

## XIX CONGRESO DE LA SOCIEDAD ARGENTINA DE MICROBIOLOGÍA GENERAL

22 al 25 de octubre del 2024

Centro cultural y Pabellón Argentina de la Universidad Nacional de Córdoba, Córdoba, ARGENTINA.



Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

## **METAGENOMIC EXPLORATION OF HALOPHILE MICROBIAL COMMUNITIES OF SALINA DE AMBARGASTA IN NORTHERN ARGENTINA**

Zerda Moreira, A.<sup>1</sup> - Parada, Andrés<sup>3</sup> - Manta, Bruno<sup>3,4</sup> - Kurth, Daniel<sup>2#</sup> - González, Javier M.<sup>1\*</sup>

1) Instituto de Bionanotecnología del NOA (INBIONATEC), CONICET-UNSE - Santiago del Estero - Santiago del Estero - Argentina

2) Planta Piloto de Procesos Industriales Microbiológicos (PROIMI)-CONICET - San Miguel de Tucumán - Tucumán - Argentina

3) Institut Pasteur de Montevideo - Montevideo - Uruguay

4) Universidad de la República - Montevideo - Uruguay

Contacto: dgkurt@gmail.com

Salinas de Ambargasta (SA) is a salt flat located in northern Argentina with an extension of 4700 km<sup>2</sup> and is part of Cuenca Saliniana, one of the largest saline complexes in the world. The Ambargasta region experiences a semi-arid climate with hot, rainy summers and cold, dry winters. These climatic conditions, together with its unique geomorphological and sedimentological characteristics, make SA an interesting location to explore its halophile adapted microbial community. In this study, we analyzed the microbial diversity in two distinct areas of the eastern zone of SA: vegetated areas (VA) and non-vegetated areas (NVA). Shotgun metagenomic sequencing was performed on environmental DNA extracted from each area. A total of 78,324,438 paired-end reads were generated for the VA sample, with a GC content of 64.26%, and 73,257,256 paired-end reads for the NVA sample, with a GC content of 61.98%, using Illumina technology. Trimmomatic (version 0.39) was employed for quality control and adapter removal. Functional and taxonomic profiles of the microbiome were obtained through the direct analysis of raw metagenomic reads and from assembled reads obtained with MegaHit (version 1.2.9). Further metagenome processing for raw reads was carried out through MetaPhlAn and HUMAnN, and for assembled reads, Semibin, Checkm, and GTDBtk were used to obtain Metagenome Assembled Genomes (MAGs). For MAGs metabolic estimation, Anvio's metabolism suite of programs was used. The metagenomic data provided a comprehensive taxonomic characterization of both SA areas. Both areas were dominated by Bacteria, with some differences in taxa abundance distribution. Proteobacteria was the dominant phylum in both VA and NVA, but with distinct secondary phyla: NVA was enriched in Firmicutes and Bacteroidetes, whereas VA lacked Firmicutes and exhibited a higher abundance of *Euryarchaeota*, which was exclusive to VA. At the family level, *Halanaerobiaceae* and *Halomonadaceae* were predominant in NVA, while VA was characterized by the presence of *Halomonadaceae* and *Saccharospirillaceae*. Genes essential for survival in extreme environments were

identified as *Ars* genes (*arsC*, *arsR*, *arsD*) involved in arsenic resistance, and *uvr* and *recA* genes critical for DNA repair under UV radiation, particularly significant in high solar incidence environments like SA. From VA, eleven high-quality MAGs were recovered. In contrast, from NVA, 28 MAGs were recovered. From these MAGs, only twelve were classified to the genus level, pointing to unusual microorganisms at these locations. To our knowledge, this is the first metagenomic investigation of the microbial communities of Salinas de Ambargasta. The findings highlight the diversity and functional potential of these extremophilic communities, laying the groundwork for future research aimed at understanding the ecological roles and adaptations in one of the largest saline environments of northern Argentina.

Palabras clave: metagenomics - halophiles - DNA sequencing