Complete Genome Sequence of IME15, the First T7-Like Bacteriophage Lytic to Pan-Antibiotic-Resistant Stenotrophomonas maltophilia

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T7-like bacteriophages are a class of virulent bacteriophages which have a clearer genetic background and smaller genomes than other phages. In addition, it grows faster and is easier to culture than other phages. At present, the numbers of available T7-like bacteriophage genomes and Stenotrophomonas maltophilia genomes are small, and IME15 is the first T7-like virulent Stenotrophomonas phage whose sequence has been reported. It shows effective lysis of S. maltophilia. Here we announce its complete genome, and major findings from its annotation are described.

Stenotrophomonas maltophilia is one of the most prevalent opportunistic bacteria causing nosocomial infections. It has become problematic because most isolates are resistant to multiple antibiotics (3), and therefore, development of phage therapy is now considered a good alternative biocontrol method to inhibit the pathogen (12). Bacteriophage products were considered "generally recognized as safe" by the U.S. Food and Drug Administration (FDA) in 2006 (4). The long history of bacteriophage therapy in some eastern European countries such as Georgia and Poland (5) convinced us that the phage therapy approach could be useful for inhibiting pathogenic Stenotrophomonas strains.

T7-like bacteriophages are a class of virulent bacteriophages which have a clearer genetic background and smaller genomes than other phages. In addition, it grows faster and is easier to culture than other phages. Due to these characteristics, T7-like bacteriophages are thought to be the ideal anti-Stenotrophomonas maltophilia agents. S. maltophilia bacteriophage IME15 was isolated from hospital sewage using a strain of clinically isolated S. maltophilia. Biological experiments showed it had a suitable burst size which exceeded 100 (data not shown) and that it effectively lysed pan-antibiotic-resistant S. maltophilia strains. However, the number of whole genomes of T7-like bacteriophages in GenBank is small and includes only viruses of Enterobacteria (10), Pseudomonas (7), Salmonella (6), Versinia (13), Vibrio (11), Morganella (14), Kluuyvera (8), Erwinia (2). IME15 is the first T7-like S. maltophilia bacteriophage whose genome sequence has been reported.

Genomic DNA was extracted from the phage stock by the proteinase K–SDS method (9). Whole-genome sequencing of this organism was performed with the FLX Titanium genome sequencer system (149× 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 IME15 has a length of 38,513 bp with a G+C content of 53.7%. Of the 45 ORFs identified, 41 were annotated as known genes. This genome contains functional genes related to phage structure and packaging (major capsid protein, capsid and scaffold, collar protein, internal virion protein, and internal virion DNA packaging protein A), tail structure for host interaction (tail fibers, phage tail fiber protein/T7-like tail tubular proteins A and B, and host range protein), head (T7-like phage head-to-tail joining protein), replication and transcription (T7-like phage primase/helicase protein, exonuclease, DNA liga- gase, T7-like phage DNA-directed RNA polymerase, single-stranded DNA-binding protein, T7-like phage DNA polymerase, endonuclease, HNS binding protein, and DNA maturation protein), host lysis (lysin and bacterial RNA polymerase inhibitor), and additional functions (S-adenosyl-l-methionine hydrolase, protein kinase, N-acetylmuramoyl-l-alanine amidase, endopeptidase, and so on).

The complete genome of this phage provides new insights and information regarding the phage’s genetic characteristics and the phage’s interactions with S. maltophilia.

Nucleotide sequence accession number. The complete genome sequence of Stenotrophomonas phage IME15 was submitted to GenBank under the accession number JX872508.

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