

Biogeosciences Discuss., author comment AC2  
<https://doi.org/10.5194/bg-2021-51-AC2>, 2021  
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## Reply on RC2

Aditi Sengupta et al.

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Author comment on "Disturbance triggers non-linear microbe–environment feedbacks" by Aditi Sengupta et al., Biogeosciences Discuss., <https://doi.org/10.5194/bg-2021-51-AC2>, 2021

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### General comments:

This is an interesting paper and I think it represents an important advance in linking microbial community structure with function by using an experiment to support a revised conceptual framework. In this study, Sengupta et al. find that beyond a desiccation threshold, microbial communities experience strong homogeneous selection for a subset of taxa and respiration rates plummet. Interestingly, stronger deterministic selection (likely due to strong environmental filtering) is associated with reduced respiration (again likely due to strong environmental controls on this function), with a transition towards less favorable OM thermodynamic conditions as a putative mechanism connecting the community with the function. I enjoyed reading the study and offer more detailed suggestions below to increase the clarity of the manuscript.

- Thank you for your feedback and comments. We will address the comments in detail in our revision. Below we summarize how we will respond to each comment.

I know there is probably a word limit for the abstract, but having read it before reading the full manuscript, I was unclear about the study's aims and how to interpret the results from the study. I think there are some really interesting results that perhaps could be more clearly articulated in the abstract.

- We will rework the abstract to improve the messaging.

The introduction is somewhat long (11 paragraphs). As a reader, I was losing sight of the big picture. In particular, one major contribution of this paper is a modification of the Hall et al. framework, which I think is somewhat buried in the introduction. What about making an additional section (starting on Line 53) called "Refining the link between microbial communities and ecosystem functions" or something that would better emphasize the conceptual contributions of this manuscript?

- We will edit the introduction per the reviewer's suggestion to help make it more succinct and highlight conceptual contributions of this manuscript. We will also

summarize main findings of the Hall et al., study as commented as a line-specific comment below.

Specific comments:

Lines 11-14: Can the essence of the conceptual framework be communicated more specifically? Perhaps emphasize the causal linkages (from Fig. 1) so the reader will understand the context of the results presented in the abstract (see also line 21)?

- Will attempt.

Line 16: Maybe specify that these are bacterial communities

- Will edit.

Lines 18-20: I understand what this means after looking at figures 3 and 4, but maybe "relationships among community assembly, respiration, and OM thermodynamics" could be rephrased slightly so it doesn't appear to conflict with the description of respiration as a step function (line 18, referring to transitions with duration of drying). What about something like "While these responses were step functions of desiccation, we found that in deterministically assembled active communities, respiration was lower and thermodynamic properties of organic matter were less favorable."? Just a suggestion, maybe the sentence is clear for other readers.

- Will edit.

Lines 38-42: Because of the crucial role that the framework by Hall et al. plays in this manuscript, I think the framework could be briefly described with a bit more detail here. It is somewhat difficult to keep track of what the Hall framework was prior to being modified here. Maybe a sentence clarifying that "Microbial membership influences community properties and microbial processes, which in turn regulate ecosystem fluxes; all of these components can be further modified by environmental variation (Hall et al. 2018)." This would also help readers who haven't read Hall et al. 2018.

- Will edit.

Figure 1 is great, but is it missing a direct link from environment to function? Or is this implied by the combination of arrow 3 and 5?

- This was on purpose and is implied by the combination of arrows 3 and 5.

Lines 75-86: On the one hand, I understand the use of "emergent property" here because the relative influence of determinism and stochasticity is unpredictable on the basis of membership alone. But on the other hand, the relative contribution of stochastic and

deterministic processes is a tally of the processes that shape microbial community membership, which could be said to emerge from the assembly processes. So, I suppose I'm getting turned around here about what is emergent: microbial community structure or the ecological processes that generate structure from which they were inferred? I'm not suggesting a change to this terminology, I'm just noting my conflicting thoughts about it and maybe looking for some clarification in the text on why the processes are an emergent property of the community, instead of vice versa.

- A very interesting point, thank you for raising it. We agree, it is a little fuzzy in terms of what comes first and what 'counts' as an emergent property. Taking inspiration from Hall et al. (2018) it seems that the quantitation of assembly is an emergent property, per their definition of any property: "Microbial community properties (Fig. 2) represent an integrated characteristic of the microbiome that has the potential to predict or at least constrain the estimates of microbial processes." They go on to state "It is generally agreed that emergent properties refer to a quality of the whole that is unique and distinguishable from the additive properties of its constituents." As the reviewer noted, this suggests that the balance between stochastic and deterministic assembly fits squarely into the definition of an emergent property. However, we also see the reviewer's point that stochastic and deterministic factors lead to microbial membership. On the other hand, because assembly is influenced by biotic interactions, membership itself influences assembly. Given all of that, we elected to add a few sentences about this in the Introduction and modify the conceptual model to have a double headed arrow between microbial membership and microbial properties. We feel this might often be a reflection of reality, whereby other kinds of emergent properties (e.g., biomass density) may feedback to influence membership.

