

Interactive comment on “Comparison of greenhouse gas fluxes and microbial communities from tropical forest and adjacent oil palm plantations on mineral soil” by Julia Drewer et al.

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Received and published: 12 November 2020

Anonymous Referee #2 Drewer and colleagues present a manuscript about greenhouse gas emissions from tropical forest and oil palm plantation soils in the SABAH landscape of Southeast Asia. They compare emissions of N₂O, CH₄, and CO₂ between the two different land use systems, want to upscale their results and try to find links between microbial communities and greenhouse gas fluxes.

Response: We thank the reviewer for taking the time to read and comment on our manuscript. We reply to individual comments in turn below.

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I think you should exclude the whole microbial part of the manuscript to strengthen the greenhouse gas flux part. It is hard to see a substantial link between your results from microbial analysis and the greenhouse gas fluxes. The microbial part of the discussion remains very speculative because you are comparing diversity/composition with greenhouse gas fluxes. It would have been better to have process rate measurements in the field (e.g. nitrification etc.) linked to functional gene abundance in soil samples where you had installed your static chambers (e.g. all the N-cycling genes, *mcrA* and/or *pmoA*). That would have been a sound story. Now you are reading two stories in one manuscript that do not strengthen each other.

Response: We could have done many other things but our goal here was to both describe how the treatments affect broad microbial communities, but also use this data in the predictive models. We still believe the microbial data helps in identifying differences between sites and use the microbial metrics in the models to try and explain fluxes.

The study design is the major drawback of the present manuscript. I do not understand why static chambers were not randomly installed. There was no plot selection as far as I can see. Why? There are only sites and per site you installed a different number of chambers (this is $n=1$) without any design! How do you want to compare fluxes between land use systems if there are not enough replicates but only pseudoreplicates? How do you test differences of soil properties between the different land use systems?

Response: The referee misunderstands the sampling design we used, and we have clarified this in the manuscript. We did install approximately equal numbers of chambers at each site, though this was not exact. To clarify the SAFE design, there were replicate sites for each land-use, with chambers installed at random locations within these sites. We had 3 forest sites each with 8 chambers, and 3 OP sites with 8 or more chambers. The only anomaly was OP7, where we tried to capture topographic variation, so had 12 chambers. The riparian was the outlier with only 4 but we don't focus on that in the land-use comparison. Our statistical analysis does not assume a balanced design, and can cope with the slight difference in the number of samples between sites.

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We did not aim to test for differences in soil properties between the different land use systems, only whether these could explain the variability in N₂O fluxes.

In my opinion the argument that Bayesian methodology is used to overcome the disadvantages of small sample size and high variability is very weak in your case.

Response: The methodology does not overcome the problem of small sample size and high variability, but makes the uncertainty associated with this very clear, by characterising the posterior probability distribution properly. It is thereby an appropriate method to use in this context.

You could have easily selected few random plots within each site and then installed the same amount of chambers within each plot to overcome the different problems.

Response: See response above, this is basically what has been done with one exception.

Interactive comment on Biogeosciences Discuss., <https://doi.org/10.5194/bg-2020-297>, 2020.

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