**Amplicon sequencing of SiteA reveals a community shift and subsequent recovery following the rain**

In order to investigate the taxonomic composition dynamics of the halite microbial communities, Site A (top of the Salar Grande 1 hill) was sampled approximately once a year for four years. The rain that occurred at the end of 2015 fell between sample 2 (2015-06) and sample 3 (2016-02). The 16S rDNA from the collected samples was amplified and sequenced to estimate the relative taxonomic composition of the samples. The changes in community composition over time was investigated at higher (Super kingdom), medium (Phylum), and lowest (OTU) taxonomic ranks.

To look at the community structure at the highest taxonomic rank, we measured the relative Archaea to Bacteria abundance ratios. In the samples collected before the rain, the relative Archaea abundance was robust and stable: 83.1±2% in 2014-09 and in 78.8±6.3% in 2015-06. However, the relative Archaea abundance dropped to 60.5±4.3% in 2016-02, indicating a significant drop approximately 4 months after the rain. In the following year, the Archaea abundance increased back to 77.7±3% in 2017-2, returning to the pre-rain baseline.

To investigate the taxonomic shifts between time-points at the finer taxonomic ranks, we looked for dynamics in the relative abundances of different phyla. We found that Cyanobacteria, Green algae (estimated by chloroplast rDNA abundance), and Bacteroidetes significantly increased in relative abundance following the rain, and gradually lowered back to baseline abundance in the following year. On the other hand, the abundance of Halobacteria (the major Archaea phylum in this community) significantly decreased and subsequently recovered following the rain.

To compare halite samples at the lowest taxonomic rank, we clustered reads from ribosomal amplicon sequencing into operational taxonomic units (OTUs), and constructed a Weighted Unifrac dissimilarity matrix, which relates the taxonomic composition of all samples to each other. Principal component analysis of this matrix reveals the relative dissimilarity between the samples in terms of the abundances of the OTUs that go into their microbiomes. We found that the pre-rain replicates from 2014-09 and 2015-06 cluster together and are not significantly different. However, the samples from 2016-02 cluster separately from these samples, revealing a significant community composition shift following the rain. Samples gathered in 2017-02 clustered away from 2016 samples, and much closer to the 2014 and 2015 samples, indicating a recovery in overall community structure in the year following the rain.

**Amplicon sequencing of SiteB further supports a gradual recovery of the community following the rain**

To further characterize the recovery of the halite communities after the rain at the end of 2015, SiteB (bottom of the Salgar Grande 1 hill) was sampled at finer time intervals. Halites were samples in 2016-02 (4 months after the rain), 2016-07 (7 months), 2016-10 (10 months), and 2017-02 (14 months). The 16S rDNA amplicons were sequenced to estimate the relative taxonomic composition of the samples.

We observe a recovery in relative Archaea abundance from 41.42±5.3% in 2016-02 to 60.10±6.7% in 2017-02, similar to SiteA. Moreover, the Archaea abundances in 2016-07 (50.14±9.2%) and 2017-10 (50.33±5.1%) indicate a relatively gradual and incremental recovery in this metric. At lower taxonomic ranks, we observe similar trends to Site A. Between 2016-02 and 2017-02, Cyanobacteria and Green algae decrease in abundance, while Halobacteria gradually increase.

**Whole metagenomic sequencing of halite communities confirms their higher-order structure resilience to perturbations**

To validate the shift and subsequent recovery of halite community composition, as well as characterize changes in the functional potential, the DNA from SiteA samples was additionally sequenced with whole genome sequencing. Taxonomic profiling of the quality-controlled reads with KRAKEN confirmed that the community composition at higher taxonomic ranks remained largely unchanged in the two years preceding the rain (2014-09 and 2015-06), changed significantly following the rain (2016-02), and returned back to the pre-rain state in the following year (2017-02). In particular, we observed a significant decrease and subsequent recovery in the relative abundance of Halobacteria, and an increase and subsequent decrease in the relative abundance of Bacteroidetes.