

SOIL Discuss., referee comment RC1
<https://doi.org/10.5194/soil-2021-88-RC1>, 2021
© Author(s) 2021. This work is distributed under
the Creative Commons Attribution 4.0 License.



Comment on soil-2021-88

Anonymous Referee #1

Referee comment on "The function and composition of active bacterial communities diverge during the hydration and desiccation of desert biocrust - a field study" by Capucine Baubin et al., SOIL Discuss., <https://doi.org/10.5194/soil-2021-88-RC1>, 2021

General comments:

The manuscript entitled "The response of desert biocrust bacterial communities to hydration-desiccations cycles" is an interesting manuscript which focusing on the effects hydration-desiccations cycles on biocrust bacterial communities. The introduction sets scene very nicely and the authors also clearly show the need for studying hydration-desiccations cycle, but see comments below for several ideas that need justification and/or more details. Some parts of the approaches are not appropriate and need more clarification (see comments below about major concern). Although this paper focused on bacterial communities but the results did not provide typical diversity analysis such as alpha and beta diversity. Discussion and conclusion will need to be revised when the major concern has been addressed. Overall, I think that the manuscript idea is interesting and will be valuable for the scientific community. However, additional work is needed to address major concerns and improve several parts of this manuscript to be more transparency and justified.

Title

The title indicates what this research is about but it does not provide any information about key results. I would suggest revising the title to be more specific. What is the key

result?

Abstract

Line 20: How does rain-mediated dynamics were assessed? Please explain experimental setup briefly? And provide brief details about bacterial communities measurement.

Line 20: What does active community mean? Active crust community? Active bacterial community? Please be more specific, it is unclear.

Line 22-24: Why focus only on phototrophs? What about other bacteria?

Line 27-28: When Cyanobacteria increased and Actinobacteria decreased, what does it really mean for biocrust?

Introduction

In general, hydration-desiccation cycles were introduced very nicely. However, this paper focused on bacterial communities, but very little information about biocrust bacterial communities was introduced. There are other studies which also focused on biocrust bacterial communities, please introduce them here. What have they done? What were the general bacterial composition? Were there any patterns that other researchers found about biocrust bacterial communities? Is there a reason why this paper should specifically focus on Cyanobacteria and Actinobacteria? Are these the only two phyla found in biocrust?

Line 48 "of soil respiration(Castillo-Monroy et al., 2011)" – add space before parenthesis

Line 50 "trace gases(Meier et al., 2021; " – add space before parenthesis

Materials and Methods

There are many types of biocrusts. What kind of biocrusts were collected? Were they all the same biocrust types?

Line 86-87: Please provide a reference.

For section 2.6 Community analysis, please report the number of reads in each step (number of raw reads, filtered reads, after chimera removals, etc.).

What is the average number of reads per sample? And what is the range (min – max)?

MAJOR CONCERN! Since the length of the sequences are different because of different platform, please provide details about how the analysis were performed to account for this issue. This section is also crucial in case other researcher would like to follow or repeat the analysis. Please make sure that all the details required for the experiment are included. Currently, it is not sufficient.

Line 172-173: What is the criteria for picking out "genes of interest"?

Results

Generally, simple diversity analysis (alpha and beta diversity) should be provided for microbiome paper. However, only relative abundance plot was provided. I would suggest including alpha and beta diversity analysis to confirm significant differences that were found in relative abundances comparison.

Line 190-201: Statistical test must be provided, reporting p-value only is not sufficient. Please check how statistical test results should be reported. Please also indicate significant differences in figures. Currently, the plots do not have these information.

Line 209-210: In total, how many bacterial phyla were found in these data?

Line 212-216: Please use appropriate statistical results report format. Reporting p-value only is not sufficient.

Figure 3: **MAJOR CONCERN!** Unless the author provide detailed explanation about how different sequencing platform and primers were accounted for. I think the differences might have been because of different platform used.

Discussion

Line 250: What exactly is "cyanobacterial activity" that was measured? How do we know that it is cyanobacterial activity not other bacteria?

Line 276: Perhaps beta diversity might help confirming this claim.

Conclusion

This might change when different sequencing platforms were taken into account.