

Biogeosciences Discuss., referee comment RC1  
<https://doi.org/10.5194/bg-2021-41-RC1>, 2021  
© Author(s) 2021. This work is distributed under  
the Creative Commons Attribution 4.0 License.



## Comment on bg-2021-41

Anonymous Referee #1

---

Referee comment on "Plant genotype controls wetland soil microbial functioning in response to sea-level rise" by Hao Tang et al., Biogeosciences Discuss., <https://doi.org/10.5194/bg-2021-41-RC1>, 2021

---

General Comments: The paper by Tang et al. uses an experimental marsh organ set up to examine the interaction of plant genotype (those adapted to flooding vs those unadapted) to flooding duration (daily, weekly, monthly). The authors hypothesized that flooding effects on microbial enzyme activity, decomposition, and community structure will be stronger in soils where the plant is not adapted to flooding than in systems where the plant is adapted to flooding. In general the paper is well written (though personally, I am not a fan of the extensive use of passive voice), the data are clear and well-presented and the results make an important contribution to the literature. My primary concern with the results, as presented, is in the lack of description for tests of assumptions for the statistical analyses. No data are presented on whether tests of assumptions were performed prior to ANOVAs, the the enzyme activity and decomposition variables, nor for the PERMANOVA. in fact, the authors highlight the differences in the variability of the microbial community as a function of genotype, which technically violates the assumption of equal variances that underlies PERMANOVA analyses. The conclusions fo the paper would be stronger if the authors documented the results for the tests of assumptions (e.g. levene's test, betadisper, etc.) along with their statistical analyses. Lastly, both in the abstract and the discussion, the authors continually refer to the effects of climate change on microbial activity/structure. I would recommend that the authors use caution with this broader construct. Their work was very specifically about flooding, not the myriad other affects of climate change. The authors argue that flooding/sea level rise is the most important climate change impact in coastal systems, which may be true, but this does not change the fact that there experiment was not a multifaceted climate change experiment, it was a single environmental factor x genotype experiment. Therefore conclusions such as " adaptive genetic variation in plants can suppress or facilitate the effects of climate change on soil microbial communities" over-states what can be concluded from this work. I would recommend that the authors keep statements regarding the conclusions of this work firmly grounded in the effects of flooding, rather than the effects of climate change more broadly

Specific comments:

Line 49: this seems like an over-statement. There are several examples of work that has been done on linking plant infraspecific variability to C cycling, some of which was published by these authors (e.g. Mueller et al.). I also find the "has not been done yet" argument to be less convincing than stating why it is important that the work be done. Perhaps switch this statement around to make it more clear why this study is needed and what knowledge gap it will fill rather than suggesting that there has been no work done on the topic.

Fig. 1: there is a decent amount of redundancy between the figure caption and the text, so if you are short on space you could edit this caption down.

Section 2.5: were tests of the assumptions underscoring these stats performed? This tests should be described in the methods and the results should be outlined in the results section.

Fig. 3: I find this figure to be really confusing, and it isn't clear to me what it adds that cannot already be gleaned from Figure 2. It isn't exactly clear what is being compared - did the authors pick whichever max-min was largest from among the 4 enzymes or is this averaged across enzymes and averaged across flooding treatments? Perhaps it is because I wasn't entirely clear on what the figure was showing, but it made it difficult for me to figure out what it added to the story. I would think that the authors could remove it all together, or if they choose to keep it, it would be helpful to have more clarity around how they aggregated their data and what conclusion can be drawn (e.g. is it average EEA change across all flooding treatments, sum of all EEA changes?).

Line 260: One of the assumptions of permanova is that variances are equivalent. This appears to violate that assumption and should be tested for using beta dispersion tests. This would support your assertion that the variability is higher in the unadapted genotypes, but it would mean the authors would need to rethink their permanova.

Line 266: the authors should be commended for not conflating the taxonomic composition of their microbial communities with what might occur in situ.

Discussion (first paragraph, principally) - I think the authors should keep the focus of their work on flooding, rather than climate change more broadly, as flooding was the only facet of climate change that was directly tested in this study.