

Draft Genome Sequencing of *Bacillus* sp. Strain M2-6, Isolated from the Roots of Korean Ginseng, *Panax ginseng* C. A. Meyer, after High-Hydrostatic-Pressure Processing

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A bacterium, designated M2-6, was isolated from Korean ginseng, *Panax ginseng* C. A. Meyer, roots after high-hydrostatic-pressure processing. On the basis of 16 rRNA gene phylogeny, the isolate was presumptively identified as a *Bacillus* sp. Here we report the draft genome sequence of *Bacillus* sp. strain M2-6 (= KACC 16563).

High-hydrostatic-pressure (HHP) processing is an efficient food-processing method for maintaining the natural characteristics of food components. The processing can be also used as an alternative method of more efficiently extracting ginsenoside metabolites from the roots of *Panax ginseng* without laborious steaming (4). Most terrestrial bacteria do not survive under high pressure above 60 MPa (11, 12). The loss of viability through HHP is probably due to the disruption or breakdown of cell wall components of microorganisms. However, if some bacteria survive such a condition, they could be a serious food safety threat. The resistance of microorganisms to high pressure is highly variable, depending mainly on the type of organism and the food matrix involved; e.g., spores show great resistance to such inactivation (7). Here we report the genome sequence of a bacterial strain, designated M2-6, isolated from Korean ginseng, *P. ginseng* C. A. Meyer, roots after HHP processing at 350 MPa for 30 min.

The genome sequence of strain M2-6 was obtained with a combination of the Illumina HiSeq 2000 (100-bp paired-end sequencing yielding 46,523,946 reads; >1,225-fold coverage) and Roche 454 (8-kb insert paired-end sequencing yielding 329,506 reads; >28.5-fold) sequencing systems. A total of 67 contigs generated by hybrid assembly using CLC genomic workbench (CLC Bio), GS Assembler 2.3 (Roche Diagnostics, Branford, CT), and CodonCode Aligner (CodonCode Co.). The draft genome of strain M2-6 consisted of 3,795,647 bases with a 41.1% G+C content, 4,058 open reading frames (ORFs), 61 tRNAs, and four rRNA operons. The annotations were conducted by homology search against the COG and SEED databases (1, 10). Among the COG categories, R (general function prediction only; 323 ORFs) and S (function unknown; 321 ORFs) were abundant, followed by category E (amino acid transport and metabolism; 306 ORFs).

The Eztaxon-e database (2) was used for the identification of isolates in which the 16S rRNA gene sequence of strain M2-6 showed 100% similarity to those of *Bacillus aerophilus* 28K^T, *Bacillus stratosphericus* 41KF2a^T, and *Bacillus altitudinis* 41KF2b^T (8). Since the genome sequence information of the latter species is not available, we could not identify our isolate to the species level.

The members of the genus *Bacillus* are regarded as an indicator of food-borne pathogens in a variety of food processes (5) because they are highly resistant to desiccation, high temperature, and UV

radiation (3, 6). These characteristics of *Bacillus* bacteria even increase their survival rate by allowing them to escape from many extreme environments (8). They may also survive after HHP processing, which is a method of food treatment with minimal heat exposure (9). *Bacillus* sp. strain M2-6 was deposited in the Korean Agricultural Culture Collection under accession number KACC 16563. Further analyses and more experimental work are under way to determine the potential pathogenicity of this isolate in HHP food processing.

Nucleotide sequence accession numbers. The genome sequence of *Bacillus* sp. strain M2-6 was deposited at GenBank under accession no. [AJWW000000000](https://www.ncbi.nlm.nih.gov/nuccore/AJWW000000000). The version used here is the first version, [AJWW010000000](https://www.ncbi.nlm.nih.gov/nuccore/AJWW010000000).

ACKNOWLEDGMENT

This study was supported by a grant from the Korea Food Research Institute (projects E0122301 and E0124104), Ministry of Knowledge Economy, Republic of Korea.

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Received 2 October 2012 Accepted 4 October 2012

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doi:10.1128/JB.01939-12

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