**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 (line 2) |
| The first sentence of the abstract should be deleted, as this is common knowledge to the readership a microbial ecology journal. | We agree and removed the redundant first sentence (line 45) |
| 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 (line 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 (lines 2, 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…” (lines 56-57) |
| 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 the introduction and methods (lines 150-153, 237), and a figure of Salar Grande and halite nodules (Fig. S1). |
| 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 187, however we removed all mention of this abbreviation until it is properly defined in the results. |
| Ln 141: Are these “whole genomes” or metagenomes? They sound like metagenomes. | We clarified this by replacing with “whole-genome metagenomic sequencing” on line 187. 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 313 |
| 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 might be carried by completely different organisms (which would result in a RI=1, but no net change). Edits were made on lines 368-382 |
| 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 (lines 170-177). |
| 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. | We agree that more context is necessary to put the community changes in perspective. We extensively surveyed public weather databases and found reports from a nearby town that illustrated long-term climate changes in the area (new Fig. S2, see Methods lines 218-224). This weather data helped put the community changes in perspective, as the climate at the 2016 and 2017 sampling times was relatively similar, supporting that the shift resulted from the precipitation. We discuss this in lines 421-427. In doing this analysis, we also found that we overlooked an even bigger 20.1mm rain event in November 2015, which is closer to the sampling date (line 172, Fig S2). We also added discussion comparing the observed shifts to what had been observed about the system in 2013. Finally, we added additional discussion about the results from the alternate site, and how they support our findings (lines 449-454, 788-789). |
| 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. | We indeed did not explain this clearly. In this section of the results the goal was to characterize the taxonomic composition changes at high-level taxonomic ranks (domains and phyla), as opposed to the later parts of the MS that focus on fine-level taxonomic compositions (especially for members of the Halobacteriain Figs 2A and 4A and B for example). Figs S3 and S5 show the 4 most abundant phylogenetic groups at the phylum levels that were differentially abundant after the rain. We added some clarification to this section of the results (lines 435-447), and the captions of figures S3 and S5 in the supplementary materials. The rationale for grouping Halobacteria lineages under one taxonomic group for these figures is the fact that these lineages are extremely numerous and showed similar patterns in relative abundances over time. |
| 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? | We changed the wording for this section to indicate that the composition at the phylum level only partially recovered (431-435). We also added that the 2017 samples were significantly different from those of 2014/2015 (PERMANOVA, line 433). We demonstrated the partial recovery by performing a t-test on the pairwise distances between samples (as mentioned in the results, and described in the methods lines 296-303), which revealed that the 2017 samples were more similar to 2014/2015 samples than to 2016 (lines 434-435).  As for the phyla, we added explicit explanation for why we chose to showcase these (lines 440-443)– they are the community’s most abundant taxonomic groups, as can be seen in the new stacked bar graph (html plots in Data S2 and S3). We also changed the wording regarding results from Site 2, where the only notable shifts after the rain were some of the phyla (line 453). To show these changes better, we split the Site 2 figures (formely S3) into two figures – Fig S4, which now shows the Archaea shift and PCoA of the Weighted Unifrac matrix, and Fig. S5, which shows the 4 dominant taxonomic groups. We also included the stacked bar plots from all the samples in Site 1 and Site 2 (html plots in Data S2 and S3).  We did not remove chloroplast sequences from our 16S rRNA gene data for the purpose of using their abundances as a proxy for algal abundances. From our whole genome metagenomic data and previous work (Robinson et al., 2014; Crits-Christophs et al. 2016) we know that there is only one alga in the community and that it contains only one chloroplast, validating our approximations. Together with the Cyanobacteria, this alga plays an important role for the community by fixing carbon, and therefore its abundance changes should be taken into consideration. We clarify these assumptions in lines 442-445. |
| 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. | In response to this comment, we added several supplementary data files:. Data S1 contains the OTU tables of both Site 1 and Site 2 with OTU representative sequences, taxonomy, and abundances across the timeline. Data S2 and S3 include the raw OTU information, and interactive stacked bar plots of the community across time timelines for both sites. Data S4 contains details about MAG taxonomy, statistics, and abundance. |
