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# Taxonomic analysis of white gypsum-halite precipitations from Laguna Verde

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The Argentine Puna represents a unique environment, characterized by high UV radiation, low oxygen pressure and extreme temperature fluctuations. There we find saline water deposits such as Laguna Verde (Salar de Antofalla, 3300 m.a.s.l.) surrounded by large extensions of white gypsum-halite precipitating crusts. These crusts harbor microbial communities distributed in layers (microbial mats) defined by physicochemical requirements, light and oxygen. These mats colonize both solid and sedimentary surfaces.

Metagenomic, physiological and geochemical studies reveal a series of strategies that allow these communities to survive in hypersaline wetlands by performing photosynthesis and serving as CO<sub>2</sub> sinks. The goal of this job was to determine the biodiversity associated to these large evaporitic biofilms surrounding the lake.

It was observed that the microorganisms are organized in two layers in the salt crust, an upper yellow layer, and a lower green layer. Samples were taken using a cut off sterile 10-ml syringe, were fixed immediately in RNAlater and transported to the laboratory on ice. Total genomic DNA was isolated from each of the layers using the FastDNA™ SPIN Kit for Soil (MP Biomedical) and it sequenced with Illumina HiSeq. Raw data obtained, was uploaded to the European Bioinformatic Archive (ENA). Once uploaded, it was analyzed using the MGnify Annotation Pipeline developed by Dr. Rob Finn's Team at EMBL-EBI. This pipeline performed the taxonomic annotation of the raw reads.

The taxonomic annotation obtained, showed that the orange layer is dominated by oxygenic photoautotrophic bacteria (Cyanobacteria, ca. 65%) followed by anoxygenic photoautotrophs (Proteobacteria, ca. 10%) from the classes Alphaproteobacteria and Gammaproteobacteria and heterotrophic bacteria (Bacteroidetes, ca. 10%). The green layer is dominated by the phyla Proteobacteria, ca. 50% followed by Bacteroidetes, ca. 30% and Cyanobacteria, ca. 20%. In both layers, the phyla Actinobacteria and Euryarcheota represent at least 1% of the relative abundance.

**KEY WORDS:** Taxonomy, Metagenomic