

Draft Genome Sequence of *Halomonas* sp. Strain HAL1, a Moderately Halophilic Arsenite-Oxidizing Bacterium Isolated from Gold-Mine Soil

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We report the draft genome sequence of arsenite-oxidizing *Halomonas* sp. strain HAL1, isolated from the soil of a gold mine. Genes encoding proteins involved in arsenic resistance and transformation, phosphate utilization and uptake, and betaine biosynthesis were identified. Their identification might help in understanding how arsenic and phosphate metabolism are intertwined.

Halomonas sp. strain HAL1, which has a high level of tolerance to arsenite, was isolated from the soil of a gold mine in Daye County, Hubei Province, central China. Strain HAL1 is a heterotrophic, arsenite-oxidizing gammaproteobacterium under aerobic conditions. It is also moderately halophilic and can grow at NaCl concentrations ranging from 0.2 M to 2.0 M in LB, the optimal concentration being 0.8 M. Interest in arsenic and phosphate metabolism in *Halomonas* was sparked by a recent controversial report claiming that arsenate could replace phosphate in DNA (6, 10). It was therefore desirable to obtain the genomic sequence of a *Halomonas* strain able to survive in extremely low phosphate concentrations in the presence of arsenic.

The genome of *Halomonas* sp. strain HAL1 was sequenced using a 454 GS FLX sequencer (3) and was assembled using GS *de novo* assembler ("Newbler"), version 2.5.3. The assembled contigs were submitted to the RAST annotation server for subsystem classification and functional annotation (1). The protein-coding genes (CDSs) were assigned using BLASTp with the KEGG orthology (KO) database. GC content was calculated using an in-house Perl script. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; <http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) was employed for gene annotation in preparation for submission to GenBank.

The draft genome sequence of *Halomonas* sp. strain HAL1 comprises 4,347,024 bases at 36-fold coverage. The assembled genome consists of 89 large contigs (>500 bp) with an average contig size of 102,049 bp and a G+C content of 54.1%. The draft genome sequence contains 4,082 CDSs, 54 tRNAs, and 8 rRNAs. For the CDSs, 3,439 proteins could be assigned to Cluster of Orthologous Groups (COG) families (9). One thousand nine hundred fifty-four proteins have orthologs (bit score of >60) with the five reference strains, *Halomonas elongata* and four others, *Chromohalobacter salexigens* DSM 3043, *Hahella chejuensis* KCTC 2396, *Cellvibrio japonicas* Ueda107, and *Pseudomonas entomophila* L48, identified by RAST as the closest neighbors to HAL1.

The *Halomonas* sp. strain HAL1 genome carries multiple genes potentially involved in arsenic resistance. There are two arsenic resistance operons containing genes encoding ArsC, ArsH, and ACR3 but only one operon with a gene encoding ArsR. One of these operons is adjacent to two genes, *aioA* and *aioB*, that encode the enzyme arsenite oxidase (4, 7). There is also a *pst* operon in the

immediate vicinity of this arsenic cluster that might play a role in integrating phosphate and arsenic metabolism. In addition, there is another *pst* operon on the chromosome. Furthermore, a number of genes were predicted to encode proteins conferring resistance to metals and metalloids, such as seven putative heavy and transition metal-translocating P-type ATPases. Additional genes related to inert substances ("compatible solutes") were identified, and they may reduce osmotic pressure and promote survival in a hypersaline environment (2, 8). Eight genes related to betaine biosynthesis were found, including three copies of *betB*, along with three genes responsible for ectoine biosynthesis.

The 16S rRNA gene sequence of *Halomonas* sp. strain HAL1 exhibited a high level of sequence similarity (99.0%) to *Halomonas boliviensis* (5). However, current experiments (such as physiological and biochemical experiments, morphological tests, and DNA-DNA hybridization, etc.) suggest it may potentially be a novel species in *Halomonas*.

Nucleotide sequence accession numbers. The genome sequence has been deposited in DDBJ/EMBL/GenBank under accession number [AGIB000000000](https://www.ncbi.nlm.nih.gov/nuccore/AGIB000000000). The version described in this paper is the first version, AGIB000000000.

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