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Complete Genome Sequence of the *Streptococcus suis* Temperate Bacteriophage *ϕ*NJ2

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Streptococcus suis **is an important cause of meningitis, arthritis, and sudden death in young piglets and of meningitis in humans. A novel temperate *S. suis*-specific bacteriophage (*ϕ*NJ2) was identified. The phage was induced from the *S. suis* strain NJ2 by using mitomycin C, and the whole genome sequence was determined. The *ϕ*NJ2 genome is 37,282 bp in length and contains 56 open reading frames (ORFs). While 31 ORFs (55%) encoded hypothetical proteins, other ORFs were predicted to be functional, clearly indicating the novelty of *ϕ*NJ2.**

Received 3 October 2012 **Accepted** 22 October 2012 **Published** 24 January 2013

Citation Tang F, Bossers A, Harders F, Lu C, Smith H. 2013. Complete genome sequence of the *Streptococcus suis* temperate bacteriophage *ϕ*NJ2. Genome Announc. 1(1): e00008-12. doi:10.1128/genomeA.00008-12.

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Streptococcus suis infection is considered to be a major problem in the swine industry worldwide. *S. suis* can cause severe invasive infections in piglets, e.g., meningitis, arthritis, and sepsis (1). *S. suis* can also cause disease in humans. Humans are at risk mainly after contact with contaminated pigs or pig meat (2, 3).

Due to their highly specific host recognition, bacteriophages have potential as therapeutic agents in the treatment of infections (4, 5). Until now, only one lytic bacteriophage specific for *S. suis* has been described (6). In addition, several prophages could be identified in the whole genome sequences of various *S. suis* isolates (7–9). So far, however, the lytic capacities of these prophages are unknown.

Here, we report the full genome sequence of a novel temperate bacteriophage induced from the *S. suis* isolate NJ2. NJ2 was isolated from a diseased pig in China, and its temperate phage, designated *ϕ*NJ2, was isolated from the host strain after induction with mitomycin C. The bacteriophages obtained were used for the isolation of the phage DNA. The genomic DNA of the bacteriophage *ϕ*NJ2 was isolated using SDS-proteinase K and phenol-chloroform extraction methods (10). Genome deep-sequencing was performed using paired-end libraries (sets of two 150-bp sequences obtained with Nextera tagmentation sequencing kits [Epicentre, Madison, WI]) on an Illumina MiSeq sequencer. The quality filtered reads were subsequently assembled *de novo* using the ABySS algorithm (abyss-pe version 1.3.3), and the overall phage genome coverage was approximately 680-fold. Putative open reading frames (ORFs) were identified by GeneMarkS (11). BLASTP analyses of the putative ORFs against the NCBI nonredundant proteins (NR) database and Pfam analysis (http://pfam.sanger.ac.uk/search) were used to assess their putative functions. The prediction of tRNA sequences was carried out using the tRNAscan-SE 1.23 software (12).

The phage *ϕ*NJ2 contains a circular double-stranded DNA genome of 37,282 bp with a G+C content of 39%. A total of 56 ORFs were predicted. Thirty-one of the ORFs (55%) encoded hypothetical proteins, clearly indicating the novelty of the *ϕ*NJ2 phage. Based on Pfam homology searches, the putative functions of the putative ORFs could be categorized into five functional modules comprising proteins for (i) lysogeny (putative recombinase), (ii) DNA replication and modification (putative endodeoxyribonuclease RusA, putative C-5 cytosine-specific DNA methylase, and putative MazG nucleotide pyrophosphohydrolase), (iii) head and tail morphogenesis (phage tail protein and minor capsid protein), (iv) packaging (putative phage portal protein and putative terminase of large subunit and small subunit), and (v) host lysis (putative holin and phage amidase protein). No tRNA sequences could be identified.

The phage *ϕ*NJ2 genome showed a high level of similarity (68% query coverage, displaying 84 to 97% identity) to sequences present in the *S. suis* isolate ST1, whereas it showed almost no similarity (less than 1% query coverage) to the lytic *S. suis* phage SMP (6).

Nucleotide sequence accession number. The complete genome sequence of the *S. suis* temperate bacteriophage *ϕ*NJ2 is available in GenBank under accession number JX879087.

ACKNOWLEDGMENTS

This study was supported by grants from Chinese National Programs for Fundamental Research and Development (2012CB518804).

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