Draft Genome Sequence of the Extremely Halophilic Archaeon

Halogranum salarium B-1T

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Halogranum salarium is an extremely halophilic archaeon isolated from evaporitic salt crystals and belongs to the family Halobacteriaceae. Here, we present the 4.5-Mb draft genome sequence of the type strain (B-1T) of H. salarium. This is the first report of the draft genome sequence of a haloarchaeon in the genus Halogranum.

The genome Halogranum was created by Cui et al. (1) based on the description of a single species, Halogranum rubrum, for two novel extremely halophilic archaea (haloarchaeal) belonging to the family Halobacteriaceae. Later, the description of the genus was emended by Cui et al. (2) with the description of two more species, Halogranum gelatinilyticum and Halogranum amylyticum. Until recently, all strains belonging to the genus Halogranum were isolated from marine solar salters in China, reflecting their extremely halophilic nature. More recently, three haloarchaeons, strains B-1T, B-3, and B-4, were isolated from evaporitic salt crystals collected along the seashore of Namhae, South Korea. According to their phylogenetic positions based on 16S rRNA gene sequences and their polar lipid profiles, strains B-1T, B-3, and B-4 were found to belong to the genus Halogranum. Subsequently, the three novel isolates have been classified as the novel species Halogranum salarium, on the basis of the RNA polymerase subunit B’ gene (rpoB’) sequence dissimilarity, low genomic relatedness (<40%), and phenotypic differences with respect to the three aforementioned species (5).

The genome sequence of H. salarium B-1T was determined using the GS FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb-span paired-end library (130,033 reads, ~38.4 Mb) and Illumina GA IIx (San Diego, CA) with 100-bp paired-end information (13,941,775 reads, ~1,408.1 Mb). All reads were assembled into 17 contigs (N50, 588,306 bp; maximum contig size, 821,749 bp) using GS Assembler 2.6 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 5.0 (CLC bio, Denmark); total coverage over the whole genome reached ~322-fold. Putative protein-coding sequences (CDSs) were predicted using Glimmer 3.02 (3). The tRNAs and rRNAs were detected using tRNAscan-SE 1.21 (7) and RNAmmer 1.2 (6), respectively. The predicted CDSs were annotated by searching against the RefSeq (9), COG (10), and SEED (4) databases.

The draft genome was 4,492,306 bp in length, with a G+C content of 62.2 mol%, and no plasmid was found. Of the 4,824 CDSs that were predicted, 3,008 (62.4%) were assigned to 22 COG functional categories. The genome also contained 63 tRNA genes and 5 rRNA operons.

H. salarium B-1T harbored the genes encoding, in order, non-histone chromosomal protein MD1, dihydroorotate oxidase, valyl-tRNA synthetase, phenylalanyl-tRNA synthetase subunit α, and β, tryptophanyl-tRNA synthetase, tRNA intron endonuclease, DNA topoisomerase I, haloacid dehalogenase-like hydrolase, DEAD/DEAH box helicase, lipoic acid synthase, pyruvate dehydrogenase E1 component subunit α and β, pyruvate dehydrogenase E2 component, and dihydrolipoamide dehydrogenase in the upstream of the 16S rRNA gene. This gene order was consistent with those of Haloferax volcanii DS2 and Halogeometricum borinquinense DSM 11551T (8), which supported their close relationship in the complete rpoB’ gene-based phylogeny (5). More detailed analysis of the genome will provide further insight into the genomic differences with respect to other haloarchaeon and metabolism of the extreme halophiles.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALJD0000000. The version described in this paper is the first version, ALJD01000000.

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**REFERENCES**


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