients allows a higher primary production and hence a higher methanogenic substrate production. Many tundra wetlands on the other hand are meso- to oligotrophic. The paper by Glagolev et al does not infer that the observed differences are related to climate only, as is suggested in line 26-28. Moreover the paper of Glagolev is based on surface flux measurements, while incubation experiments would be a more appropriate to assess climate-related differences between microbial communities.

Page 16335 line 20-23. It is not clear how the parameters for the wetland methane emission model were calibrated. This information is crucial however. The Walter-Heiman model has a large number of parameters that are poorly quantified and often need to be calibrated, including microbial population parameters like the methane production rate, the temperature sensitivity, but also other parameters like plant transport rate and oxidation within the root system. These parameters tend to influence each other, as is demonstrated in a paper on sensitivity analysis of the Walter-Heimann model by Van Huissteden et al (Biogeosciences, 6:3035-3051, 2009). If several of these parameters are poorly constrained by experimental data, it is impossible to obtain

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reliable estimates of one of the parameters by optimization, since equifinality of parameter sets may occur. Equifinality results in widely differing parameter sets, all with a good model-data fit. So, if you use optimization to obtain a Q10 value for methanogenesis, the constraints on other microbial population parameters and any other parameter that influences the surface flux, should be well defined. If not, the resulting optimization may give invalid results. For instance, in the Walter-Heimann model the value assumed for oxidation during plant transport may strongly influence optimization results for the methane production rate and temperature sensitivity parameters, as is demonstrated in the sensitivity analysis cited above.

Page 16335 line 27-30. Q10 values between 9.7 and 11.7 are unrealistically high. Data from incubation experiments in general do not indicate such high values. This indeed makes me worry about the optimization from which these values have been derived.

Page 16336 line 1-2. Again, the paper by Lupasco does not consider latitudinal differences on the scale of the West Siberian Lowlands, but differences between wetland vegetation types.

Page 16336 line 3-4. Q10 is not the only microbial population parameter in the Walter-Heimann model. Why is the methane production rate R0 not considered here – this may be equally responsible for the high fluxes in the south?

Page 16338 line 22-23. 'Population shifts were modeled as a complete replacement of northern microbial species abundances with those of the south'. This is nonsense. It is completely unknown how the microbial population parameters in the Walter-Heimann model relate to microbial species abundances.

Page 16338 line 23-25. Please explain the parameter abbreviations in the text.

Page 16340 line 21-24. How is GWP calculated? This deserves more attention than it is given here, see e.g. Frolking et al., Journal of Geophysical Research, 11, 2006.

Page 16343 line 12-13. As detailed above, the large increase in methane emission can

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be quite well an artefact of the optimization of Q10.

Page 16348 line 19. More can be added to the list of model oversimplifications. I miss any references to the uncertainties resulting from the optimization procedure. Another oversimplification is that changes in wetland nutrient status, topography and vegetation composition by thawing permafrost are not included. This might even be more important than changes in microbial communities by climate change.

Page 16348 line 24-25. The lack of data, noted here by the authors, confirms that spatially varying microbial population parameters are still rather hypothetical. However, I wonder why the authors did not support their case by using literature on incubation experiments and (eventually) metagenomic analysis of microbial populations, rather than considering surface flux observations only. Surface flux observations do not give explicit clues to microbial population variation.

Overall evaluation:

Does the paper address relevant scientific questions within the scope of BG? Yes. Does the paper present novel concepts, ideas, tools, or data? Yes. Are substantial conclusions reached? Yes, although these are insufficiently supported by the methods used. Are the scientific methods and assumptions valid and clearly outlined? No, see above. Are the results sufficient to support the interpretations and the conclusions? No. Is the description of experiments and calculations sufficiently complete? No, in particular the optimization by which crucial model parameters are obtained is not described in sufficient detail in this paper. Do the authors give proper credit to related work and clearly indicate their own new/original contribution? Yes. Does the title clearly reflect the contents of the paper? Yes. Does the abstract give a concise and complete summary? Yes. Is the overall presentation well structured and clear? Yes. Is the language fluent and precise? Yes. Are mathematical formulae, symbols, abbreviations and units correctly defined and used? No, in some cases model parameter abbreviations are not explained in the text. Should any parts of the paper be clarified, reduced, combined or

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eliminated? No. Are the number and quality of references appropriate? No, see above. In at least two cases inappropriate conclusions are drawn from the references. Is the amount and quality of supplementary material appropriate? Not applicable.

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