**Referee #1:**

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| Referee comment | Author response |
| Title: This could be more simple and specific. A “catastrophic climate event” is rain in the Atacama. These extremophiles are halophiles. There was no adaptation “mechanisms” reported. The running title could also be more specific. | We re-wrote the title to address concern brought up by both referees |
| The first sentence of the abstract should be deleted, as this is common knowledge to the readership a microbial ecology journal. | We agree, and dropped the redundant first sentence |
| Ln 42-44: There are enough studies of temporal dynamics of microbial communities in extreme environments that this should be deleted or rephrased to specify that you mean extremophilic community responses to disturbance. | Rephrased to be more specific; lines 46-48. |
| One sentence summarizing the methods would be useful in the abstract before describing the results. I do not yet know whether this study is cultivation-based, metagenomic, or other, how many samples, from what geographic locations, etc. At least some of that information should be here. | Added introductory overview on the study’s design; lines 51-53. |
| Why not mention in the abstract that the samples come from the Atacama Desert? That would get my attention. | Added mention in the title and abstract; line 49 |
| Ln 50: As far as I can tell, there is no “proteome” studied here. Presumably, the authors mean “predicted proteins” from metagenomics? | This was misleading. Changed to “…broad predicted proteins…”; line 56 |
| Ln 123: What is a “halite nodule”? Some basic information would be useful here, for example, what is the approximate size and/or mass of a nodule or sample? Would one sample be a collection of many tiny halite nodules, or one or more larger nodules? | We added some details about the nature of halite nodules in te introduction and methods; lines 109-111, 144. |
| Ln 133: Please change “16S rDNA” to “16S rRNA gene” throughout the manuscript, including text, figures, and tables | We fixed this inaccuracy throughout the manuscript, the legends, and supplementary materials. |
| Ln 140: What is WMG? | WMG sequencing is defined as “whole-metagenomic” on line 278, however we removed all mention of this abbreviation until this is properly defined in the results. “WMG sequencing” is replaced with “shotgun metagenomic sequencing” in lines 160, 193, and 251 |
| Ln 141: Are these “whole genomes” or metagenomes? They sound like metagenomes. | We clarified this by replacing with “whole-genome metagenomic sequencing” on line 161. However, we would prefer to explicitly refer to shotgun sequencing of microbial community DNA as “whole metagenome sequencing” instead of just “metagenomic sequencing”. By definition of the term, community rRNA gene sequencing is also technically “metagenomic”, which causes some confusion in the field. |
| Ln 181: typo, should be “--use-metaspades” | Thank you for catching this. Fixed on line 209 |
| Ln 210-221: Do you have a reference for this “taxonomic rearrangement index”? If this is something new that you are introducing (I see later that it is), I suggest reconsidering the name. As far as I can tell, this is a measure of the difference in abundance of each functional prediction (more accurately, the abundance of each contig with a particular functional prediction, under the assumption that the contig abundance is the same as the gene abundance, which is a caveat that should be explicitly stated) between two samples. I do not understand how this relates to rearrangement. | We apologize for the confusion – this calculation was not well explained. We added clarifications to the MS. The RI does not measure the change in total abundance of gene functions. Instead, it measures the change in the abundance of the organisms that carry them. Note that the formula calculates the weighted average of the absolute values of the contig abundance changes. For example, the total abundance of photosynthesis genes between two samples might stay the same, but they might be carried by completely different organisms (which would result in a RI=1, but no net change). Edits made on lines 257-268 |
| Ln 241-257: most of this belongs in the methods section | We moved the section into the methods, and the sentence about specific rain information into the introduction. |
| Ln 248-249: I appreciate that sample collection must be exceedingly difficult and expensive. However, you are describing evidence of community compositional shifts and resilience in response to disturbance based on only four time points, and the first time point after the rain event (disturbance) was 6 months later. Do you have other evidence (e.g., geochemical data) to show that you would expect to see differences at these time points that would be generally representative of before + after disturbance, as opposed to just temporal differences? Having five biological replicates per time point helps with spatial heterogeneity at least, and the slightly higher temporal resolution samples collected after the event help too, but those data are all buried in the supplementary material. | * Mention alex paper taxonomic distribution * Make yearly weather plot * Bring out the high-res sample more |
| Ln 271-274: Only these four phyla are shown in the figure. Why were they chosen, and where are the rest of the taxa? From a superficial scan of the OTU table on github, it looks like the vast majority of sequences were from different lineages of Halobacteria, and grouping them at the phylum level does not seem meaningful. |  |
