**METHODS**

**Sample collection**

In this study, halites from three sites were harvested in Salar Grande in the Atacama Desert – site 1 (used for pre- and post-rain replicates) at the at 20°57’12.006”S 70°1’10.5996”W 680m above sea level, site 2 (used only for post-rain samples) at the bottom of that hill at 20°57’8.5212”S 70°1’1.2612”W 664m above sea level, and site 3 (sequenced for supplementary sequencing to improve binning results) at 20°55’48.18”S 70°0’49.32”W 676m above sea level. At each site, an area approximately 50m by 50m was randomly sampled. Halite nodules were randomly broken with a geological hammer into smaller pieces (<20cm), and pieces of halite with visible green coloration (indicative of colonization), were stored in sterile Whirl-Pack bags. Colonized halite powder was pooled from 1-3 nodules until sufficient material was collected. The halite samples were stored in dark, dry conditions until DNA extraction in the lab.

**Cell and DNA extraction**

Using a dull sterilized knife, the halite pieces with visible green colonization were manually scraped to extract a green powder. Because the halites are comprised of primarily NaCl salt, the powder could be dissolved in water to release the cells. In a 50ml falcon tube, 2g of halite powder was mixed with 2ml of 20% NaCl. After a 5-minute acclimation period, 6ml of ultrapure water was added with a syringe, adding the water drop wise over the course of 2 minutes while vigorously mixing the halite mixture to prevent cell lysis due to osmotic shock. The mixture was left for two minutes to allow larger debree to settle, and then the supernatant was transferred to a new 50ml tube. The cells in the suspension were then spun down in a centrifuge at 8000g for 10 minutes. The cell pellet was suspended again by using 500ul of the supernatant, and transferred to a 1.5ml tube, where the cells were spun down one more time at 13000g for 10 minutes. The supernatant was discarded and the resulting pellet was stored at -20°C. The DNA was extracted from the cells by using the DNAeasy Powersoil DNA extraction kit from QIAGEN. 300ul of the liquid in the bead tubes was used to re-suspend the cell pellet and transfer to the bead tube. After addition of 60ul of the C1 buffer, the rest of the DNAeasy protocol was followed without alterations. The final DNA was eluted in 50ul of C6 elution buffer, and quantified by using the Qubit dsDNA HS Assay Kit from Invitrogen.

**Ribosomal amplicon library preparation**

The V4 region of the community 16S ribosomal DNA was amplified with 515F (ACACGACGCTCTTCCGATCTGTGYCAGCMGCCGCGGTAA) and 926R (CGGCATTCCTGCTGAACCGCTCTTCCGATCTCCGYCAATTYMTTTRAGTTT) primers using the Phusion High-Fidelity PCR kit (New England BioLabs). The PCR mixture was put together according to the kit specifications with a total reaction volume of 50ul, and using the recommended DMSO component. 40ng of environmental DNA was used as the template. The PCR was performed with the following cycle: 30 seconds at 98°C, followed by 20 cycles of 10 seconds at 98°C, 15 seconds at 55°C and 15 seconds at 72°C, and with a final step of 5 min at 72°C. 10ul of the reaction was run out on a 2% agarose gel using the 1kb Plus DNA Ladder kit from New England BioLabs to verify that the reaction worked. If viable ~411bp amplicons were produced, the product was then cleaned up with DNA-binding Sera-Mag SpeedBeads from GE Healthcase Life Sciences. 40ul of Sera-Mag beads were added to the remaining 40ul of PCR product and incubated 5 minutes at room temperature. The tubes were then placed on a magnetic rack for 3 minutes and then the beads were washed gently 2 times with 200ul of 80% ethanol. After drying the beads for 5 minutes, the DNA was eluted in 20ul of UltraPure water for 3 minutes. MiSeq sequencing adapters and unique barcodes were then added to the purified rDNA amplicons with a second PCR reaction. Finally, the samples were quantified again with the Qubit dsDNA HS Assay Kit from Invitrogen, pooled together to equal molarity, and sequenced on a MiSeq Illumina platform at (see Victoria paper) sequencer. Where? How?

**Amplicon sequencing analysis pipeline**

The de-multiplexed and quality trimmed 16S amplicon reads from the MiSeq sequencer were processed with MacQIIME v1.9.1 [26]. The samples from the two sites described in this paper (main and supplementary) were processed separately. The reads were clustered into OTUs at a 97% similarity cutoff with the pick\_open\_reference\_otus.py function (with --suppress\_step4 option), using the SILVA 123 database [27] release as reference and USEARCH v6.1.554 [28]. The OTUs were filtered with filter\_otus\_from\_otu\_table.py (-n 2 option), resulting in a total of 624 OTUs for the main site (top of hill) and 173 OTUs for the supplementary site (bottom of hill). The taxonomic composition of the samples was visualized with summarize\_taxa\_through\_plots.py (default options). The beta diversity metrics of samples in the two sites were compared by first normalizing the OTU tables with normalize\_table.py (default options), and then running beta\_diversity.py (-m unweighted\_unifrac, weighted\_unifrac). The sample dissimilarity matrices were visualized on PCoA plots with principal\_coordinates.py (default options, but providing the mapping file with sample information) and on heat maps with Seaborn v0.8 [29].

**WMG library preparation**

The whole genome sequencing libraries of the halite DNA were prepared using the KAPA HyperPlus kit (Roche). The fragmentation was performed on 5ng of input gDNA for 6 minutes to achieve peaks around 800bp. Library amplification was done with dual-index primers for a total of 7 cycles, and the product library was cleaned up 3 times with XP AMPure Beads (New England BioLabs) with the following bead ratios: 1X ratio (discard unbound), 0.4X (discard beads), and 0.6 (discard unbound). The other steps were performed according to the kit’s recommendations. The final 35 libraries were quantified with Qubit dsDNA HS kit, inspected on a dsDNA HS Bioanalyzer, pooled to equal molarity, and sequenced on the HiSeq 2000.

**WMG sequence data analysis pipeline**

The de-multiplexed WMG sequencing reads were processed with the complete metaWRAP pipeline [25] on a UNIX cluster with 48 cores and 1024GB of RAM available. Read trimming and human contamination removal was done by the metaWRAP Read\_qc module (default parameters) on each separate sample. The taxonomic profiling was done on the trimmed reads with the metaWRAP Kraken module (default parameters, standard KRAKEN database). The reads from all samples were co-assembled with the metaWRAP Assembly module (--use-metastades option). For improved assembly and binning of low-coverage community members, reads from all the halite samples sequenced in the HiSeq run were pooled together. The co-assembly was then binned with the metaWRAP Binning module (--maxbin2 --concoct --metabat2 options) while using all the available samples for differential coverage information. The resulting bins were then consolidated into a final bin set with metaWRAP’s Bin\_refinement module (-c 70 –x 5 options). The bins and the contig taxonomy were then visualized with the Blobology module (--bins option specified), classified with the Classify\_bins module (default parameters), and quantified with the Quant\_bins module (default parameters). Gene prediction and functional annotation of the co-assembly was done with the JGI Integrated Microbial Genomes & Microbiomes (IMG) annotation service.