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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Klebsiella pneumoniae* Phage JD001

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***Klebsiella pneumoniae* is a member of the family *Enterobacteriaceae*, opportunistic pathogens that are among the eight most prevalent infectious agents in hospitals. The emergence of multidrug-resistant strains of *K. pneumoniae* has became a public health problem globally. To develop an effective antimicrobial agent, we isolated a bacteriophage, named JD001, from seawater and sequenced its genome. Comparative genome analysis of phage JD001 with other *K. pneumoniae* bacteriophages revealed that phage JD001 has little similarity to previously published *K. pneumoniae* phages KP15, KP32, KP34, and phiKO2. Here we announce the complete genome sequence of JD001 and report major findings from the genomic analysis.**

Klebsiella pneumoniae is an important opportunistic pathogen that causes hospital-acquired pneumonia, sepsis, and urinary tract infections. Multidrug resistance is emerging worldwide among *K. pneumoniae* strains at an alarming rate and raises the problem of antibiotic choice (2, 7). It sometimes causes severe infection, and some of the infectious diseases caused by antibiotic-resistant bacteria cannot be treated in time (5). The use of bacteriophages to treat some infectious diseases was tried once they were discovered (1, 6). To develop bacteriophage cocktails as an alternative biocontrol agent for *K. pneumoniae*, *K. pneumoniae* phages have been isolated by using *K. pneumoniae* clinical isolates as the host organisms in our group. A novel *K. pneumoniae* phage, JD001, were isolated from a seawater sample collected at an estuary of the East China Sea near Shanghai, China. It belongs to the *Myoviridae* family, according the transmission electron microscopic image, and efficiently lyses *K. pneumoniae* strain JDM777, which was isolated in a hospital.

The bacteriophage was purified by discontinuous CsCl centrifugation, and phage genomic DNA was extracted by 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. The assembly of quality filtered reads was performed by 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 (3) and GeneMark.hmm (9), respectively. Conserved protein domain analysis of predicted ORFs was also carried out by using the BLASTP nr database and InterProScan programs (10). tRNA was predicted by the use of tRNAscan-SE software (8).

The complete circular double-stranded DNA genome of *K. pneumoniae* phage JD001 showed a 48,814-bp length with a GC content of 48.53%. The genome sequences of JD001 had little similarity to those of previously published *K. pneumoniae* phages KP15, KP32, KP34, and phiKO2 (4). There were 68 predicted ORFs and no tRNA, and 40 of the ORFs encode hypothetical proteins. The others were expected to encode proteins with conserved domains or similarity to a pectate lyase, DNA/RNA polymerases, a helicase, a tetracycline transcriptional regulator, an integrase, an endonuclease, metallo-dependent phosphatases, a terminase, a J-like baseplate assembly protein, a phage head morphogenesis domain, a tail spike protein (gluconolactonase), a prophage protein, and some phage-related proteins whose functions are still unknown. In addition, ORF JD001-59, which is predicted to encode a lysozyme, has 54% identity to previously published data.

Overall, the genome sequences of JD001 had little similarity to previously published *K. pneumoniae* phages KP15, KP32, KP34. and phiKO2 (4). These genome data constitute an important resource for us to study and engineer phages or the lysozyme they encode to control specific bacterial species.

Nucleotide sequence accession number. The whole genome sequence of *K. pneumoniae* phage JD001 has been deposited in GenBank under accession no. JX866719.

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