Draft Genome Sequence of the Polyextremophilic *Halorubrum* sp. Strain AJ67, Isolated from Hyperarsenic Lakes in the Argentinian Puna

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The high-altitude Andean Lakes (HAAL) consist of several shallow lakes located in a desert known as Puna, located at >3,000 m altitude. They are exposed to extreme environmental conditions, such as high UV radiation levels, elevated salinity, and heavy metals and metalloids, mainly arsenic (1–5). Interestingly, *Halorubrum* was identified as the dominant halorarchael taxon in HAAL.

The extremely halophilic archaeon *Halorubrum* sp. strain AJ67 was isolated from Laguna Antofalla located in Catamarca, Argentina, in the Argentinian Puna. The 16S rRNA gene sequence shows a relationship to species of the genus *Halorubrum*, with a close relationship to *Halorubrum chaoviator* (98.74% identity). AJ67 belongs to a single euryarchaeotal order (*Halobacterales*) that inhabits hypersaline environments (3 to 5 M), such as salt lakes, salt ponds, and marine salterns. The genus *Halorubrum* belongs to the family *Halobacteriaceae* (6). Previous molecular ecological studies showed that archaeal halophiles dominate these ecosystems (7–9) and that the genus *Halorubrum* (6, 10) is widely distributed in hypersaline habitats (11–13). The cells are Gram-negative, rod shaped, and motile. The colonies are small, red-orange pigmented, and smooth. AJ67 is a chemo-organotrophic and aerobic archaeon.

The genome sequence was obtained using a whole-genome shotgun (WGS) strategy with a 454 GS Titanium pyrosequencer at the Instituto de Agrobiotecnología Rosario (INDEAR), Argentina. Assembly was done using 454 Newbler version 2.6, using the -urt option, with 8.25x coverage. This assembly generated 50 scaffolds. The draft genome is 4,225,006 bases in length. The G+C content of the genomic DNA is 63.71 mol%. Genome annotation was done using the standard operating procedures (SOPs) from the Integrative Services for Genomic Analysis (ISGA) (14) and our own prokaryotic annotation pipeline. The RAST annotation server was also used for subsystem descriptions (15). A total of 3,370 coding sequences (CDSs) and 49 structural RNAs (43 tRNAs) were predicted. A total of 1,086 CDSs (32%) were classified as hypothetical proteins. According to RAST, the annotation identified 489 CDSs (14%) into RAST subsystems. The genome of *Halorubrum* sp. AJ67 presents 21 genes devoted to resistance to toxic compounds, such as antibiotics, arsenic, cadmium, mercury, and others, according to RAST (15). The high resistance to arsenic previously observed in AJ67 can be explained based on the greater number of genes encoding the detoxification of this compound, 17 genes in comparison to 15 genes observed in *Halocallococcus walsbyi* DSM 16790 and in *Natronomonas pharaonis* DSM 2160. A striking difference with other *Halobacteriaceae* genomes is the presence of the arsenite oxidase (aio) gene, which oxidizes arsenite and reduces oxygen or nitrate, arsenite being one of the most toxic arsenic species. This is the first report of the presence of the *aio* gene in this genus. Strain AJ67 contains a complete DNA repair system, including UvrABC (subunit A and B) and photolyase, which confers high resistance to UV radiation.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. CBVY000000000. The version described in this paper is the first version.

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REFERENCES

1. Dib J, Motok J, Zenoff VF, Ordoñez O, Farias ME. 2008. Occurrence of resistance to antibiotics, UV-B, and arsenic in bacteria isolated from extreme environments in high-altitude (above 4400 m) Andean wetlands. Curr. Microbiol. 56:510–517. http://dx.doi.org/10.1007/s00284-008-9103-2.

2. Dib JR, Weiss A, Neumann A, Ordoñez O, Estévez MC, Farías ME. 2009. Isolation of bacteria from remote high altitude Andean lakes able to grow in the presence of antibiotics. Recent Pat. Antinfect. Drug. Discov. 4:66–76. http://dx.doi.org/10.2174/157489109787236300.

