

Complete Genome Sequence of *Halalkalicoccus jeotgali* B3^T, an Extremely Halophilic Archaeon[∇]

Seong Woon Roh,^{1†} Young-Do Nam,^{1†} Seong-Hyeuk Nam,² Sang-Haeng Choi,² Hong-Seog Park,² and Jin-Woo Bae^{1*}

Department of Life and Nanopharmaceutical Sciences and Department of Biology, Kyung Hee University, HoeGi-Dong 1, DongDaeMun-Gu, Seoul 130-701, Republic of Korea,¹ and Genome Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB) and University of Science and Technology (UST), Daejeon 305-806, Republic of Korea²

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***Halalkalicoccus jeotgali* B3^T, isolated from salt-fermented seafood from South Korea, is an extremely halophilic archaeon belonging to the family Halobacteriaceae. Here, we present the complete genome sequence of the type strain *H. jeotgali* B3^T (3,698,650 bp, with a G+C content of 62.5%), which consists of one chromosome and six plasmids. This is the first complete genome sequence of the *Halalkalicoccus* species.**

Extremely halophilic archaea (haloarchaea) are adapted to hypersaline environments and grow optimally in NaCl solutions of 2.6 M or higher (12). These haloarchaea are classified within the family Halobacteriaceae in the order Halobacteriales; currently, this family comprises 28 genera (3), and only 11 complete genome sequences in Halobacteriaceae have been reported. In a study of archaeal diversity in salt-fermented small shrimp or shellfish from South Korea, our laboratory isolated and characterized 5 novel, extremely halophilic archaeal strains of Halobacteriaceae. These strains included *Natronococcus jeotgali* (9), *Halalkalicoccus jeotgali* (11), *Halorubrum cibi* (7), *Haloterrigena jeotgali* (10) and *Haladaptatus cibarius* (8). We have now sequenced the genome of *Halalkalicoccus jeotgali* B3^T; genome sequencing had not been completed or initiated for any strain in this genus when our sequencing project was begun. The genus *Halalkalicoccus* currently contains only two species, *Halalkalicoccus tibetensis* (13) and *H. jeotgali*, and these species exhibit 98.6% gene sequence similarity in their 16S rRNA. The genome of *H. jeotgali* B3^T is the first of this genus to be sequenced.

The complete genome sequence of *H. jeotgali* B3^T was determined by a whole-genome shotgun strategy using Roche 454 GS (FLX Titanium) pyrosequencing (898,168 reads totaling ~348 Mb; ~94-fold coverage of the genome) and a fosmid library (514 reads totaling ~680 kb) at the Genome Resource Center, KRIBB (Korea Research Institute of Bioscience and Biotechnology). Genome sequences from pyrosequencing were processed by Roche's software according to the manufacturer's instructions, and sequences from the fosmid library were processed by PESTAS (6). A total of 898,196 reads were assembled using Newbler Assembler 2.3 (454 Life Science), which generated 54 large contigs (>100 bp in size) with bases having quality scores of 40 and above. The gaps between contigs were closed by primer walking and sequencing of PCR products across the gaps. The annotation was done by merging

results obtained from the RAST (Rapid Annotation using Subsystem Technology) pipeline (1), Glimmer 3.02 (2), tRNAscan-SE 1.21 (5), and RNAmmer 1.2 (4).

The *H. jeotgali* B3^T genome is 3,698,650 bases long with a 62.5% G+C content. The chromosome consists of a single circular chromosome (2,809,118 bp, with a G+C content of 65.0%) and six plasmids (406,285 bp, 55.3%; 363,534 bp, 54.2%; 44,576 bp, 58.9%; 44,459 bp, 54.9%; 23,727 bp, 47.6%; 6,951 bp, 60.6%). The genome contains 3,860 predicted coding sequences and 52 RNA genes (determined using RAST). The chromosome is predicted to contain 3,101 coding sequences with a coding intensity of 90.0%, including 47 tRNA genes, 1 5S rRNA gene, 1 16S rRNA gene, and 1 23S rRNA gene. The largest plasmid contains 466 coding sequences with a coding intensity of 81.2% and 2 tRNA genes, while the other five plasmids contain 425, 44, 48, 29, and 5 coding sequences with coding intensities of 80.2%, 84.2%, 83.0%, 69.6%, and 22.8%, respectively (determined using Glimmer3). More detailed analysis of this genome and comparative analysis with other haloarchaea will provide further insight into the genomic differences and metabolism of the extremely halophilic archaea.

Nucleotide sequence accession numbers. The complete genome of *H. jeotgali* B3^T was deposited in the NCBI GenBank database and assigned accession numbers CP002062 (chromosome) and CP002063 to CP002068 (six plasmids).

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* Corresponding author. Mailing address: Department of Biology, Kyung Hee University, HoeGi-Dong 1, DongDaeMun-Gu, Seoul 130-701, Republic of Korea. Phone: (82)-2-961-2312. Fax: (82)-2-961-0244. E-mail: baejw@khu.ac.kr.

† The first two authors contributed equally to this work.

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