| Ln 274-276: This is not what I am seeing in these figures. The abundances of the selected four phyla sort of (not really) return to pre-rain abundances in some cases, but those are only four phyla (what about the rest?), and interpreting these trends at the phylum level does not seem meaningful. The PCoA plot clearly shows a cluster of the two pre-rain samples together and two separate clusters of post-rain samples, though one could argue that separation along the PCo1 axis is stronger, suggesting a grouping of 2014, 2015, and 2017 samples separate from 2015 (do you have PERMANOVA or equivalent stats to support this grouping?). In Fig. S3, the trends for two phyla and the archaea are clear, but how are you interpreting the chloroplasts and Bacteroidetes, which do not seem to support any disturbance-related trends, and where are the other phyla, and where is the PCoA plot for the full dataset (equivalent to Fig. S2e)? Also, chloroplasts are usually removed from 16S rRNA gene amplicon analyses -- what evidence do you have that considering their abundances as representative of algal abundances is reasonable? |  |
| There is no information about the predicted taxonomy of any of the MAGs or of the 16S rRNA gene sequences, and there is no information about why the authors chose to focus on a very small number of specific taxa for many of their interpretations. I see that the OTU table with taxonomy is publicly available on github, but this OTU table (and preferably a summary figure with the taxonomic data and relative abundances, e.g., a stacked bar graph) should at least be in the supplementary material. |  |
| Ln 360-361: Please place the isoelectric points for your study in context. Yes, there are changes in the isoelectric points, but how big or small are these changes, relative to other studies? What is a normal range of isoelectric points at different salinity ranges? If this information is not known, then it is difficult to interpret these results. |  |
| Ln 367: I do not see any evidence that any analyses were done at the strain level. All analyses seem to have been done at the 97% OTU or population level. Please remove “strain” throughout the manuscript. | While the implications of the study suggests changes to the strains composition of the community, we agree – the term is misleading in the context of our results, since even contigs do not represent true strains. We replaced all uses of “strain composition” to “fine-scale taxonomic composition” or similar, except where appropriate (discussion and interpretation). |
| I think that the figures labeled and described in the text as “PCAs” are actually PCoAs, right? Please correct this throughout the manuscript. | Figures 1C and 3C are principle component analysis (PCA) plots, performed with the PCA module from sklearn\_decomposition. However, you are correct about figure S2E was mislabeled – it was actually done from principle coordinate analysis (PCoA) with principle\_coordinates.py from Qiime. We fixed this typo in the figure itself, and in the Figure S4 caption. |
| Figure 1: The figure title, “Taxonomic and functional resilience after recovery period” does not describe all of these figures, and it is too interpretive. Something like “Phylogenetic and predicted functional composition of halite microbial communities over time” would be better. In the caption, please link the text “significance bars denote …” directly to what the reader sees in the figure. For example, in panel B, what do the three dots above each line mean, and what does each of those lines represent (some sort of significant grouping?)? | We changed the title to “Community taxonomic composition and functional potential over time” to be more specific. We moved the statistical information explanation from the end of the caption to the panel B explanation. |
| Figure 2: If I understand correctly, this is an exclusively bioinformatic analysis of predicted proteins recovered from metagenomes and not a direct measurement of isoelectric points or of proteins. If so, “proteome” in the title is misleading, and “adaptations” is interpretive. A more appropriate title would be something like, “Differences in predicted protein isoelectric points and potassium uptake potential over time.” | This is also fair - we changed the title to the suggested name to be more accurate. |
| Figure 3: These are all just differences in microbial community composition and predicted function over time, right? If so, the title is not intuitive and may be incorrect. “Rearrangement” evokes changes in chromosome architecture, but I think that you are just trying to say that the community changes or shifts (rearranges). I recommend changing "rearrange" to "shift" throughout the manuscript. For the 16S rRNA gene analyses, are these 97% nucleotide identity OTUs? If so, this analysis is probably not resolving strain-level differences. The same goes for MAG abundances, which are presumably measured at the population (not strain) level. I would change the title to something like, “Differences in microbial community composition and predicted function over time.” For panel D, the rearrangement index is not an intuitive set of units for the y-axis. At a minimum, please include the equation for the rearrangement index in the figure caption, and I would recommend a more intuitive y-axis label. | This figure is meant to