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Complete Genome Sequence of the Podoviral Bacteriophage YMC/09/02/B1251 ABA BP, Which Causes the Lysis of an OXA-23-Producing Carbapenem-Resistant Acinetobacter baumannii Isolate from a Septic Patient

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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Podoviral Bacteriophage YMC/09/02/B1251 ABA BP, Which Causes the Lysis of an OXA-23-Producing Carbapenem-Resistant *Acinetobacter baumannii* Isolate from a Septic Patient

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The emergence of carbapenem-resistant *Acinetobacter baumannii*, responsible for causing nosocomial infections, has been becoming a significant global health issue. In this article, we report the complete genome sequence of bacteriophage Bϕ-B1251 (YMC/09/02/B1251 ABA BP), which causes lysis of a carbapenem-resistant *A. baumannii* strain. The bacteriophage belongs to the family *Podoviridae* and has a double-stranded circular DNA genome with a length of 45,364 bp and a 39.05% G+C content. Genome analysis showed that it had no similarity to other previously reported bacteriophages capable of infecting *A. baumannii*.

Acinetobacter baumannii causes severe infections, including septicemia, in immunocompromised patients (8, 13). Recently, the emergence of multidrug-resistant *A. baumannii* strains that are even resistant to carbapenem, the last resort for the treatment of severe Gram-negative bacterial infections, has increased worldwide concerns (5, 6). In this study, we reveal a novel carbapenem-resistant *A. baumannii* lytic bacteriophage, Bϕ-B1251 (YMC/09/02/B1251 ABA BP), which was isolated from a sewage sample obtained from a university hospital in South Korea. The bacteriophage was purified by the agar double-layer method (6, 12), using an OXA-23-producing carbapenem-resistant *A. baumannii* strain isolated from a septic patient. It was classified as a member of the family *Podoviridae* by using electron microscopy.

The genomic DNA of Bϕ-B1251 was sequenced using an Illumina Genome analyzer (Illumina, Inc.) with approximately 152-fold coverage. Gap filling was carried out by using standard PCR and subsequent Sanger sequencing. The whole-genome sequence was analyzed by using Newbler assembler 2.3 (Roche), CodonCode Aligner (CodonCode, Co.), and CLC Genomics Workbench 4.8 (CLCbio). Open reading frames (ORFs) were predicted by the NCBI ORF Finder (11) and GenMark.hmm (3), and the gene was annotated by homology searches of the GenBank (2) and Clusters of Orthologous Groups (COG) (10) databases. Similarity scores between all putative proteins were determined by PSI-Search (http://www.ebi.ac.uk/Tools/sss/fasta/) and BLASTP (1). The prediction of tRNA was identified using the tRNAscan-SE program (7).

The genome consists of a double-stranded circular DNA with a length of 45,364 bp and a G+C composition of 39.05%, with no tRNAs identified. Among the 62 total putative ORFs, 37 (57%) indicated hypothetical proteins. Fifty-one ORFs were on the plus strand and only 11 ORFs on the minus strand. The sequences appeared to contain three functional groups, as follows: (group 1) replication and modification (gp1, putative restriction-modification protein; gp9 and gp10, putative phage replication proteins), (ii) DNA package and structure/morphogenesis (gp22, putative head morphogenesis protein; gp21 and gp25, putative phage structural proteins; gp27, putative major capsid protein; gp49, putative tail protein), and (iii) lysis (gp51, putative endolysin). The sequence did not show similarity to other previously studied bacteriophages capable of infecting *A. baumannii*, such as phage phiAB1 (GenBank accession no. HQ186308), phage AB1 (GenBank accession no. HM368260), and phage AP22 (GenBank accession no. HE806280), according to the results from the BLASTN program(http://www.ncbi.nlm.nih.gov/blast/Blast.cgi/).

Double-stranded DNA phages generally use endolysin to rapidly degrade the peptidoglycan cell wall, which consequently causes lysis of the host bacteria (4, 14). gp51 showed only 51% identity to the endolysin of *Erwinia* phage vB_EamP-S6 (GenBank accession no. HQ728266).

To the best of our knowledge, Bϕ-B1251 is a novel bacteriophage that can lyse OXA-23-producing carbapenem-resistant *A. baumannii* isolates from a septic patient. Strains of this type have evoked worldwide concern. The bacteriophage could be a useful strategy for prevention of infections with multidrug-resistant bacteria (5, 9). Therefore, characterization of Bϕ-B1251 would facilitate the development of an alternative tool to control the spread of multidrug-resistant *A. baumannii*.

Nuclotide sequence accession number. The complete genomic sequence of the *Acinetobacter* bacteriophage Bϕ-B1251 has been deposited in GenBank under accession no. JX403940.

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