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GENOME SEQUENCES

Draft Genome Sequence of *Haloferax volcanii* SS0101, Isolated from Salt Farms in Samut Sakhon, Thailand

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ABSTRACT *Haloferax volcanii* SS0101 is a halophilic archaeon isolated from salt farms in Thailand. The genome sequence of *H. volcanii* SS0101 contains a gene encoding capreomycidine synthase, a key enzyme for capreomycidine biosynthesis. This 3.8-Mb draft genome sequence of *H. volcanii* SS0101 will provide the tools for investigating genes involved in capeomycidine production in haloarchaea.

Haloferax volcanii is an extremely halophilic archaeon (1–3) and aerobic chemoorganotroph (1). Cells of *H. volcanii* are Gram negative, pleomorphic, and mostly flattened or disk shaped (1). The optimal growth temperature of *H. volcanii* is 35°C (1). The salt concentration for optimal growth is approximately 2.5 M (1). The major polar lipid components of *H. volcanii* are phosphatidylglycerophosphate (PGP) and sulfated diglycosyl diether (S-DG) (1). *H. volcanii* is an important cellular model system for the genetic, molecular biological, and biochemical study of archaea (4).

Strain SS0101 was isolated from soil samples collected from salt farms (13°30′47″N, 100°22′29″E) in Samut Sakhon, Thailand. One gram of soil was dissolved in phosphate buffer containing 3.4 M NaCl, and the extinction dilution method was performed to isolate strain SS0101. Strain SS0101 was grown in JCM169 broth containing 3.4 M NaCl at 37°C with shaking at 250 rpm. Genomic DNA (gDNA) of strain SS0101 was extracted with the phenol chloroform method described by Sambrook and Russel (5). The quality and quantity of gDNA were determined using a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA). The sequencing library was prepared using the Ion Plus fragment library kit and the Ion PI Hi-Q OT2 200 template kit. The sequencing was performed on the Ion Proton sequencer using the Ion PI Hi-Q sequencing 200 kit and the Ion PI chip (Thermo Fisher Scientific, USA). The average read length was 101 bp. There were 5,993,233 raw reads (155× depth of coverage) generated from the sequencing run. The quality of the raw reads was determined using AfterQC 0.9.6 with default parameters (6). *De novo* genome assembly of the raw reads was performed with SPAdes 3.13.1 in the careful mode (7). The genome was decontaminated using Automated Contamination Detection and Confidence (ACDC) 1.02 with default parameters (8). The genome assembly metrics of the decontaminated contigs of *H. volcanii* SS0101 were determined using QUAST 5.0.2 with default parameters (9). The draft genome sequence of *H. volcanii* SS0101 consists of 3,784,342 bp in 593 contigs with an N_{50} value of 18,910 bp and a 66.08% G+C content. Gene prediction was performed using Prokka 1.13.7 with default parameters (10). The annotated genome sequence of *H. volcanii* SS0101 contains 3,853 protein-coding sequences along with 51 tRNAs, 1 rRNA operon, and 7 CRISPR regions.

The draft genome sequence of strain SS0101 was identified using the Genome-to-

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Genome Distance Calculator (GGDC) 2.1 with default parameters (11, 12). The archaeal strain SS0101 was affiliated with *Haloferax volcanii* DS2 (GenBank accession number CP001956) with an 80.6% supported value of the digital DNA-DNA hybridization (dDDH). The difference in G+C content between strain SS0101 and *H. volcanii* DS2 (CP001956) was 0.56%.

There is one annotated locus of the capreomycidine synthase gene in the *H. volcanii* SS0101 genome. Capreomycidine synthase is a key enzyme for capreomycidine synthesis. Capreomycidine is a nonproteinogenic amino acid, an important residue found in the tuberactinomycin family of antitubercular peptide antibiotics (13).

Data availability. The whole-genome shotgun sequence of *Haloferax volcanii* SS0101 has been deposited at DDBJ/ENA/GenBank under the accession number VMTR00000000 and SRA number SRR9831208.

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