showcase the permanent changes in fine-scale taxonomic composition changes, as opposed to Figure 1, which showed the change and recovery in the higher-order taxonomic composition. To eliminate this confusion, we expanded the Results section to include bare-minimum interpretations about what the data implies (while the Discussion section expands on the interpretation) and the Methods section to clarify the meaning of the RI (now TTI). We thank the reviewer for the suggestion to avoid using “rearrangement” due to the term’s connotations with chromatin – we had not made this connection. We replaced “rearrangement” to “taxonomic composition turnover”, which we felt captured our findings more accurately. To account for these adjustment, we changed the figure title to “Fine-scale taxonomic turnover across time” to be more precise, but still clearly distinguish the content from Figure 1. We felt that the full explanation of TTI would be too verbose for the caption, but we included a brief description and reference to the methods section. We changed the y-axis title of panel D to “taxonomic turnover within gene categories”. |
| Figure 4: The caption only describes the model. Please also walk the reader through exactly what is presented in the figure, and/or add additional labels to the figure. What are the axes of the grey graphs at the top? For the colored graphs below the grey graphs, are the abundances of individual taxa represented by their spread along the y-axis? What does the spread along the x-axis mean (does “community functions” mean that each block is a different function?), and what does it mean when colors are light vs. dark for a particular taxon and function? Is the seed bank meant to represent all rare taxa? | We greatly thank the reviewer for pointing this mistake out. We added explanations necessary for the interpretation of the figure to the caption. |

**Referee #2:**

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| Title. I would not call this a catastrophic event. Rainfall is very rare (from a human perspective) in extremely dry deserts, but is definitely not a catastrophic event. Also, “adaptation” might not be the best term to represent what you have done in this study. | We re-wrote the title to address concern brought up by both referees |
| Line 53. Change “can” to “could potentially be” You have explained this point in a much nicer manner in the conclusion section. | Thank you for pointing that out. Fix made at line 58. |
| Lines 68-71. No need for invoking functional redundancy here. Other studies have also demonstrated that losses in microbial diversity and changes in microbial community composition can result in important changes in functional rates (e.g., in soils and freshwater ecosystems). | ??? |
| Line 121-130. Rewrite for clarity. This part is confusing. Why were some of the temporal samplings conducted at 5km from each other? Shouldn’t all samples have been collected in the exact same locations? Or nearby? How many replicates were collected within each location/time? | This section was largely re-written to emphasize that there were two longitudinal analysis in this work – the main time course from S1 (2014-2017), and the post-rain time course from S2 (2016-2017) shown in figure S3. Each time course consisted of samples harvested in one 502m area. |
| Line 289. Change “fate” to “changes” | Changed section name to “Differences in salt adaptations likely drove changes in salt-in strategists” |
| Lines 304-307. Can this permanent rearrangement in the microbial community be a consequence of the potential existence of relic DNA from bacterial and archaeal communities (which abundance was increased immediately after the rainfall event)? Statements such as “The permanently altered OTU composition of the community…” (line 311) cannot be supported by your current study. The same issue applies to lines 314-333. Perhaps you should not put the focus on these results. |  |
| Line 336. Was functional diversity (number of retrieved functional genes) affected? Also, you might want to clarify that all these analyses are based on potential functioning (relative gene abundance). Even if contingent taxa occupied the left functional niches after the rainfall event, and even if all functional gene were maintained in the community after such event, functional rates were not measured in this study, and therefore, whether ecosystem functionality was lost or gained cannot be addressed here. |  |
| Lines 367-376. Did you consider that perhaps the changes in microbial communities after the rainfall events were related to the microbial community contained within the water from the rainfall? e.g., see <https://www.pnas.org/content/115/48/12229.> Considering the low microbial biomass typically found in this type of deserts, and the fact that sequencing only sequences a % of all reads in a given sample, this could be an issue. i.e., how do you know whether these new microbial communities were ever active/alive? I mean, for how long can a water pulse of 4.1mm influence environmental moisture in a desert? A few days? Are you indirectly measuring how the DNA which was contained within the water from the rainfall degrades over time, rather than the changes in active microbial communities? All these issues should be properly discussed. |  |
| Figure S1 could be moved to the main text. This is a great figure. | We took up this suggestion and made Fig. S1 into Fig. 1, which also shifted the names of all the other figures. |