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GENOME SEQUENCES

Draft Genome Sequence of Red-Heat-Causing *Halomonas eurihalina* MS1, a Moderately Halophilic Bacterium Isolated from Saline Soil in Alicante, Spain

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ABSTRACT Here, we report the draft genome sequence of *Halomonas eurihalina* MS1, which was isolated from saline soil in Alicante, Spain, and causes the condition known as "red heat" in salt-packed cured hides, decreasing their commercial value for leather production.

Strain MS1, which belongs to the *Halomonas eurihalina* species, is in the class *Gammaproteobacteria* (1–3). *Halomonas* species have been designated as slight to moderate halophiles, with the potential to grow in concentrations of sodium chloride of 0.1 to 32.5% (wt/vol) (4). The genus *Halomonas,* a leading member within the family *Halomonadaceae* (5), was first characterized after the isolation of *Halomonas elongate* from the solar saltern in the Netherlands (1, 5). *Halomonas eurihalina* is a Gram-negative, nonmotile, rod-shaped, aerobic, moderately halophilic bacterium (2) with the ability to propagate in diverse saline environments, such as solar salterns, intertidal estuaries, hydrothermal vents, hypersaline lakes, and open ocean (2, 3).

Strain MS1 of *H. eurihalina* was obtained from the saline soil of Alicante, Spain (37°58′40″N, 0°41′0″W). The saline source is located 22.97 m above sea level on the southeastern Mediterranean coast of Spain and contains 17% NaCl. Isolation of the MS1 strain was executed by filtering (0.22-μm filter) water from the saline soil and culturing the filter for 24 h at 32°C in Luria broth (LB) agar containing 10% (wt/vol) NaCl (https://haloarchaea.com/wp-content/uploads/2018/10/Halohandbook_2009_v7.3mds.pdf). This strain demonstrated growth under saline conditions (i.e., 5.0 to 25%), with an optimum of 10%, while no growth was found in the absence of saline conditions. This phenomenon eventually indicated that the strain is a moderate halophile.

MS1 was streaked onto an LB agar plate containing 10% (wt/vol) NaCl and was incubated at 32°C for 24 h. DNA was isolated from a single colony scraped from the LB plate. Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified using a Qubit 3.0 fluorometer (Life Technologies, Carlsbad, CA). The genomic DNA library was prepared using the Nextera Flex DNA library preparation kit (Illumina, San Diego, CA), which generated ~600-bp fragments. The library was analyzed for concentrations and denatured for loading into a flow cell for cluster generation. The denatured library was sequenced on an Illumina MiniSeq platform. A total of 1.9×10^6 sequencing reads were obtained by using 150-bp paired-end sequencing. Read quality was assessed with FastQC (version 1.0.0; Illumina BaseSpace Labs). Reads were assembled *de novo* using SPAdes (version 3.9.0). Default parameters were used for all software unless otherwise noted. Multilocus sequence type, coding sequences (CDSs), mRNAs, rRNAs, tRNAs, genes, and pseudogenes were determined using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (version 4.3).

The genome characteristics were as follows: genome size, 3.84 Mb in 108 contigs (148-fold coverage); N_{50}, 210,983 bases; GC content, 63.01%; total number of genes,

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3,652; total number of CDSs, 3,576; number of CDS coding genes, 3,526; number of RNA genes, 76; number of rRNAs, 5; number of tRNAs, 66; number of noncoding RNAs, 5; number of pseudogenes, 50. Based on the sequencing data, the strain was identified as *H. eurihalina* by using the Bacterial Analysis Pipeline.

These genomic data will be worthwhile for understanding *H. eurihalina* MS1 prevalence and should offer a novel understanding of the persistence of this strain in salt facilities and of effective control measures against such strains, which are responsible for red heat in salt-packed cured hides.

Data availability. The whole-genome shotgun projects reported here have been deposited in DDBJ/ENA/GenBank under accession number VTPU00000000 and BioProject number PRJNA562905. The raw reads are available in the Sequence Read Archive (SRA) under accession number SRR10095887. The version described in this paper is the first version.

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