3. Fernández Zenoff V, Siñeriz F, Farías ME. 2006. Diverse responses to UV-B radiation and repair mechanisms of bacteria isolated from high-altitude aquatic environments. Appl. Environ. Microbiol. 72:7857–7863. http://dx.doi.org/10.1128/AEM.01333-06.

4. Flores MR, Ordoñez OF, Maldonado MJ, Farías ME. 2009. Isolation of UV-B resistant bacteria from two high altitude Andean lakes (4,400 m) with saline and non saline conditions. J. Gen. Appl. Microbiol. 55:447–458. http://dx.doi.org/10.2323/jgam.55.447.

5. Ordoñez OF, Flores MR, Dib JR, Paz A, Farias ME. 2009. Extremophile culture collection from Andean lakes: extreme pristine environments that host a wide diversity of microorganisms with tolerance to UV radiation. Microb. Ecol. 58:461–473. http://dx.doi.org/10.1007/s00248-009-9527-7.

6. McGinity TJ, Grant WD. 1995. Transfer of *Halobacterium saccharovorum*, *Halobacterium sodomense*, *Halobacterium trapanicum NRC 34021* and *Halobacterium lacusprofundi* to the genus *Halorubrum* gen. nov., as *Halorubrum saccharovorum* comb. nov., *Halorubrum sodomense* comb. nov., *Halorubrum trapanicum* comb. nov., and *Halorubrum lacusprofundi* comb. nov. Syst. Appl. Microbiol. 18:237–243.

7. Litchfield CD, Gillevet PM. 2002. Microbial diversity and complexity in hypersaline environments: a preliminary assessment. J. Ind. Microbiol. Biotechnol. 28:48–55. http://dx.doi.org/10.1007/s10368-001-700175.

8. Ochsenreiter T, Pfiefer F, Schleper C. 2002. Diversity of Archaea in hypersaline environments characterized by molecular-phylogenetic and cultivation studies. Extremophiles 6:267–274. http://dx.doi.org/10.1007/s00792-001-0253-4.

9. Øvreås L, Daae FL, Torsvik V, Rodriguez-Valera F. 2003. Characterization of microbial diversity in hypersaline environments by melting profiles and reassociation kinetics in combination with terminal restriction fragment length polymorphism (T-RFLP). Microb. Ecol. 46:291–301. http://dx.doi.org/10.1007/s00248-003-3006-3.

10. Kamekura M, Dyall-Smith ML. 1995. Taxonomy of the family Halobacteriaceae and the description of two genera *Halorubrobacterium* and *Na-trialba*. J. Gen. Appl. Microbiol. 41:333–350.

11. Grant WD, Kamekura M, McGinity TJ, Ventosa A. 2001. Order 1. *Halobacteriales* Grant and Larsen 1989b, 495VP (effective publication: Grant and Larsen 1989a, 2216), p 294–334. In Boone DR, Castenholz RW, Garrity GM (ed), Bergey’s manual of systematic bacteriology, 2nd ed, vol 1. Springer Verlag, New York, NY.

12. Trigui H, Masmoudi S, Brochier-Armanet C, Maalej S, Dukan S. 2011. Characterization of *Halorubrum sfaxense* sp. nov., a new halophilic archaeon isolated from the solar saltern of Sfax in Tunisia. Int. J. Microbiol. 2011:240191. http://dx.doi.org/10.1155/2011/240191.

13. Xu XW, Wu YH, Zhang HB, Wu M. 2007. *Halorubrum arcis* sp. nov., an extremely halophilic archaeon isolated from a saline lake on the Qinghai-Tibet Plateau, China. Int. J. Syst. Evol. Microbiol. 57:1069–1072. http://dx.doi.org/10.1099/ijs.0.64921-0.

14. Hemmerich C, Buechlein A, Podicheti R, Revanna KV, Dong Q. 2010. An Ergatis-based prokaryotic genome annotation web server. Bioinformatics 26:1122–1124. http://dx.doi.org/10.1093/bioinformatics/btq090.

15. Aziz RK, Bartels D, Best AA, DeLong H, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kibala M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil IL, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. http://dx.doi.org/10.1186/1471-2164-9-75.