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Genome Sequence of *Halobiforma lacisalsi* AJ5, an Extremely Halophilic Archaeon Which Harbors a *bop* Gene

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The draft genome sequence (4,398,155 bp, with 65.35% G+C content) of *Halobiforma lacisalsi* AJ5, an extremely halophilic archaeon isolated from a salt lake, is reported here. This is the first genome report for a species of the *Halobiforma* genus.

Bacteriorhodopsin, encoded by the *bop* gene, is a membrane protein that functions as a photoactive proton pump (14). It was first found in the purple membrane of the halophilic archaeon *Halobacterium salinarum*. The structure of the protein was described later, in the early 1970s (5, 15). Due to its photoelectric properties, bacteriorhodopsin has many useful applications in biochemical and bioelectronics devices, such as three-dimensional (3D) memory systems, targeted drug delivery systems, and biocatalytic reactors (17). *Halobiforma lacisalsi* strain AJ5 is an extremely halophilic archaeon that was isolated from a salt lake in Xinjiang, China (19). The *bop* gene from this strain was obtained, and the properties of the bacteriorhodopsin were studied (21). *Halobiforma lacisalsi* AJ5 belongs to the genus *Halobiforma* (19). The *Halobiforma* genus currently contains only three species, *Halobiforma haloterrestris* (8), *Halobiforma nitratireducens* (formerly *Natronobacterium nitratireducens*) (18), and *Halobiforma lacisalsi* (19). The genome of *Halobiforma lacisalsi* AJ5 is the first of this genus to be sequenced.

Here we report the sequence of *Halobiforma lacisalsi* AJ5, which was obtained using a whole-genome shotgun (WGS) strategy, Solexa paired-end-sequencing technology (4), a 500-bp-span paired-end library (~430 Mb available reads; ~98-fold genome coverage), and a 6,000-bp-span paired-end library (~250 Mb available reads; ~57-fold genome coverage). All reads were assembled into 156 contigs (>199 bp in size) and 34 scaffolds (>560 bp in size) by the use of SOAP *de novo* version 1.04 software (http://soap.genomics.org.cn/soapdenovo.html) (12). The open reading frames (ORFs) were predicted using Glimmer version 3.0 software (6); tRNA and rRNA recognition made use of tRNAscan-SE (13), RNAmmer (11), and the Rfam database (7); the repeat sequence annotation was obtained using the RepeatMasker and Repbase databases (10); and functional annotation of translated ORFs was achieved by BLAST (1) using the nonredundant (nr), Swiss-Prot, Clusters of Orthologous Groups (COG) (16), and Kyoto Encyclopedia of Genes and Genomes (KEGG) (9) databases. Meanwhile, we used InterProScan software (2, 20) with the Pfam database (3) to obtain the gene ontology (GO) annotations.

The uncompleted genome sequence of *Halobiforma lacisalsi* AJ5 showed a genome size of 4,398,155 bp (scaffold length) and 65.35% G+C content. A total of 4,682 coding sequences (CDSs) and 43 tRNAs were identified. Partial sequences of 2 rRNA operons, 22 transposons, and 1,558 tandem repeats were found. Among the 4,682 genes identified, 2,638 were classified into 21 certain functional COG sets. Two bacteriorhodopsins and one bacteriorhodopsin-related protein with identities of 86.38%, 100%, and 58.17%, respectively, were found (determined using the nr database). The bacteriorhodopsin which has 100% identity corresponds to that found in our former study (21). These genome sequence data give us a vast pool of functional enzymes and should provide further insight into the genomic differences among strains of extremely halophilic archaea.

Nucleotide sequence accession numbers. The nucleotide sequence determined in the *Halobiforma lacisalsi* AJ5 whole-genome shotgun-sequencing project has been deposited at DDBJ, EMBL, and GenBank under accession no. AGFZ00000000. The version described in this paper is the first version (accession no. AGFZ01000000).

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