

Genome Sequence of *Lentibacillus jeotgali* Grbi^T, Isolated from Traditional Korean Salt-Fermented Seafood

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***Lentibacillus jeotgali* Grbi^T, isolated from a traditional Korean salt-fermented seafood, is a strictly aerobic, Gram-positive, nonmotile, endospore-forming, moderately halophilic bacterium belonging to the family Bacillaceae in the phylum Firmicutes. Here, the draft genome sequence of *L. jeotgali* Grbi^T (3,775,822 bp with a G+C content of 42.5%) is reported. This is the first reported genome sequence from a *Lentibacillus* species.**

The moderately halophilic bacteria grow optimally in 3 to 15% (wt/vol) NaCl (4) and usually synthesize or accumulate compatible solutes to maintain an osmotic equilibrium in response to the high-salt content of the external environment. Such compatible solutes comprise low-molecular-weight osmoregulatory organic compounds such as highly water-soluble amino acids, carbohydrates or their derivatives, sugars, and polyols (9). Jeotgal is a traditional Korean fermented seafood made from salted marine organisms, including fish, mollusks, or crustaceans. It is an important source of dietary protein and has been since AD 683 (10). It is also a source of numerous diverse bacteria belonging to the phyla *Actinobacteria*, *Firmicutes*, and *Proteobacteria*, as well as yeast and archaea (1, 8). *Lentibacillus jeotgali* Grbi^T is a Gram-positive, nonflagellated, rod-shaped, endospore-forming, moderately halophilic bacterium isolated from jeotgal made from scallops (3). Strain Grbi^T grows in 3.0 to 20.0% (wt/vol) NaCl, with optimal growth occurring in 10 to 15% (wt/vol) NaCl. Here, we present the draft genome sequence of *L. jeotgali* Grbi^T. This is the first reported genome sequence from a *Lentibacillus* species.

The genome sequence of *L. jeotgali* Grbi^T was determined using a combination of an Illumina (San Diego, CA) Genome Analyzer IIX with a 100-bp paired-end library and a 454 Genome Sequencer FLX Titanium system (Roche Diagnostics, Branford, CT) with an 8-kb paired-end library. Totals of 19,593,594 and 168,344 sequencing reads were obtained from the Illumina (508.8-fold genome coverage) and Roche 454 (10.7-fold genome coverage) systems, respectively. The Illumina and Roche 454 sequencing reads were assembled using CLC Genomics Workbench 4.7.2 (CLC bio, Denmark) and GS Assembler 2.5.1 (Roche Diagnostics, Branford, CT), respectively. The sequences were assembled into 31 large contigs (>1 kb in size) organized into eight scaffolds (N_{50} contig size of approximately 312.4 kb) totaling 3,775,822 bp, with a G+C content of 42.5%.

Genes were predicted using Glimmer 3.02 (2) and

tRNAscan-SE 1.23 (5) and annotated using an in-house annotation system with several open-access databases (6, 7, 11, 12). The uncompleted draft genome contains 53 predicted tRNA genes and 12 predicted rRNA genes (three copies of 5S rRNA genes, four copies of 16S rRNA genes, and five copies of 23S rRNA genes). Of the 3,731 predicted coding sequences, 2,668 were predicted to fall into 18 cluster of orthologous group (COG) categories (J, K, L, D, O, M, N, P, T, C, G, E, F, H, I, Q, R, and S). The genome contains 299 predicted genes for amino acid transport and metabolism and 109 predicted genes associated with the biosynthesis of compatible solutes (betaine, glutamate, and glutamine) and the transport of osmolytes (choline-glycine betaine transporter, ABC-type proline/glycine betaine transporter, potassium transporter [TrkA], sodium symporter/antiporter, and mechanosensitive channels). These results perhaps reflect the food grade ecological niche occupied by an organism present in salt-fermented seafood.

Nucleotide sequence accession numbers. The draft genome sequence of *Lentibacillus jeotgali* Grbi^T reported in this paper has been deposited in DDBJ/EMBL/GenBank under accession number AGAV00000000 and in GenBank under Genome Project identification number 71453. The version described in this paper is the first version (accession number AGAV01000000).

This work was supported by a grant from the Next-Generation BioGreen 21 Program (PJ008208), Rural Development Administration, Republic of Korea.

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