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GENOME ANNOUNCEMENT

Complete Genome Sequence of Bacteriophage BC-611 Specifically Infecting *Enterococcus faecalis* Strain NP-10011

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***Enterococcus faecalis* is an opportunistic pathogen that causes serious infections in humans and animals and is also an important bacterium for dairy and probiotic supplement production. Therefore, bacteriophages infecting *E. faecalis* may be useful for phage therapy against multidrug-resistant strains or may threaten industrial fermentation. We isolated a virulent *Siphoviridae* bacteriophage, BC-611, specifically infecting *E. faecalis* strain NP-10011 but not infecting other *E. faecalis* strains or other enterococci. Although the genome sequence of BC-611 resembled that of enterococcal bacteriophage SAP6, BC-611 was marked by its narrow host specificity.**

Enterococcus faecalis is an opportunistic pathogen that causes serious infections such as urinary tract infections, bacteremia, and infective endocarditis in humans and animals (14) and is a major cause of nosocomial infections (9). Since a multidrug-resistant *E. faecalis* strain is refractory to most therapeutic options, it may become a target of bacteriophage therapy (13). Conversely, *E. faecalis* is an important bacterium in fermentation industries, especially for cheese production (5, 8), and the cells are used for dietary supplement production (11). Lysed *E. faecalis* cells were shown to improve the intestinal flora disturbed by antibiotics (12), to improve clinical symptoms in allergic rhinitis (10), and to suppress active cutaneous anaphylaxis and local accumulation of eosinophils (11). While bacteriophages should be the natural enemy against pathogenic bacteria, they are the primary cause of fermentation failure in the food, chemical, pharmaceutical, feed, and pesticide industries (3, 4). We isolated a virulent bacteriophage, BC-611, capable of specifically infecting *E. faecalis* strain NP10011, which was isolated and identified by Nichinichi Pharmaceutical Co., Ltd., but not infecting 10 other *E. faecalis* strains or eight enterococci tested. This study reports the morphogenetic properties and complete genome sequence of the virulent *E. faecalis* bacteriophage BC-611.

The morphological characteristics of bacteriophage BC-611 were examined by transmission electron microscopy. Bacteriophage particles were negatively stained with 2% aqueous uranyl acetate on a carbon-coated grid and examined. They were also observed by scanning electron microscopy. Genomic DNA of BC-611 was isolated according to the method described for bacteriophage λ (7). Purified genomic DNA was fragmented by physical shearing or restriction enzyme digestion, and fragmented DNAs were cloned into the pBluescript II vector and introduced into *Escherichia coli* DH5α. Recombinant plasmids were subjected to sequencing by CEQ 2000XL DNA analysis system (Beckman Coulter, Miami Lakes, FL). The assembled sequence was confirmed by Roche Genome Sequencer FLX sequencing. Open reading frames (ORFs) were predicted by the Genetyx-Mac program (Genetyx Co., Tokyo), and genes were annotated by homology searches of the GenBank database (2).

Electron microscopic observation of BC-611 indicated that bacteriophage BC-611 was classified in the family *Siphoviridae* (1). The BC-611 genome consisted of 53,996 bp, with a G+C content of 40.45%, including 341-bp direct repeats at its termini. The genome contained 57 ORFs, among which 30 were annotated as hypothetical proteins. The others were expected to encode terminase subunits, homing endonucleases, portal protein, head proteins, minor capsid protein, tail proteins, tail fiber protein, minor structural protein, *N*-acetylmuramoyl-L-alanine amidase, DNA polymerase, DNA primase, DNA replication protein, replicative DNA helicase, transcriptional regulator, adenylate kinase-like protein, nucleoside triphosphate pyrophosphohydrolase, cytidine deaminase, and lipopolysaccharide (LPS) glycosyltransferase. The BC-611 genomic sequence is highly homologous to that of enterococcal bacteriophage SAP6 (58,619 bp; GenBank accession number JF731128) (6): amino acid sequence identities of homologous proteins between BC-611 and SAP6 ranged from 73 to 100%. It is noteworthy that understanding the infection mechanism of the bacteriophage will give us measures of protection against its infection.

Nucleotide sequence accession number. The whole-genome sequence of phage BC-611 has been deposited in DDBJ under accession number AB712291.

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