Line 344-360: I'm not sure I fully understand what to do with the CPI output. The writing here is clear. I get the concept, I get the computation of the metric, and I get the interpretation of the metric in terms of the relative contributions of each bioreactor. But I'm kind of missing an explicit statement of what the CPI values can tell us about microbial processes in temporally varying environments in this study. It tells us about the variation among replicates, which should, in principle, be rather low if the sediment community was well homogenized. But what would it mean (ecologically, in the context of the conceptual framework) if a CPI value was close to 0.5 or 1? Maybe a hypothetical example or some hypotheses relating desiccation frequency to CPI in the context of Fig. 1 (arrow 5) would be helpful.

- In the context of this kind of experiment we think of the treatments as potentially changing the probability of outliers (i.e., hotspots) emerging. That is, we hypothesize the frequency of wet/dry transitions and/or the duration of drying could lead to different levels of variation (e.g., in microbial communities) across replicates. For example, each time sediments go dry, the exact spatial distribution of water films that remain will differ across the replicates. In turn, it seems plausible that greater among-replicate variation would be expected in treatments with more wet/dry transitions. High values of CPI require variation across interrogated locations/times (in our case, treatment replicates) because high CPI results from large contributions from hot spots/moments. In turn, a hypothesis is that CPI will increase with the number of wet/dry transitions. That hypothesis was rejected in this experiment, though we feel it deserves additional evaluation, potentially in studies with larger sample sizes per treatment to more robustly quantify CPI.

Lines 361-429: I appreciate the extraordinarily clear presentation of the results. It was a

joy to read. Lots of interesting aspects of this study to weave together and it was very expertly done here by the authors.

- Thank you.

Lines 452-453: I think this is an important point that could be emphasized more strongly. Why is this particular aspect of the study so crucial? That many microbes in the environment are inactive, and that active microbes remain sensitive to abiotic stresses while also being responsible for ecosystem functioning seems like a key detail to highlight in the context of the framework.

- Will edit and reflect this aspect.

Lines 469-473: One reference that might be helpful for the discussion is Chase (2007) Drought mediates the importance of stochastic community assembly, PNAS.

- Will add.

Lines 482-489: Great point. Yes, I think the environmental effects are strong drivers of the relationships observed here. There could also be a biomass effect if the desiccated treatments simply have fewer cells, most of which may be inactive due to desiccation stress.

- Agreed. Thank you

Lines 517-520: This is a really cool aspect of the study! Interesting way to show the link between desiccation in the environment and thermodynamic favorability for microbial growth.

- Thank you

Lines 539-544: One thought about the CPI output here is that the difference between the 31- and 34-day treatments is actually greater than their nearby position on the continuous x-axis might imply. The 34-day treatment experienced more or less constant conditions, and was only rewetted during the incubation. The 31-day treatment experienced a single pulse of water followed by a subsequent redrying event prior to the incubation. Perhaps this pulse generated among-replicate variation in the microbial community such that the reactor with high function was also very different in community composition. While homogeneous selection dominated this treatment overall, if the null model was constructed using all taxa observed in the study, it's not surprising only a subset of these taxa was able to survive desiccation (hence low beta-NTI). But if different taxa survived in different replicates, this could explain the high CPI. Is raw beta-diversity (or a within-treatment beta dispersion metric) of the active *community a better predictor of CPI than the beta-NTI metric for this study?*

- Really cool idea, thank you. We will evaluate the degree to which raw beta-diversity

and beta-dispersion can explain variation in CPI.

Lines 556-558: Yes, very interesting hypothesis and I suspect this is likely to be the case as long as environmental stresses (like desiccation) are homogeneously distributed in space/time. If stresses are spatio-temporally asynchronous, you might find high CPIs as hot spots/moments shift in space and time in response to environmental forcing.

- Thank you

Technical corrections:

Line 79: Seems like there's a typo here. "is an emergent property" maybe?

- Will edit

Line 107: "preferential use of OM"

- Will edit

Line 141: "biogeochemically"

- Will edit

Line 303: "reference framework graphic" should probably be "Figure 1"

- Will edit

Line 467: "outcomes"

- Will edit