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GENOME ANNOUNCEMENT

Complete Genome Sequence of Enterococcal Bacteriophage SAP6

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***Enterococcus faecalis* is an important bacterium for use as a probiotic and is an opportunistic pathogen in human beings. The antibiotic resistance acquired by *E. faecalis* is restricted to antibiotics used in the clinical setting. While screening for alternative antibiotics for use against multidrug-resistant *E. faecalis*, we isolated a virulent enterococcal bacteriophage, SAP6, belonging to the family *Siphoviridae*. To our knowledge, this study is the first to report the complete genome sequence of bacteriophage SAP6, which might be used as a therapeutic agent in combination with alternative antibiotics for multidrug-resistant *E. faecalis*.**

Enterococcus faecalis is used as a starter for fermented food and probiotics (5). However, it can also cause infectious diseases in human beings and biogenic amine production in foods (3). Moreover, acquired resistance of *E. faecalis* to aminoglycosides, glycopeptides, and other antibiotics is being increasingly reported in isolates, and the therapeutic effect obtained in these multidrug-resistant strains is limited (14). Acquired resistance to various antibiotics is mediated by various mechanisms such as conjugation or gene transfer. Biocontrol involving biological treatment (e.g., use of bacteriophages) has recently been used to minimize the risk of infection with *E. faecalis* (8, 12). Bacteriophages have been intensively studied and used for various practical applications such as phage therapy (13), bacterial pathogen detection (2), foodborne-pathogen biocontrol (6, 7), and bioremediation (16). This study reports the morphogenetic properties and complete genome sequence of the virulent enterococcal bacteriophage SAP6, which was newly isolated from sewage.

The morphological characteristics of bacteriophage SAP6 were examined by transmission electron microscopy. Bacteriophage particles were negatively stained with 2% aqueous uranyl acetate on a carbon-coated grid and examined. The genomic DNA of SAP6 was isolated using the method reported by Manfioletti and Schneider (10). Its genomic sequence was determined using ultra-high-throughput Genome Sequencer FLX (GS-FLX) sequencing. The nucleotide sequences were compared with those of other genes in GenBank by using the BLAST program (15). The open reading frames (ORFs) were identified using the NCBI ORF Finder (15). The molecular weight and isoelectric point were calculated using the ExPASy Compute pI/M_w program (4). The tRNA sequences were analyzed using the tRNAscan-SE program (9). Conserved protein domain analysis was performed using BLASTP and the NCBI CDD (11).

Morphological analysis showed that bacteriophage SAP6 belonged to the family *Siphoviridae* (1). The genomic sequence of SAP6 was composed of 58,619 bp, with a G+C content of 40.00%. The genome showed 44 ORFs, and the tRNA sequences could not be determined. A BLASTN search of the genomic sequences did not indicate any significant similarity between the genomic sequence of SAP6 and those of other previously reported bacteriophages. ORFs from the SAP6 genome were involved in DNA packaging, morphogenesis, replication, DNA manipulation, and host lysis. The morphogenesis modules and DNA packaging modules contained head morphogenesis-related proteins (major head protein, head morphogenesis protein, minor capsid protein, minor structural protein), tail morphogenesis-associated proteins (major tail protein, tail fiber protein, major tail protein), a terminase, and a phage portal protein. The genome encoded replication-related proteins and DNA manipulation proteins (DNA helicase, primase, polymerase, replication protein, transcriptional regulator, deaminase, metalloprotease, glycosyltransferase, endo-DNase, endonuclease, methyltransferase, pyrophosphohydrolase). Bacteriophage SAP6 also contained an *N*-acetylmuramoyl-L-alanine amidase for host lysis.

In conclusion, to our knowledge, this study is the first to report the morphology and complete genome sequence of the virulent enterococcal bacteriophage SAP6. Further study of this bacteriophage might enable its use as a therapeutic agent in combination with alternative antibiotics against multidrug-resistant *E. faecalis*.

Nucleotide sequence accession number. The complete genome sequence of bacteriophage SAP6 is available in GenBank under accession number JF731128.

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