**Sequencing reveals community structure resilience**

In order to investigate the taxonomic composition of the halite microbial communities, two sites at the top and the base of a hill - SG1-Top and SG1-Bot – we independently sampled and investigated with both ribosomal DNA 16S amplicon and whole metagenome sequencing. Samples were collected at different times over the course of 4 years. SG1-Top was sampled once a year – twice before the rain and twice after, and SG1-Bot was sampled at approximately 4-month intervals after the rain.

In SG1-Top ribosomal amplicon sequencing, we observed a relatively robust baseline relative Archaea abundance in the time points before the rain – 83.1+/-2% in September 2014 and 78.8+/-6.3% in June 2015. However, we observed a significant shift in the relative Archaea abundance to 60.5+/-4.3% in February 2016 – approximately 4 months after the rain. In the following year, the relative Archaea abundance increased to 77.7+/-3% in February 2017, returning to the pre-rain baseline. This result was also recapitulated with whole metagenomic sequencing of these time-points. Unfortunately, we do not have samples from before the rain in SG1-Bot, but we are able to investigate composition changes at shorter time intervals. Here as well, we observe a recovery in relative Archaea abundance from 41.42+/-5.3% in February 2016 to 60.10+/-6.7% in February 2017. Moreover, the July and October time-points in 2016 show that this recovery is gradual and incremental.

To investigate the taxonomic shifts between time-points at the finer taxonomic ranks, we looked for dynamics in the relative abundances of different phyla. In both SG1-Top and SG1-Bot, we found that Cyanobacteria, Green algae, 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 significantly decreased and subsequently recovered following the rain. These results were found in both ribosomal amplicon sequencing of SG1-Top and SG1-Bot and whole genome metagenomic sequencing of SG1-Top.

To compare halite samples at the lowest taxonomic rank, we clustered reads from ribosomal amplicon sequencing into operational taxonomic units (OTUs), and constructed a dissimilarity matrix relating all samples to each other. Principal component analysis of this matrix reveals the relative similarity between the halite sample replicates in terms of all the OTUs that go into the microbial communities. In SG1-Top, we found that the pre-rain replicates from 2014 and 2015 cluster together and are not significantly different. However, the samples gathered in February 2016 clustered separately from these samples, revealing a significant community composition shift following the rain. Samples gathered in February 2017 clustered away from 2016 samples, and much closer to the 2014 and 2015 samples, indicating a recovery in overall community composition in the year following the rain back to the pre-rain state. In SG1-Bot, we were also able to show that the samples from February 2016 and 2017 cluster separately from each other. Furthermore, we found that July and October 2016 samples fell in-between the February 2016 and 2017 samples, further reinforcing the gradual nature of this transition.