| 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. | In the discussion, we added context for our pI findings in relation to previous reported pI points for these halophiles, as well as previous studies linking pI levels and high-salt adaptations in salt-in strategists (lines 668-765). |
| 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 suggest 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 2C and 4C are principle component analysis (PCA) plots, performed with the PCA module from sklearn\_decomposition. However, figure S3E was mislabeled – it was actually done from principle coordinate analysis (PCoA) with principle\_coordinates.py from Qiime. We fixed this error in the figure itself and its legend. |
| 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 “Halite microbial community taxonomic composition and functional potential over time” to be more specific (line 1180). We moved the statistical information explanation from the end of the caption to the panel B explanation (line 1184). |
| 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 a very good point - we changed the title to the suggested name to be more accurate (line 1190). |
| 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 (lines 561-563, 587-628) 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, lines 368-381). We thank the reviewer for the suggestion to avoid using “rearrangement” due to the term’s connotations with chromatin. We replaced “rearrangement” to “taxonomic compositional shift” and “composition turnover”, which we felt captured our findings more accurately. To account for these adjustment, we changed the figure title to “Fine-scale taxonomic shifts across time” to be more precise (line 1200), but still clearly distinguish the content from Figure 2. 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 (lines 1205-1206). 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 thank the reviewer for pointing this out. We added explanations to walk the reader through the figure and its for the interpretation (lines 1213-1218). |

**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 2) |
| 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 (fixed at line 60). |
| 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). | We thank the reviewer for bringing up this point and made the corresponding adjustments in the introduction (lines 76-79). |
| 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 analyses in this work – the main time course from S1 (2014-2017), and the post-rain time course from S2 (2016-2017) shown in figure S4. Each time course consisted of samples harvested in one 502m area. (lines 227-239) |
| Line 289. Change “fate” to “changes” | Changed section name to “Differences in salt adaptations likely drove changes in salt-in strategists” (line 546) |
| 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. | This is an extremely interesting question and one that we failed to address. If significant fractions of the sequenced DNA were relic DNA, then we would not expect to see the disappearance of many MAGs/contigs after the rain (Figs 4B, S6). The rain was not significant enough to “wash away” the DNA (24mm cumulative precipitation), but it likely transiently filled the rock’s pores with water, impacting the internal osmotic conditions. Because of these reasons we believe that we observed a taxonomic shift *despite* any potentially present relic DNA, not because of it. As for introducing relic DNA from the rain, we do not observe this to occur at detectable levels because the DNA found in all the samples belonged almost exclusively to known halophiles groups, while the taxonomic composition of air/rainwater would likely contain a greater variety. We added this important discussion to the manuscript (lines 780-786). |
| 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. | This is an excellent idea and after extensive testing at different coverage cut-offs, we conclude that the overall functional diversity was not affected. We added this information to the end of this section (lines 657-660), and added the analysis approach to the Methods section (lines 358-359). As for the study measuring functional potential as opposed to functioning, we completely agree that this is a major caveat of this analysis. We changed the name of this section to be more precise (line 636), and made it more clear that these results are based purely on gene abundance (lines 647-650). |
| 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. | This is certainly a possibility, and we thank the reviewer for inciting this discussion. The linked paper was also useful in supporting our point. Introduction of foreign microbiota from the atmosphere is unlikely to occur at significant levels relative to the native biomass of the halites, since the DNA found in all the samples belonged almost exclusively to known halophiles, while the taxonomic composition of air/rainwater would likely contain a greater variety. We added this important discussion to the manuscript. We also added a discussion on the potential impact of relic/foreign DNA on this study (lines 780-786).  Further analysis of local weather changes over the course of the study (which was prompted by reviewer #1) led us to find a second overlooked rain event shortly before the 2016 sampling, so the cumulative precipitation was 24.2mm (see line 172, lines 218-224, and Fig S2). |
| Figure S1 could be moved to the main text. This is a great figure. | We took up this suggestion and made this Fig. 1 in the main text (line 1177). Fig S1 now shows an image of halite nodules, and S2 now shows the climate data for the time series, as requested by Referee #1 (see sup. files). |