

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 #2

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Review on the manuscript titled ‘Exploring the response of West Siberian wetland methane emissions to future changes in climate, vegetation, and soil microbial communities’, submitted for publication in Biogeosciences by Bohn and Lettenmaier.

The presented manuscript aims at evaluating the impact of shifts in the responses of microbial communities towards environmental drivers under future climate change. The study focuses on the West Siberian Lowlands as a target region, comparing trends in methane emissions between a reference historic period and the final decades of the 21st century as a response to changes in biogeophysical and biogeochemical param-

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eters. With very high potential increases in CH₄ emissions to be expected from high latitude wetlands in the upcoming century, and at the same time significant uncertainties associated with the feedback mechanisms between changes in environmental drivers of the carbon cycle and the microbial communities, this research topic is very relevant to improve our capability to simulate the fate of northern carbon reservoirs under climate change.

The manuscript is well written and structured, and the major elements of the research presented are in most cases clearly described and supported by citations. Also the discussion addresses most of the weak points in the presented study in a straightforward way. However, there are certain shortcomings in the methodology, and sometimes in the description of it, that need to be straightened out in the revised version of the manuscript. One main element that needs to be changed in my opinion is the objective of the paper: As I see it, the authors describe rather a thought experiment than realistic scenarios of future trajectories of the fate of the WSL region. This needs to be stated clearly from the beginning, instead of talking about ‘brackets’ every now and then. Their scenarios, both the adaptation and the shift version, appear to be arbitrary, subjectively chosen from a large portfolio of setups, along the lines of ‘imagine what would happen if . . .’. It becomes neither clear why these setups were chosen, nor how sensitive the presented results are towards modifications in the scenarios. Therefore, the authors need to add a justification for the selected scenarios, and also need to add more setup options to provide a range of potential responses, instead of just those two.

Further aspects to be improved include: i) how robust is the internal structure of the Walter-Heimann model towards shifts in just one of its parameters, as implemented when adjusting the T_{mean} value in the ‘adaptation’ scenario. In other words, is the output, the net feedback towards a suite of environmental drivers, still plausible when shifting one parameter and leaving the others constant, or will (parts of) the output be distorted? The effect of adjusting T_{mean} should e.g. be tested based on the historic dataset.

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ii) How were the chosen parameter settings in the Walter-Heimann model derived, and how trustworthy/robust are the chosen settings for this study?

iii) What other setups could be used to simulate adaptation towards modified environmental conditions under future climate change? Why was the current version (i.e. adjusting Tmean based on averaged shifts in temperatures) chosen?

iv) Is it sufficient to simply focus on mean climatological shifts when evaluating the future responses of microbes to changes in environmental drivers? What would be the effect of more pronounced climate extremes (drought periods, heat waves, summer-time peak temperatures) towards the stability and functionality of the microbial community?

v) The 'shifts' scenario, which entirely replaces the northern microbial community with the southern one, appears to be a rather extreme example. One (or more) additional scenarios that apply a more moderate setup, e.g. selective replacements based on e.g. the distribution and/or extent of wetlands, certain climatological features, etc., would clearly strengthen the message of this manuscript.

Summarizing, the authors should make clear from the beginning that they are testing the relative impact of nonlinear shifts in microbial community responses to climate change for a range of hypothetical scenarios, and not necessarily present realistic forecasts. It would clearly strengthen the paper if a thorough discussion would be provided how likely these scenarios are. In addition, results should be supplemented with uncertainty ranges, taking into account e.g. the confidence in the chosen parameter settings, the spread of the CMIP5 climate scenarios, etc. I do not think that such modifications would change the main message of this manuscript, i.e. that adaptation processes in biogeochemical responses to climate change might have a significant impact on forecasts, but that the range of results is considerable since we do not know enough about such nonlinear processes. Still, additional scenarios and an extended discussion on uncertainties are highly important to strengthen this message. I therefore recommend

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to accept this paper for publication only after major revisions along the lines outlined above.

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