Draft genome sequence of the halophilic Halobacillus mangrovi KTB 131 isolated from Topan salt of the Jeon-nam in Korea

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A B S T R A C T

The draft genome sequence of the halophilic bacterium Halobacillus mangrovi KTB 131, isolated from Topan salt of the Jeon-nam in Korea, was established. The genome comprises 4,151,649 bp, with a G + C content of 41.6%. The strain displays a high number of genes responsible for secondary metabolite biosynthesis, transport, and catabolism compared to other Halobacillus bacterial genus members. Numerous genes responsible for various transport systems, solute accumulation, and aromatic/sulfur decomposition were detected. The first genomic analysis encourages further research on comparative genomics and potential biotechnological applications. The whole draft genome sequence of Halobacillus mangrovi KTB 131 is now available (Bioproject PRJNA380285).

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/CP020772.1.

2. Introduction

The genus Halobacillus was created by Spring et al. with the description of two novel species, Halobacillus litoralis and Halobacillus trueperi, and represents a large group of halophilic aerobic bacteria (Gram-positive, rod-shaped, heterotrophic, endospore-producing) belonging to the family Bacillaceae [1]. To date, 20 species have been described within the genus Halobacillus, which are widely distributed among diverse natural saline environments such as marine salterns, salt lakes, saline soils, salt-fermented foods, and salt-preserved food products [2,3]. Hence, more investigations at the genomic level are required to improve our understanding of its ecology, genetics, and potential biotechnological applications. The Halobacillus mangrovi KTB 131 strain was isolated from the Topan salt of Shin-Ahn tae-pyung saltern in Korea. Topan defines a marine solar saltern’s floor turned into red-clay using a Korean traditional method. To date, the whole-genome analysis of Halobacillus mangrovi had not been reported. To fill this gap, Halobacillus mangrovi KTB 131 was chosen to perform genome sequencing.

3. Materials and methods

Genome sequencing was accomplished using a single molecule real-time (SMRT) sequencing platform on the PacBio RS II (Pacific Biosciences, Menlo Park, CA) [4]. Genomic DNA was isolated using a standard genomic DNA isolation kit (Promega, USA). The whole
genome sequencing of strain SAH-A6 was accomplished using single SMRT cell with a single 180-min movie (Paciﬁc Biosciences) with P6C4 chemistry [5]. The open reading frames of the assembled genome were predicted and annotated using the hierarchical genome-assembly process (HGAP) [6] protocol RS HGAP Assembly 2 in SMRT analysis version 2.3.0 (Paciﬁc Biosciences; https://github.com/PaciﬁcBiosciences/SMRT-Analysis), IMG-ER [7], NCBI COG function [8], Pfam information [9], and EzTaxon [10] database. The rRNA and tRNA genes were identiﬁed using RNAmmer 1.2 [11] and tRNA scan-SE 1.23 [12], respectively. The whole genome sequence of SAH-A6 was annotated using the Rapid Annotation System Technology (RAST) server. The pie chart showed the counts for each subsystem feature as well as the subsystem coverage.

4. Data description

Moderately halophilic KTB 131 strain grows at NaCl concentrations ranging between 5 and 20% (w/v), with optimum growth obtained at 10% (w/v). Growth occurs at temperatures of 10–45 °C and pH 7.0–9.0. The KTB 131 strain showed the ability to hydrolyze skim milk, starch, and tween 80. A phylogenetic tree was built based on a neighbor joining tree obtained from the alignment of the 16S rRNA gene sequences (~1400 bp), showing the relationship between Halobacillus sp. genomes available for KTB 131 using MEGA 6 (Supplementary Fig. 1). The draft genome sequence of Halobacillus mangrovi KTB 131, isolated from Topan salts of the Shin-Ahn tae-pyung saltern, Korea, was determined. The assembled genome comprises 4,151,649 bp, with a G + C content of 41.6%. Strain KTB 131 displays a G + C content similar to those observed in other Halobacillus sp. (Table 1). The strain possesses a high number of genes that are responsible for secondary metabolites biosynthesis, transport, and catabolism compared to other bacteria from the Halobacillus genus. In addition, strain KTB 131 uses universal strategies toward enabling extreme adaptation, as indicated by its genome. Numerous genes responsible for various transport systems, solute accumulation, and aromatic/sulfur decomposition were detected. Additionally, as shown in Fig. 1, this strain displays many genes involved in the Serine-glyoxylate cycle, sporulation gene orbits, the glycolipid and glycerophospholipid metabolisms, fatty acid biosynthesis FASII, maltose and maltodextrin utilization, ribosomal LSU production, and modiﬁcation of tRNA involved in peptidoglycan synthesis. The results obtained from the subsystem category distribution statistical analysis for Halobacillus mangrovi KTB 131 are shown in Fig. 1.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.gdata.2017.07.010.

Verification and authentication

The whole draft genomic sequence of Halobacillus mangrovi KTB 131 (Bioproject PRJNA380285) has been deposited at NCBI GenBank database under accession numbers CP020772. This strain is available from Korean Collection for Type Cultures (KCTC) with the accession number KCTC 33901.

Conflict of interest

The authors have nothing to disclose.
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