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MS16 GENOME SEQUENCE ANALYSIS OF BACTERIA HIGHLY TOLERANT TO ARSENIC, ISOLATED FROM HIGH ALTITUDE ANDEAN LAKES (HAAL)

Omar F Ordoñez¹, Daniel G Kurth¹, Adrian Turjanski², Martin Vazquez³, Maria E Farias¹, Nestor Cortez⁴.

¹Laboratorio de Investigaciones Microbiológicas de Lagunas Andinas (PROIMI-CONICET). ²Departamento de Qca-Inorgánica, Analítica, Qca y Fca (Facultad de Ciencias Exactas-UBA). ³Plataforma de Secuenciación Genómica y Bioinformática (INDEAR-CONICET). ⁴Instituto de Biología Molecular y Celular de Rosario (IBR-CONICET & UNR).

omar_federico@yahoo.com.ar

High Altitude Andean lakes (HAAL) comprise a system of shallow lakes formed during the tertiary period (1.8-65 million years ago) distributed across the Puna (high plateau) at altitudes varying from 4,200 m to 6,000 m above sea level (asl). These aquatic ecosystems present extreme environmental conditions such as high levels of Ultraviolet Radiation (UVR), a wide range of salinity (from 0.4 to 117 ppm), large daily temperature fluctuations ranging from 20° C to -40° C, low nutrient concentrations and the presence of heavy metals and metalloids, mainly arsenic. The presence of arsenic resistance mechanisms has been explored in several microbiological studies in arsenic-rich environments. The most characterized arsenic resistance mechanism is the *ars* operon located either in plasmids or chromosomes of prokaryotes. Bacterial As detoxification involves the reduction of arsenate (As[V]) to arsenite (As[III]) via a cytoplasmic arsenate reductase (*arsC*). Later on As[III] will be extruded by a membrane-associated ArsB efflux pump. Other genes like *arsR*, *arsD* and *arsA* form part of *ars* operon along with *arsB* and *arsC* in most of the As tolerant prokaryotes. HAAL isolates show enhanced resistance compared to other bacteria carrying the *ars* operon. This could be explained by the presence of additional genes related to this function, including extra copies of the *ars* operon or supplementary extrusion pumps. The aim of this study was to elucidate the genetic mechanisms of

tolerance to high arsenic concentrations, taking advantage of the available genomes of three UV resistant bacterial strains, recently isolated from HAAL extreme environments. Moreover, the presence of the *ACR3* gene as a possible resistance mechanism was assessed by degenerate oligonucleotides. We studied the strains *Acinetobacter* sp. Ver3 and *Exiguobacterium* sp. N30 and S17, isolated from shallow water (Laguna Verde and Laguna Negra), and from modern stromatolites (in Laguna Socompa) respectively. Maximal arsenic concentration was 33.81 mg/L. Genome sequences were obtained using a whole-genome shotgun strategy with a 454 GS Titanium pyrosequencer at INDEAR, Argentina. Genomes were annotated and analyzed in the RAST annotation server. PSI-BLAST and ClustalW were used to compare and align sequences, and phylogenetic trees were built using Mega5. The effect of As[V] and As[III] during growth in rich media was also evaluated by different protocols. The strains *Exiguobacterium arantiacum* DSMZ 6208 and *Acinetobacter baumannii* DSM 30007 were used as controls during tolerance profiles measurements. Organisms with high tolerance to this metalloid, isolated in pure culture from environments such as HAAL, could be good candidates for studies of bioremediation of metals and metalloids, a methodology considered of low cost and environmentally friendly.