

Complete Genome Sequence of the *Edwardsiella ictaluri*-Specific Bacteriophage PEi21, Isolated from River Water in Japan

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We present the complete genome sequence for a novel *Edwardsiella ictaluri*-specific bacteriophage, PEi21, isolated from river water in Japan. An initial comparative genome analysis revealed that the phage was closely related to the previously reported *Edwardsiella tarda* phage MSW-3 isolated from a red sea bream farm in Japan.

Received 27 February 2014 Accepted 13 March 2014 Published 3 April 2014

Citation Yasuike M, Kai W, Nakamura Y, Fujiwara A, Kawato Y, Hassan ES, Mahmoud MM, Nagai S, Kobayashi T, Ototake M, Nakai T. 2014. Complete genome sequence of the *Edwardsiella ictaluri*-specific bacteriophage PEi21, isolated from river water in Japan. *Genome Announc.* 2(2):e00228-14. doi:10.1128/genomeA.00228-14.

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Edwardsiella ictaluri, a Gram-negative bacterium, causes enteric septicemia of catfish (ESC), the most serious infectious disease in the channel catfish (*Ictalurus punctatus*) industry in the United States (1). *E. ictaluri* also infects other catfish species and is found in Southeast Asia (2–4). For a long time there had been no records of this bacterium in Japan. However, in 2007, *E. ictaluri* infections of wild ayu (*Plecoglossus altivelis*) were first found in some rivers of Japan (5, 6) and have been continuously observed since then (7).

Three *E. ictaluri*-specific bacteriophages (phages), eiAU, eiDWF, and eiMSLS, have been isolated from catfish aquaculture ponds in the United States and classified within the family *Siphoviridae* (8, 9). Recently, *E. ictaluri*-specific phages have also been isolated from rivers in Japan, in association with *E. ictaluri* infections of ayu (7). These phages exhibited the morphology of the family *Myoviridae* (7). To further characterize the *E. ictaluri* phages isolated from the Japanese rivers, we determined the complete genome sequence of the *E. ictaluri*-specific bacteriophage PEi21.

Whole-genome shotgun sequencing of PEi21 was performed using the Roche 454GS-FLX Titanium sequencing platform. *De novo* assembly of sequence reads was performed using Newbler 2.8. The complete genome sequence was annotated using the Rapid Annotations using Subsystems Technology (RAST) server (10) and BLASTP (11) against the viral sequence database (*E* value threshold of $1E-3$).

The complete genome sequence of PEi21 was assembled as a circular contig. The circularly permuted genome showed a 43,378-bp length, with a GC content of 52.6%. The genome contained 71 predicted open reading frames (ORFs), of which 59 encode conserved hypothetical proteins or novel proteins and 12 have a predicted function. A phylogenetic analysis based on portal proteins revealed that PEi21 was closely related to dwarf myoviruses (12). The *E. tarda* phage MSW-3, which was isolated from a seawater sample obtained from a red sea bream (*Pagrus major*) farm in Japan (13), was the closest phage to PEi21, followed by *Klebsiella* phage JD001 (14), Iodobacteriophage ϕ PLPE (15),

Vibrio phages 138 and CP-T₁ (12), and *Pectobacterium* phage ZF40 (12). CoreGenes3.5 (16) analysis (with the BLASTP threshold score set at 75) also confirmed these results, showing that PEi21 shared 54 homologous genes with MSW-3, while PEi21 has 40, 28, 31, and 20 homologous genes in common with *Klebsiella* phage JD001, Iodobacteriophage ϕ PLPE, *Vibrio* phages 138 and CP-T₁, and *Pectobacterium* phage ZF40, respectively. Thus, it will be interesting to investigate the function of the unique genes among these phage genomes in future studies, which will increase our understanding of the evolution of these phages and their host specificity. Furthermore, this *E. ictaluri* phage genome information provides a novel resource for detection of *E. ictaluri* in natural freshwater, for elucidating the transmission route of *E. ictaluri* (7), and for various applications of phages in the control of ESC and other *E. ictaluri* infections in aquaculture (17).

Nucleotide sequence accession number. The complete genome sequence of the *E. ictaluri* phage PEi21 was submitted to DDBJ under the accession number [AP013057](https://www.ncbi.nlm.nih.gov/nuclseq/AB013057).

ACKNOWLEDGMENTS

This study was supported by a Grant-in-Aid (Marine Metagenomics for Monitoring the Coastal Microbiota) from the Ministry of Agriculture, Forestry and Fisheries of Japan.

We thank Kristian von Schalburg (Centre for Biomedical Research, University of Victoria, Canada) for his help in preparing the manuscript. We also thank Ayako Kondo and Haruka Ito for support in genome sequencing.

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