Draft Genome Sequence of *Halomonas* sp. Strain KM-1, a Moderately Halophilic Bacterium That Produces the Bioplastic Poly(3-Hydroxybutyrate)

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We report the draft genome sequence of *Halomonas* sp. strain KM-1, which was isolated in Ikeda City, Osaka, Japan, and which produces the bioplastic poly(3-hydroxybutyrate). The total length of the assembled genome is 4,992,811 bp, and 4,220 coding sequences were predicted within the genome. Genes encoding proteins that are involved in the production and depolymerization of poly(3-hydroxybutyrate) were identified. The identification of these genes might be of use in the production of the bioplastic poly(3-hydroxybutyrate) and its monomer 3-hydroxybutyrate.

*Halomonas* sp. strain KM-1 was deposited in the International Patent Organism Depositary (IPOD, AIST, Japan) as FERM BP-10995 (3). Strain KM-1 is a heterotrophic gammaproteobacterium that exhibits a higher level of poly(3-hydroxybutyrate) (PHB) production under aerobic conditions than other species (4). This strain is moderately halophilic and can grow in SOT medium containing NaCl concentrations ranging from 0.1% to 10% (2, 4). Strain KM-1 has attracted much attention in terms of practical bioplastic PHB production using biodiesel waste glycerol without pH adjustment (3). The complete genome sequence of *Halomonas elongata* (11) and the draft genome sequences of *Halomonas* sp. strain HAL1 (5), *Halomonas* sp. strain TD01 (1), *Halomonas boliviensis* LCI, and *Halomonas* sp. strain GFAJ-1 (14) have been reported. It was therefore considered desirable to obtain the genomic sequence of a *Halomonas* strain that produces a higher level of PHB than other strains using glycerol and compare the genes involved in PHB synthesis by high- and low-productivity strains.

The genome of *Halomonas* sp. strain KM-1 was sequenced using a 454 GS FLX sequencer (6), and the sequence was assembled using the GS de novo assembler Newbler, version 2.0.00.20. The assembled contigs were submitted to the Microbial Genome Annotation Pipeline ver.1.060 (MiGAP; http://www.migap.org/index.php/en) annotation server for subsystem classification and functional annotation (12). Protein coding sequences (CDSs) were assigned using the MetaGene annotator with the NCBI RefSeq microbial sequence database (8). MiGAP was employed for gene annotation in preparation for submission to the DDBJ database.

The draft genome sequence of *Halomonas* sp. strain KM-1 comprises 4,992,811 bases at 41-fold coverage. The assembled genome consists of 173 contigs (>663 bp) with an average contig size of 28,860 bp and a G+C content of 63.9%. The draft genome sequence contains 4,648 CDSs, 56 tRNAs, and one rRNA. Among the CDSs, 4,220 proteins could be assigned to Clusters of Orthologous Groups families (13). The number of proteins with orthologs (bit score of >60) among the 134 reference strains was 3,978. *Halomonas elongata* and *Chromohalobacter salexigens* DSM 3043 were identified by MiGAP as the closest neighbors of strain KM-1, in addition to *Halomonas* sp. strain HAL1 (5).

As expected for an organism that synthesizes PHB and as has been reported for other *Halomonas* strains (9), the requisite *phbA*, *phbB*, and *phaC* genes, as well as the PHB depolymerase structural gene *phaZ*, were found in the genome of strain KM-1. The *Halomonas* sp. strain KM-1 genome also carries multiple genes that are potentially involved in arsenic resistance, as has also been reported for *Halomonas* sp. strain HAL1 (5) and *Halomonas* sp. strain GFAJ-1 (14). *Halomonas* sp. strain KM-1 has two arsenic resistance operons that contain genes encoding the proteins *ArsR* and *ACR3* and the proteins *ArsB* and *ArsC*, respectively (7, 10).

The 16S rRNA gene sequence of *Halomonas* sp. strain KM-1 exhibited a high level of sequence similarity (99.0%) to *Halomonas* species (3).

**Nucleotide sequence accession numbers.** The genome sequence described here has been deposited in the DDBJ database under accession numbers BAEU01000001 to BAEU01000173.

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