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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Virgibacillus halodenitrificans* 1806

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***Virgibacillus halodenitrificans* 1806 is an endospore-forming halophilic bacterium isolated from salterns in Korea. Here, we report the draft genome sequence of *V. halodenitrificans* 1806, which may reveal the molecular basis of osmoadaptation and insights into carbon and anaerobic metabolism in moderate halophiles.**

Halophilic bacteria are excellent model microorganisms for investigating the molecular mechanisms underlying osmoadaptation in hypersaline environments (2, 3, 12). Recently, several *Virgibacillus* strains were isolated from salterns, fermented seafood, and deteriorated mural paintings (4, 6–8, 10, 11, 13), and their 16S rRNA gene sequences are similar to those of *Oceanobacillus* and *Lentibacillus* (10). *Virgibacillus* strains are Gram-positive, motile, rod-shaped, and spore-forming halophiles. Some species can metabolize fructose and grow anaerobically (5, 6, 14), indicating that these features are species-dependent phenotypes (11). The draft genome sequence of *V. halodenitrificans* 1806 will help to reveal not only the molecular basis of prokaryotic osmoadaptation but also the molecular mechanisms underlying distinct metabolic pathways in this genus.

The genome sequence of strain 1806 was determined by a whole-genome shotgun strategy using an Illumina HiSeq 2000 instrument. Quality trimming of paired-end reads produced from a 500-bp genomic library (2,322.9 Mb, 592-fold coverage) and *de novo* assembly were performed using CLC Genomics Workbench version 4.8. We obtained 92 contigs of more than 200 bp (3,920,549 bp, 37.4% G+C) with an N_{50} of 79,346 bp and a maximum contig size of 230,247 bp. The same data set was also subject to analysis using Velvet version 1.2.01 (15), resulting in 77 large scaffolds (total length = 3,961,615 bp and N_{50} = 263,346 bp) out of 111 contigs, which was the best result obtained with a *k*-mer size of 93. The assembly results from these two *de novo* assemblers were consistent with each other, but the tRNA prediction results were very different (46 versus 60), probably due to improper representation of tRNA genes located near to or within the multicopy rRNA operons.

Automatic genome annotation, based on CLC-generated assembly, was performed using the RAST server (1). Of the predicted 3,949 protein-coding genes, 45% were assigned subsystem categories. The genome size of strain 1806 inferred from the total contig length was similar to those of *Oceanobacillus iheyensis* HTE831 (3,530,528 bp, 35.7% G+C), which was ranked as the closest neighbor according to RAST genome analysis, and *Geobacillus thermoglucosidasius* C56-YS93 (3,893,306 bp, 44.0% G+C). PROmer-based comparison (9) between contigs and complete genome sequences of HTE831 revealed fairly good alignment, with only 20 mismatched contigs (61.0 kb in total).

Strain 1806 contains genes related to osmolarity for the uptake of compatible solutes from hypersaline environments (3). For example, several osmotically activated L-carnitine/choline ABC transporters, glycine betaine transporters, Na^+/H^+ antiporters, and Na-dependent phosphate transporters were identified, together with a glucose-fructose oxidoreductase responsible for protecting the bacterium against osmotic shock in sugar-rich environments. Genes involved in fructose metabolism (14) (e.g., fructose-specific II ABC components, DeoR family transcriptional repressors, fructokinase, and PfkB family kinases) were also identified. Another feature of strain 1806 is its ability to grow anaerobically, which might be supported by genes involved in alternative respiration pathways, including menaquinone biosynthesis, nitrate reductase, and lactate dehydrogenase. Thus, the draft genome sequence of *V. halodenitrificans* strain 1806 will not only facilitate further evolutionary study of this genus but also provide insights into the molecular mechanisms underlying osmoadaptation in hypersaline environments.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number ALEF00000000. The version described in this paper is the first version, ALEF01000000.

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