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GENOME ANNOUNCEMENT

Complete Genome Sequence of Wide-Host-Range *Staphylococcus aureus* Phage JD007

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Methicillin-resistant *Staphylococcus aureus*-related infections have become a serious problem worldwide. Bacteriophage therapy is an alternative approach against this threat. *S. aureus* phage JD007, which belongs to the *Myoviridae* family according to transmission electron microscopic imaging, could lyse nearly 30% of the *S. aureus* strains from Ruijin Hospital, Shanghai, China, and was isolated from chicken feces in Shanghai, China. The complete genome showed that JD007 is a linear, double-stranded DNA phage 141,836 bp in length with a GC content of 30.4% encoding 217 open reading frames. A BLAST search of the JD007 genome revealed that it was very similar to that of phage GH15.

Staphylococcus aureus is a Gram-positive bacterium that can cause skin and soft tissue infections, especially in some immunocompromised patients. Methicillin-resistant *S. aureus* (MRSA) has been commonly found in hospital-acquired infectious diseases worldwide, and community-acquired MRSA infections also have been reported (10). Attempts to use bacteriophages to treat infectious diseases have been made since they were discovered (5), and they are still being used in some former Soviet Union countries like Georgia and Poland. Some clinical tests and animal models have proved that *S. aureus* phage can effectively treat infectious diseases caused by *S. aureus*, particularly some multidrug-resistant strains (2, 3, 7, 9, 11, 12). *S. aureus* phage JD007 was isolated from chicken feces in Shanghai, China. It belonged to the *Myoviridae* family according to transmission electron microscopic imaging and could efficiently lyse nearly 30% of the *S. aureus* strains isolated at Ruijin Hospital, Shanghai, China.

The bacteriophage was purified by discontinuous CsCl centrifugation, and phage genomic DNA was extracted using the Aidlab kit (Aidlab Biotechnologies Co., Ltd.). It was sequenced by using the Roche 454 genome sequencer at the Chinese National Human Genome Center in Shanghai. Assembly of quality filtered reads was performed using the platform the 454 Life Sciences Corporation provided, and the prediction of open reading frames (ORFs) and their confirmation were conducted by using GLIMMER and GeneMarkS, respectively (1, 4). Conserved protein domain analysis of predicted ORFs was also carried out by using the BLASTP nr database and InterProScan programs (13). tRNA was predicted by the use of tRNAscan-SE software (8).

The complete linear, double-stranded DNA genome of *S. aureus* bacteriophage JD007 showed a 141,836-bp length with a GC content of 30.4%. The complete genome of JD007 encodes a predicted 217 ORFs, 157 of which encode hypothetical proteins. On the basis of a homology search, putative functions of the remaining 60 ORFs were identified. The structural proteins include a major capsid protein, a major tail protein, a portal protein, a tail lysine, and a tail sheath protein. Nonstructural proteins include a DNA ligase, a DNA polymerase, a DNA primase, an exonuclease, a helicase, a nicotinate phosphoribosyltransferase, a nucleoside 2-deoxyribosyltransferase, a resolvase, a ribose-phosphate pyrophosphokinase, a ribonucleoside-diphosphate alpha subunit, a ribonucleoside-diphosphate beta subunit, a ribonucleotide reductase stimulatory protein, a prohead protease, a recombinase, a resolvase, an RNase, and a large terminase. The JD007 genome also encodes four tRNAs, i.e., Asp-tRNA, Phe-tRNA, Trp-tRNA, and a Met-tRNA. The regions that encode them span nucleotides 50344 to 50417, 50424 to 50496, 50503 to 50574, and 72975 to 73046, respectively.

Furthermore, the *S. aureus* phage JD007 genome was 97% identical to *Staphylococcus* phage GH15, with 93% coverage (6). These genome data constitute an important resource for us to further study or use the phage to treat clinical infectious diseases caused by *S. aureus*, especially multidrug-resistant strains.

Nucleotide sequence accession number. The whole genome sequence of *S. aureus* bacteriophage JD007 was deposited in GenBank under accession number JX878671.

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