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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Novel Marine Siphovirus, pVp-1, Infecting *Vibrio parahaemolyticus*

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Among the abundant bacteriophages that belong to the order *Caudovirales* in the ocean, the genome sequences of marine siphoviruses are poorly investigated in comparison to those of myo- or podoviruses. Here we report the complete genome sequence of *Vibrio* phage pVP-1, which belongs to the family *Siphoviridae* and infects *Vibrio parahaemolyticus* ATCC 33844.

Marine viruses are the most abundant biological entities in the ocean (10), which makes the analysis of their genomes essential for a better understanding of their enormous genetic diversity (1). Most of the marine viruses reported to date are bacteriophages that belong to the order *Caudovirales*, which is divided into three families: *Myoviridae*, *Podoviridae*, and *Siphoviridae* (10). Among the marine phages whose genomes have been sequenced, siphoviruses are relatively poorly investigated (9) and only two of them, including phiHSIC (7) and SIO-2 (1), were studied and reported to infect *Vibrio* spp. Here we report the complete genome sequence of a novel marine siphovirus, pVp-1, which was isolated from the coastal water of the Yellow Sea in Korea and infects *V. parahaemolyticus* ATCC 33844, which was isolated from a patient with food poisoning.

Genomic DNA was extracted as previously described (8) and sequenced using standard shotgun sequencing reagents and a 454 GS-FLX Titanium Sequencing System (Roche) by Macrogen in Korea (approximately 50× coverage). The full-length genome sequence was obtained by sequence assembly using the SeqMan II sequence analysis software (DNAStar). The putative open reading frames (ORFs) were predicted using Glimmer 3.02 (2) and GeneMark.hmm (6), and putative ORF functions were analyzed by BLASTP and InterProScan (12). Putative tRNA genes were searched for using tRNAscan-SE (v. 1.21) software (5).

The double-stranded and nonredundant DNA genome of pVp-1 was 111,506 bp in length with a G+C composition of 39.71%. A total of 157 ORFs containing more than 40 amino acid residues and 19 tRNAs (including 1 pseudogene) were identified, suggesting this as the first marine phage genome in the family *Siphoviridae* with a large number of tRNAs capable of infecting *V. parahaemolyticus*. Forty-eight ORFs showed no homology to proteins in the GenBank database, while 69 and 40 of the other ORFs code for proteins with some homology to known phage- and bacterium-related proteins, respectively. Of the 40 bacterium-related genes in phage pVp-1, 5 ORFs (*orf34*, *orf38*, *orf79*, *orf85*, and *orf97*) were highly homologous to *Vibrio*-related proteins and 35 ORFs shared some similarities with unrelated bacteria spanning a wide range of phyla.

Bioinformatic analyses were performed for the assignment of putative functions to 69 phage-related ORFs, and those ORFs were clustered together by at least three functional roles, i.e., DNA metabolism (*orf2*, *orf3*, *orf4*, *orf6*, *orf7*, *orf12*, *orf14*, *orf15*, *orf16*, *orf17*, *orf18*, *orf21*, *orf28*, *orf32*, *orf42*, and *orf52*), viral morphogenesis (*orf139*, *orf141*, *orf143*, *orf144*, *orf148*, *orf149*, *orf153*, *orf155*, *orf156*, and *orf157*), and lytic properties (*orf73*, *orf82*, and *orf83*). Interestingly, most of the ORFs containing DNA metabolism and viral morphogenesis genes were clustered together at each end of the sequenced genome by functional roles and were similar (≤79%) to those of T5 (11) or T5-like (3, 4) phages, thus indicating a close genetic relatedness between pVp-1 and those phages.

In contrast, there were no sequence similarities to marine *Vibrio* phages belonging to the family *Siphoviridae* (phiHSIC and SIO-2), and a large proportion of the genes in pVp-1 were not similar to those of other sequenced phages or bacteria. Based on these results, newly sequenced *Vibrio* phage pVp-1 could be considered a novel T5-like virus and will help to advance our understanding of the biodiversity of marine phages belongs to the family *Siphoviridae*.

Nucleotide sequence accession number. The genome sequence of *Vibrio* phage pVp-1 was deposited in the GenBank database under accession number JQ340389.

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