Genome Sequences of *Listeria* Phages Induced from Lysogenic Isolates of *Listeria monocytogenes* from Seafood and a Seafood Processing Environment in Thailand

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**ABSTRACT** We report here the complete genome sequences of three *Listeria* phages (PSU-VKH-LP019, PSU-VKH-LP040, and PSU-VKH-LP041), which were newly induced from lysogenic isolates of *Listeria monocytogenes* from seafood and a seafood processing environment in Thailand. The three phages show circularly permuted double-stranded DNA genomes with sizes of 38.6, 39.6, and 48.3 kb.

Phage diversity is of interest since prophages are commonly present in the genomes of *Listeria monocytogenes* strains (1, 2). They play an important role in the evolution (3), survival, and persistence (4, 5) of *L. monocytogenes*. We have an ongoing project for screening lysogenic isolates of *Listeria* from various sources, including seafood and a seafood processing environment. Of these lysogenic isolates, an induced form of prophage(s) from selected isolates of *L. monocytogenes* was examined to understand the prophage diversity. We report here the complete genome sequences of three induced phages, PSU-VKH-LP019, PSU-VKH-LP040, and PSU-VKH-LP041 (hereafter referred to as LP019, LP040, and LP041, respectively).

Phage DNA was extracted by the phenol-chloroform method, as previously described (6). Fragmentation of DNA was performed, and high-quality sequencing libraries were sequenced using the Illumina HiSeq 2500 platform with 100-bp paired-end reads at Macrogen, Inc. (Seoul, South Korea). Then, low-quality reads were filtered by Trimmmomatic (7). SOAPdenovo2 was utilized for de novo assembly (8) before a prediction of open reading frames (ORFs) using Glimmer 2 (9) was made. An automatic genome annotation was performed by RAST (10) and Phaster (11) and then verified by BLAST (12), InterPro (http://www.ebi.ac.uk/interpro) (13), and Artemis (14). tRNA was detected using the tRNAscan-SE search server (15).

Sequencing of the induced phages by the Illumina HiSeq 2500 platform yielded 7 to 11 million reads, with an average sequencing coverage of 15,000X. De novo assembly resulted in a single contig for each phage, suggesting a complete genome. These genomes were circularly permuted terminally redundant double-stranded DNA genomes. The genome sizes of these phages ranged from 38 to 48 kb, which is consistent with the size range of previously reported temperate *Listeria* phages (16–19). A lysogeny module, including integrase and transcriptional regulator/repressor genes, was observed, thus confirming the temperate characteristic of these sequenced phages. No tRNAs were found in the genomes of these phages.

Phage LP019 was induced from a lysogenic *L. monocytogenes* isolate, PSU-KVH-134LM, obtained from a seafood product (fish stick) using *L. monocytogenes* FSL J1-208 as a propagating host (20). This phage is 38,601 bp in length, with a GC content of...
35.7%. A total of 66 ORFs were detected, of which 28 ORFs were assigned functions. Genome comparison by BLASTN of phage LP019 with the NCBI database showed 93% similarity with 62% sequence coverage to Listeria phage vB_LmoS_188, which was previously isolated from wild mushroom (21).

Two phages, LP040 and LP041, were induced from lysogenic L. monocytogenes isolate PSU-KV-036LM (from a seafood processing environment) using F2365 and FSL F2-695 as propagating hosts, respectively (H. T. K. Vu, S. Benjakula, and K. Vongkamjan, submitted for publication). Phage LP040 presents a genome size of 39,585 bp, with a GC content of 37.1%, whereas phage LP041 is 48,286 bp in length, with a GC content of 35.8%. For phage LP040, a total of 67 ORFs were detected, of which 32 ORFs were assigned functions. For phage LP041, a total of 81 ORFs were detected, but only 24 were assigned functions. Nucleotide sequence comparison by BLASTN revealed that LP040 showed a 91% similarity with 77% sequence coverage to Listeria phage vB_LmoS_293, isolated from mushroom compost (20). The genome of phage LP041 showed 96% similarity with 82% sequence coverage to phage B054 (16) previously induced from Listeria innocua WSLC 2054 (21).

**Accession number(s).** The genome sequences of these three induced Listeria phages, LP019, LP040, and LP041, have been deposited in GenBank under the accession no. MH341451, MH341452, and MH341453, respectively.

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