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Complete Genome Sequence of *Bacillus cereus* Bacteriophage BCP78

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***Bacillus cereus* is generally found in soil habitats, and it contaminates a wide variety of foods, causing food poisoning with symptoms such as vomiting and diarrhea. To develop a novel biocontrol agent to inhibit this pathogen, bacteriophage BCP78 belonging to the *Siphoviridae* family was isolated from a fermented food sample. Here we announce the complete genome sequence of BCP78, which may be useful for understanding its inhibition mechanism against *B. cereus*, and describe major findings from the genome annotation.**

Bacillus cereus is a soil bacterium and is generally propagated to vegetables and foods (4, 6, 7). It sometimes causes severe food poisoning with symptoms such as nausea, vomiting, and diarrhea (4, 13). Because bacteriophage treatment was allowed for use in foods by the U.S. FDA (2), it would be useful to ensure food safety from *B. cereus* contamination (9, 14). However, genomic characterization for its inhibition mechanism has not been conducted yet. The *B. cereus* bacteriophage BCP78 was isolated from a fermented food, and it belongs to the *Siphoviridae* family, efficiently inhibiting *B. cereus* and several strains of *B. subtilis* in various vegetables and foods (data not shown).

Alkaline lysis method (15) was used to isolate the phage genomic DNA, and it was sequenced using the Genome Sequencer FLX (GS-FLX) Titanium by Macrogen, Seoul, South Korea. The assembly of quality filtered reads was performed using 454 Newbler 2.3 assembler, and the prediction of open reading frames (ORFs) and their confirmation were conducted using the Glimmer 3.02 (3), GeneMark.hmm (10), and FgenesV softwares (Softberry, Inc., Mount Kisco, NY), respectively. Conserved protein domain analysis of predicted ORFs was also carried out using the BLASTP (1) and InterProScan programs (16). Comparative codon preference analyses of the *B. cereus* and phage BCP78 genomes were performed using GCUA program (11).

The complete circular genome of *B. cereus* phage BCP78 showed a 156,176-bp length with a GC content of 39.86%, 227 ORFs, and 18 tRNAs, suggesting the first phage genome targeting *B. cereus* in the *Siphoviridae* family with the largest number of tRNAs. It is intriguing that this genome encodes many extra tRNAs, suggesting that they probably help translation of the host mRNAs or they may be involved in translation of the phage mRNAs (8). Comparative codon usage analysis of *B. cereus* strains (AH187 and ATCC 14597) and the phage showed different preferences in phenylalanine, asparagine, and serine, explaining a possible role for extra tRNAs in the phage genome. This phage genome encodes structural and packaging proteins, such as a major capsid protein, a prohead protease, minor structural proteins, baseplate proteins, a portal protein, a terminase, a tail sheath protein, tail lysins, and tail fiber proteins. This genome encodes two copies of tail lysins, probably involved in the infection mechanism (5), and an autolysin and a holin, probably involved in cell lysis (12). In addition, this genome encodes many DNA manipulation proteins (DNA polymerases, helicases, a primase and a recombinase) and nu-

lease (DNA nucleases and endo- and exonucleases). Furthermore, there are three putative sigma factors in this genome, suggesting that they are probably related to preferential transcription of the phage genes rather than the host genes. The complete-genome analysis of *B. cereus* phage provides novel information about *B. cereus*-targeting phage.

Nucleotide sequence accession number. The complete genome sequence of *B. cereus* phage BCP78 is available in GenBank under accession number [JN797797](https://www.ncbi.nlm.nih.gov/nuclseq/JN797797).

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