

Genome Sequence of Strain TW25, a Novel Member of the Genus *Ornithinibacillus* in the Family *Bacillaceae*[∇]

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***Ornithinibacillus* sp. strain TW25, belonging to the family *Bacillaceae*, was isolated from a dead ark clam during a mass mortality event. Here, the draft genome sequence of strain TW25 (3,843,870 bp, with a G+C content of 36.7%) is reported. This is the first *Ornithinibacillus* genome to be sequenced.**

Mass mortality of cage-cultured invertebrates is an annual event along the south coast of Korea. The novel strain TW25 belonging to the genus *Ornithinibacillus* was cultivated as part of an attempt to isolate and characterize putative pathogenic bacterioplankton. The genus *Ornithinibacillus* currently comprises three species; *O. baviensis* was isolated from pasteurized milk, *O. californiensis* from coastal surface sediments (8), and *O. contaminans* from a human blood sample obtained from a 75-year-old woman (5). Based on 16S rRNA gene sequences of validly published species, the isolate TW25 shows the closest similarity to *O. californiensis* (98.5%). Within the family *Bacillaceae*, a major feature that differentiates the genus *Ornithinibacillus* from *Oceanobacillus* is the inclusion of L-ornithine in the peptidoglycan (5). This study presents the genome of *Ornithinibacillus* sp. TW25; genome sequencing had not been completed or initiated for any strain in this genus when the present sequencing project was begun. *Ornithinibacillus* sp. TW25 genomic DNA was isolated from a tissue homogenate obtained from the ark clam. This strain is the first member of the genus *Ornithinibacillus* to be sequenced.

A whole-genome shotgun strategy was used for genomic DNA sequencing. Roche 454 GS FLX Titanium pyrosequencing (216,931 reads totaling ~86 Mb, ~22.4-fold coverage of the genome) was performed by GnCIBIO, Inc. (Daejeon, Republic of Korea), and genome sequences were processed with Roche software, according to the manufacturer's instructions. A total of 216,931 reads were assembled using 454 Newbler assembler version 2.3 software (454 Life Science), which generated 75 large contigs with bases containing quality scores of 40 and above. The RAST (Rapid Annotation using Subsystem Technology) pipeline (1) and the Glimmer 3.02 modeling software package (4) were used for the preliminary prediction of 3,867 and 4,019 coding sequences (CDSs), respectively, within the genome.

The unclosed draft genome includes 3,843,870 bases with a G+C content of 36.7%. tRNAscan-SE 1.23 (7) and

RNAmmmer 1.2 (6) analyses of the genome predicted 54 tRNA genes, two 5S rRNA genes, one 23S rRNA gene, and one 16S rRNA gene. L-Ornithine is the characteristic di-amino acid in the peptidoglycan of *Ornithinibacillus* species, and 15 genes were predicted to be involved in the conversion or degradation of L-ornithine, including arginase (EC 3.5.3.1), ornithine aminotransferase (EC 2.6.1.13), and ornithine cyclodeaminase (EC 4.3.1.12) (2, 3, 10).

Among the publicly available genomes for the family *Bacillaceae*, *Ornithinibacillus* sp. strain TW25 shows the closest relationship to *Oceanobacillus iheyensis* HTE831^T (9), with which it shares 2,266 genes, in addition to containing 1,645 unique genes. There are 51 and 30 predicted genes that correspond to virulence, disease, and defense in the genomes of TW25 and *O. iheyensis* HTE831^T, respectively. However, only the TW25 genome contains genes putatively involved in adhesion, bile hydrolysis, vancomycin resistance, and multidrug resistance efflux.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AEW0000000. The version described in this paper is the first version, AEW01000000. The 75 large contigs contained in the genome have been deposited under accession numbers AEW01000001 through AEW01000075.

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