**Genome Sequencing of *Bacillus subtilis* SC-8, Antagonistic to the *Bacillus cereus* Group, Isolated from Traditional Korean Fermented-Soybean Food**

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*Bacillus subtilis* SC-8 is a Gram-positive bacterium displaying narrow antagonistic activity for the *Bacillus cereus* group. *B. subtilis* SC-8 was isolated from Korean traditional fermented-soybean food. Here we report the draft genome sequence of *B. subtilis* SC-8, including biosynthetic genes for antibiotics that may have beneficial effects for control of food-borne pathogens.

The genus *Bacillus* produces broad-spectrum antibiotics with a variety of structures, such as bacteriocin-like compounds and lipopeptides (8). In particular, the biochemical and genetic properties of *B. subtilis* have been well studied (7). Antibiotics produced by *B. subtilis* have low toxicity and high biodegradability, and *B. subtilis* has been granted “generally recognized as safe” (GRAS) status (1). Due to these beneficial properties, *B. subtilis* has been widely used for the control of food-borne pathogens (6) and therefore has importance in the fermented food industry.

*B. subtilis* SC-8 was isolated from Korean traditional fermented-soybean food and was found to display narrow antimicrobial activity against *B. cereus* group species, such as *B. cereus*, *B. anthracis*, *B. mycoides*, *B. pseudomycoides*, *B. thuringiensis*, and *B. weihenstephanensis* (4, 5).

The genome sequence of *B. subtilis* SC-8 was obtained by using a combination of an Illumina GA IIx instrument (San Diego, CA) with 100-bp paired-end sequencing (29,613,94 reads; total, 2,394,595,930 bases; coverage, 578.57×) and a 454 GS FLX Titanium instrument (Roche Diagnostics, Banford, CT) with 8-kbp paired-end sequencing (181,914 reads; total, 37,497,691 bases; coverage, 9.06×). All generated reads were assembled into 17 contigs using the software programs GS Assembler 2.3 (Roche Diagnostics, Branford, CT) and CLC Genomics Workbench 4.5 (CLC Bio, Denmark).

The draft genome of *B. subtilis* SC-8 is composed of 4,138,818 bp with a 43.46% G+C ratio. *B. subtilis* SC-8 includes 4,244 protein-coding genes, 83 tRNA-encoding genes, and 30 rRNA operons in its genome.

The *B. subtilis* SC-8 genome also includes several genes related to antimicrobial products and antibiotic biosynthetic pathways, similar to the genomes of *B. subtilis* 168 (3) and *B. subtilis* BSn5 (2). Of these, genes related to lipopeptide, such as surfactin and lipo|pastatin, and polyketide synthase were found in SC-8 chromosomes. In particular, the surfactin synthetase gene cluster was composed of 5 genes (BSSC8_39740 to BSSC8_39780) in the SC-8 chromosome. Meanwhile, the *B. subtilis* 168 and *B. subtilis* BSn5 genomes include a 4-gene cluster encoding surfactin synthetase. The gene encoding subtilosin A (BSSC_04620), known to be a bacteriocin-like substance, was found and was composed of 44 amino acids (aa), unlike the subtilosin A gene of *B. subtilis* 168 (43 aa). In contrast, the SC-8 genome lacks the sublancl gene found in *B. subtilis* strain 168. Potential genes related to antibiotics that were not present in *B. subtilis* 168 and *B. subtilis* BSn5 were also found in the *B. subtilis* SC-8 chromosome (BSSC8_21740 to BSSC8_21920). These genes may encode the novel antimicrobial peptides displaying narrow activity against the *B. cereus* group, as previously described (4, 5). Therefore, *B. subtilis* strain SC-8 is a possible candidate for use as an antagonistic bacterium against food-borne pathogens, to prevent food poisoning, and as an alternative fermenting bacterium in the fermented-soybean food industry because of these features of the SC-8 genome.

**Nucleotide sequence accession number.** The draft genome sequence of *Bacillus subtilis* SC-8 was deposited in GenBank under accession number AGFW00000000.

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