SOIL Discuss., referee comment RC2
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Comment on soil-2021-29

Anonymous Referee #2

Referee comment on "The role of ecosystem engineers in shaping the diversity and function of arid soil bacterial communities" by Capucine Baubin et al., SOIL Discuss., https://doi.org/10.5194/soil-2021-29-RC2, 2021

I enjoyed reading the work presented in this manuscript. The question is straight forward and important to better understand microbial communities among patch types in arid ecosystems. The MS is written well. There are several instances in this MS where I was unsatisfied with the amount of information presented in their methods that need clarification before its clear to the reader how the study was performed. Below are specific comments regarding this issue that would ideally make the manuscript repeatable. As it stands, it is not based on the lack of information provided and significant rewrite is recommended. There are also some overall recommendations on how to present results.

Methods

- How were the soils actually sampled? There is no mention of coring instrument, number of subsamples within replicate plots. Please add in this information. Line 100 states there is 5g for molecular work and 20g for water content so must have taken multiple subsamples and pooled into a composite sample.
- Please add more information on how soil chemistry was measured. Citing standard methods and then not detailing how nitrate, ammonium, and P were extracted (what concentration of extract? How were the extracts measured – on what instrument?) is not enough information.
- Likewise to point 2, the authors must provide more details regarding their "community analysis" (I would refer to this as bioinformatics analysis and leave out the information regarding ordinations and statistics). Specifically:
  - What parameters did you use for DADA2 including trimming or truncating sequences after reviewing sequence quality?

    - Its assumed that the authors used a 99% identity cutoff for ASVs – can they confirm?
    - What additional steps were included after taxonomic assignment and what database classifer was used? Were contaminants (mitochondria, unclassified, chloroplasts) removed prior to downstream analysis?
    - Were the sequences sub-sampled at the same sequencing depth and/or normalized to account for that?
- I recommend having a separate statistical analysis section after describing how authors measured their response variable (at end of the methods). It seems as though there are statistics that were included as supplemental material but not described at all in the manuscript (e.g., adonis test included chemistry variables). Please describe all statistics used here and include any statistical software and package used (adonis is the function, but the actual test is a permutational multivariate ANOVA).

Results

- L156: I'd prefer a table of mean and standard error values for each physico-chemical variables presented along with statistical outputs.
- PCA and Figure 1: + or – signs are unnecessary. The direction of the arrows/vectors denotes the direction of change.
- L174: NMDS does not suggest any significant differences. Similar to PCA, it is just a visualization tool to view multivariate responses such as community composition. Please correct.
- Table A10 suggests either the same or a separate perMANOVA test was run with physiochemical data. This test is for categorical data. If the authors wish to understand environmental correlates, I recommend either the envfit function along with NMDS or a constrained ordination, such as redundancy analysis (or whatever appropriate analysis fits your data structure).
- Figure 2: Please include centroids or atleast ellipses around different patch types similar to Figure 1 – this is quite helpful in delineating compositional changes.
- Please separate Proteobacteria out to classes (Alpha-,Beta-,etc.) – this is important information as these classes may differ in their ecologies across ecosystems and fairly routine practice for working with 16S community data.
- What is the justification for only targeting 3 of the dominant phyla? Based on Figure 3, there are several other phyla that may be shifting among patch types, such as Bacteroidetes, Acidobacteria, and Firmicutes. These phyla, although less abundant, are important components of the community. If interested in dormancy, Firmicutes is particularly important in response to drought (see Placella et al. 2012. PNAS).
- Also consider what other taxonomic classifications are comprising these changes in phyla among patch types – I recommend digging deeper into the taxonomic classifications (dominant families or even genera that change among patch types).