




Whole-Genome Shotgun Sequence of *Halomonas* sp. Strain SBS 10, Isolated from a Hypersaline Lake in India

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ABSTRACT The whole-genome shotgun sequence of a moderately halophilic bacterium, *Halomonas* sp. strain SBS 10, was assembled and studied. The assembled genome size was 1.5 Mb, with a G+C content of 63.6%. The genome sequence of this *Halomonas* sp. SBS 10 isolate will be valuable in understanding gene clusters and functions involved in the adaptability of this bacterium to hypersaline conditions.

Hypersaline environments harbor large numbers of halotolerant and moderately and extremely halophilic species that are exposed to severe stresses such as high osmolarity and low water activity (1, 2). Along with several other bacterial species, species of the genus *Halomonas* are widely distributed throughout hypersaline environments. Some of them have been recognized for their potential use in the field of biotechnology (3, 4). Analysis of their genomes will be helpful in understanding their wide genetic diversity and the genes involved in their adaptation to these stringent environmental conditions (5, 6). In our study, we isolated a moderately halophilic strain of *Halomonas* from a hypersaline lake (Sambhar Salt Lake) located in North-Western India and characterized it using whole-genome shotgun (WGS) sequence analysis.

The bacterium described here was isolated from the saltern brines of the Sambhar Salt Lake. The isolation of strain SBS 10 was carried out by streaking a sample on tryptic soy agar (TSA) supplemented with 10% NaCl. Streaking was done three times in repetition, resulting in a single colony at 37°C. The 16S rRNA gene was amplified from the genomic DNA, as described by Embley (7), with universal bacterial primers 27 F (59-AGAGTTTGATCCTGGCTCAG) and 1492 R (59-GGTTACCTGTACGACTT) and was aligned with those related to *Halomonas* species. The phylogenetic tree was constructed using the maximum likelihood (ML) and maximum parsimony (MP) methods available in the MEGA v. 7.0 software package (8). Phylogenetic analysis based on a 16S rRNA gene sequence (1,452 bp, GenBank accession number [KT796562](https://doi.org/10.1128/MRA.01270-19)) comparison with the 10 closest species indicated that strain SBS 10 is clustered within the branch consisting of the species of *Halomonas* belonging to the *Gammaproteobacteria*. The isolate was found to be a member of the genus *Halomonas*, with the closest neighbor deemed to be the type strain *Halomonas gudaonensis* CGMCC 1.6133 (98% similarity) (9, 10).

Genomic DNA was extracted from freshly cultured tryptic soy broth (TSB) medium containing 10% NaCl using a GenElute bacterial genomic DNA kit (Sigma-Aldrich, UK),

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TABLE 1 *Halomonas* sp. SBS 10 sequencing and assembly metrics

Genome feature	Value
Sequence length (bp)	1,533,947
No. of contigs	31
Avg genome coverage (fold)	316
G+C content (%)	63.6
Shortest contig length (bp)	1,219
Median sequence contig length (bp)	43,086
Mean sequence contig length (bp)	49,482.2
Longest contig length (bp)	110,994
N_{50} (bp)	49,763
L_{50}	12

following the protocol for Gram-negative bacteria. The sequencing library was prepared using the RAD004 rapid sequencing kit (Oxford Nanopore Technologies, UK) per the instruction manual. The WGS was performed by Nanopore technology (Oxford, UK) using the MinION sequencer. In sum, a total of 71.2 Mb (316-fold coverage) was generated by the sequencing run. The quality of the 530,458 read pairs generated was assessed using FastQC v0.11.5 (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>). The resulting ultralong reads were assembled using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP), using SPAdes v. 3.10.1 (11). Annotation of the assembled contigs using PGAP and the GeneMarkS+ annotation method revealed 146 subsystems, 3,847 coding sequences, and 19 RNAs. For assembly and annotation using PGAP, default settings were used. Sequencing and assembly metrics for the strain are given in Table 1.

Data availability. The genome sequence and associated data for *Halomonas* sp. SBS 10 were deposited under GenBank accession number [RXH100000000](https://www.ncbi.nlm.nih.gov/nuclseq/RXH100000000), BioProject accession number [PRJNA479678](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA479678), SRA accession number [SRP224914](https://www.ncbi.nlm.nih.gov/sra/SRP224914), and BioSample accession number [SAMN09601649](https://www.ncbi.nlm.nih.gov/biosample/SAMN09601649).

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We declare no conflicts of interest.

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