

Complete Genome Sequence of IME11, a New N4-Like Bacteriophage

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N4-like bacteriophages are a class of virulent *Podoviridae* phages for which few genome sequences are present in GenBank. IME11, a novel lytic *Escherichia* bacteriophage with a wide host range, was isolated, and the whole genome was sequenced. It has a circular double-stranded DNA genome of 72,570 bp. Genomic analysis showed that it resembles another *Escherichia* phage, vB_EcoP_G7C. Here we announce its complete genome and major findings from its annotation.

Escherichia coli is a Gram-negative bacterium that acts as an opportunistic pathogen. It forms biofilms (9) which give rise to infections in diarrhea patients (6) and sepsis patients (2). An increasing incidence of multidrug-resistant *E. coli* strains has been reported (8). Bacteriophages have been used to control multi-drug-resistant *E. coli* strains (4). We isolated IME11 from the sewage of the no. 307 hospital in Beijing, China. The phage infected 13 of all 31 enteropathogenic *E. coli* strains from the clinical laboratory of the no. 307 hospital, which implies that it has potential as an agent against enteropathogenic *E. coli*.

N4-like bacteriophages are a class of virulent *Podoviridae* phages, for which few genome sequences are present in GenBank. They include *Escherichia* phage N4 (11), *Enterobacter* phage EcP1 (GenBank ID: HQ641380), *Escherichia* phage vB_EcoP_G7C (7), *Erwinia* phage vB_Eamp-S6 (3), *Pseudomonas* phages LIT1 and LUZ7 (5), *Silicibacter* phage DSS3φ2, and *Sulfitobacter* phage EE36φ1 (12). IME11 is a new member of the N4-like viruses.

Genomic DNA was extracted from the phage stock by the proteinase K/SDS method (10). Whole-genome sequencing of this organism was performed with the FLX Titanium genome sequencer system (350× coverage), and the raw sequences were assembled using the Roche 454 Newbler 2.5 assembler. The prediction of open reading frames (ORFs) was performed using the RAST annotation server (1) and Kodon (Applied Maths, Sint-Martens-Latem, Belgium).

The complete genome of phage IME11 revealed a length of 72,570 bp with a G+C content of 43.1%. Of the 91 ORFs identified, 18 were annotated as known functional genes. Structural proteins included major coat protein, phage neck whiskers, anchor domain protein, and phage tape measure protein, while non-structural proteins included DNA primase, DNA helicase, phage integrase, single-stranded DNA-binding protein, DNA polymerase I, RNA polymerase, and dCTP deaminase. The remaining 73 gene products were annotated as hypothetical proteins, probably due to insufficient database information about the functional genes of N4-like phage genomes. Genomic analysis showed that this phage resembles the *Escherichia* phage vB_EcoP_G7C. The complete genome of this phage provides new insights and information regarding the phage's genetic characteristics and its interactions with *Escherichia coli*.

Nucleotide sequence accession number. The complete genome sequence of bacteriophage IME11 was submitted to GenBank under the accession number **JX880034**.

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