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► **To cite this version:**

A. M. Plominsky, N. Delherbe, J. A. Ugalde, E. E. Allen, M. Blanchet, et al.. Metagenome Sequencing of the Microbial Community of a Solar Saltern Crystallizer Pond at Cahuil Lagoon, Chile. *Genome Announcements*, 2014, 2 (6), pp.e01172-14. 10.1128/genomeA.01172-14 . hal-01253989

HAL Id: hal-01253989

<https://hal.science/hal-01253989>

Submitted on 13 Jan 2016

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Metagenome Sequencing of the Microbial Community of a Solar Saltern Crystallizer Pond at Cahuil Lagoon, Chile

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Cahuil Lagoon in central Chile harbors distinct microbial communities in various solar salterns that are arranged as interconnected ponds with increasing salt concentrations. Here, we report the metagenome of the 3.0- to 0.2- μm fraction of the microbial community present in a crystallizer pond with 34% salinity.

Received 1 October 2014 Accepted 6 October 2014 Published 13 November 2014

Citation Plominsky AM, Delherbe N, Ugalde JA, Allen EE, Blanchet M, Ikeda P, Santibañez F, Hanselmann K, Ulloa O, De la Iglesia R, von Dassow P, Astorga M, Gálvez MJ, González ML, Henríquez-Castillo C, Vaultot D, Lopes do Santos A, van den Engh G, Gimpel C, Bertoglio F, Delgado Y, Docmac F, Elizondo-Patrone C, Narváez S, Sorroche F, Rojas-Herrera M, Trefault N. 2014. Metagenome sequencing of the microbial community of a solar saltern crystallizer pond at Cahuil Lagoon, Chile. *Genome Announc*. 2(6):e01172-14. doi:10.1128/genomeA.01172-14.

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Solar salterns represent unique extreme microbial ecosystems that are best studied by applying different molecular techniques (1). These habitats offer relatively low microbial diversity and are generally dominated by archaea (2). In this study, we generated an additional data set from a solar saltern crystallizer pond in Cahuil Lagoon (Chile). We will continue to use the data for comparative studies on the metabolic potential and diversity of microorganisms inhabiting an environment with 10-fold seawater salt concentration.

Cahuil Lagoon extends several miles into mainland from the coast of the South Pacific, where seawater mixes with various freshwater tributaries. Along the border of the lagoon, local inhabitants build a series of locks to distribute brackish water into a series of interconnected ponds where water evaporates until the ion activity products of the dissolved ions exceed the solubility product of halite.

Samples for this study were collected on 12 January 2012 from a final salt crystallizer pond (34°30'10"S 71°59'09"W), which had a salinity of 34.1‰, a temperature of 41.2°C, and a pH of 6.4. A volume of 5 liters was first passed through a 60- μm nylon mesh, and then 600 ml was sequentially filtered through 20- μm , 3.0- μm (polycarbonate; Millipore), and 0.22- μm -pore filters (polyethersulfone; Millipore). Community DNA was extracted from the 3.0- to 0.22- μm size fraction using the

cetyltrimethylammonium bromide (CTAB) method (3) and sequenced by pyrosequencing (Roche 454 GS-FLX system, Titanium chemistry) at the Center for Genomics and Bioinformatics, Universidad Mayor, Chile.

The raw 222,074 sequencing reads (average length, 450 bp) were quality filtered for ambiguities and homopolymers (≥ 10), and reads with $>75\%$ of the sequence having a Phred quality score of ≤ 20 were removed. Taxonomic assignment (MGTAJA [<http://mgtaxa.jcvi.org>] against NCBI RefSeq v01-07-2012) of the remaining 183,299 reads revealed that 61% stem from archaea, 19% from viruses, and 16% from bacteria. At the phylum level, 58% of the reads were assigned to *Euryarchaeota* (all from the family *Halobacteriaceae*), 9% to *Actinobacteria*, and 7% to the virus class *Caudovirales*. Several genera of the family *Halobacteriaceae* share similar levels of representation (expressed as the % of reads assigned to *Archaea*): *Haloarcula* (14%), *Haloquadratum* (11.5%), *Halorubrum* (9.5%), *Halobacterium* (9%), *Natronomonas* (9%), *Halogeometricum* (8.5%), *Halomicrobium* (6.5%), and *Halorhabdus* (6%). Although *Haloquadratum* is still an important part of the microbial community, it is not as abundant in this crystallizer pond as it is in the Santa Pola saltern (1, 4).

The data generated as part of this metagenome add valuable information for ongoing and future studies on the metabolic po-

tential of the microbial communities associated with extreme hypersaline habitats worldwide.

Nucleotide sequence accession number. This metagenome project has been deposited in the NCBI Sequence Read Archive under the accession no. [SRX680116](https://www.ncbi.nlm.nih.gov/SRA/SRX680116).

ACKNOWLEDGMENTS

This study was performed during the Ecology and Diversity of Marine microorganisms (ECODIM) VII course as part of the 12th Austral Summer Institute organized by the Universidad de Concepción (UdeC) in 2012. The course was held under the auspices of the UdeC and was supported through access to research facilities at the Marine Station of the Pontificia Universidad Católica de Chile (PUC) in Las Cruces.

Funding for the sampling and sequencing was provided by the Agouon Institute, the Gordon and Betty Moore Foundation, the Graduate School of UdeC, the Faculty of Biological Sciences of PUC, and the Center for Genomics and Bioinformatics of the Universidad Mayor. The sequence analyses were performed by A.M.P., N.D., and J.A.U. at E.E.A.'s

Laboratory at the Scripps Institution of Oceanography, UCSD, with the support of a MECESUP-PUC 2012 internship grant to A.M.P.

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