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Comment on bg-2021-51

Stephanie Jurburg (Referee)

Referee comment on "Disturbance triggers non-linear microbe–environment feedbacks" by Aditi Sengupta et al., *Biogeosciences Discuss.*, <https://doi.org/10.5194/bg-2021-51-RC1>, 2021

The authors present work of good quality, and I especially commend them for making the data available already. My biggest concern is the presentation of the experiment's hypotheses as a conceptual framework, as the notion that microbial community assembly influences and is influenced by microbial functions is not novel. Rather, the authors present what seems to be the basis for a very interesting SEM in their final figure. They might consider pursuing this! Additional comments are listed below in order of decreasing importance.

- The authors should be careful with their description and interpretation of deterministic forces throughout the manuscript. Deterministic forces are caused both by biotic interactions and abiotic forces, and the research presented cannot disentangle these two. I therefore think it is important that the authors temper their discussion of determinism as an informative emergent property. In L85, they state "a stronger influence of determinism over community assembly is hypothesized to cause higher respiration rates (a microbial processes) due to a larger contribution of well-adapted taxa (Graham and Stegen, 2017).", however this is entirely dependent on the identity of the deterministic force and the community it is exerted upon. A stronger influence of determinism on microbial community assembly can be caused by an infinity of factors, but it is these factors that determine how the community is shaped. Thus the expected effect on the community cannot be linked directly to the change in the relative influence of determinism.
- While I think that the sequencing of both gDNA and cDNA is a strong feature of this manuscript, I don't think that the authors discuss it in sufficient depth. Why might the disturbances change the relative strength of deterministic forces according to cDNA but not gDNA?
- In figure 2, the authors present the treatments in a different order than what is used throughout the rest of the manuscript (i.e., dry days). I think this is a great description of a complex experiment, and I would suggest the treatments are reordered to reflect the order in the analyses
- In figures 3 and 5, I would like to see the points colored by treatment. In 5B, the positive correlation is driven (almost?) entirely by the differences between the two treatments with most dry days and the rest. I would be curious to see whether that is

the case in the rest of the figures.