Complete Genome Sequence of *Marinomonas* Bacteriophage P12026

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Members of the genus *Marinomonas* in the *Gammaproteobacteria* are broadly distributed in marine environments where they could be infected by bacteriophages. Here we report the genome sequence of bacteriophage P12026 that can lytically infect bacterial strain IMCC12026, a member of the genus *Marinomonas*. To our knowledge, this is the first genome sequence of a lytic bacteriophage infecting the genus *Marinomonas*.

The genus *Marinomonas*, belonging to the family *Oceanospirillaceae* of the *Gammaproteobacteria*, currently comprises 21 species. Members of this genus have been found in various habitats such as seawater (15), sea ice (17), seafloor sediment (14), mucus of coral (3), and the surface of sea grass (10), suggesting a widespread distribution in marine environments. The genus has been implicated in the metabolism of various chemicals, including dimethylsulfoniopropionate, phthalate, and oil compounds (2, 5, 7). Genome sequences have been reported for 4 strains of the genus *Marinomonas*, at least three of which have prophages or CRISPR sequences (9, 12), suggesting that members of the genus interact with marine bacteriophages. To our knowledge, however, there has been no publicly available genome sequence of a lytic bacteriophage infecting strains of the genus *Marinomonas*. Here we report the complete genome sequence of phage P12026 that lytically infects strain IMCC12026, a member of the genus *Marinomonas*.

Host bacterial strain IMCC12026 was isolated from a surface seawater sample collected off the coast of the Yellow Sea. Based on the 16S rRNA gene sequence showing 100% similarity to the type strain of *Marinomonas pontica* (6) and greater than 95% similarities to the type species of the genus *Marinomonas*, IMCC12026 was tentatively classified as a member of the genus *Marinomonas* (4). Bacteriophage P12026 was isolated by using enrichment culture followed by plaque assay from a seawater sample collected from the same station. We could classify phage P12026 as a member of the *Siphoviridae*, since isometric heads and long noncontractile tails were observed by transmission electron microscopy and the genetic material was double-stranded DNA.

Genome sequencing was performed by using both 454 pyrosequencing and Illumina sequencing. Sequencing reads from each technology were separately assembled into each single contig by gsAssembler (version 2.3) and Velvet (version 1.0) (16), respectively, with only three 1-bp differences between the two contigs. Since all differences were located within homopolymeric tracts, the contig from Illumina sequencing was adopted as the final genome sequence. Gene prediction and functional annotation was carried out using the RAST server (1) and manually checked and complemented by RPS-BLAST searches against Pfam (version 26.0) and CDD (version 3.05) (11, 13).

The genome sequence of phage P12026 was 31,766 bp in length with G+C content of 46.0 mol% and had 54 open reading frames (ORFs) predicted. The genome of phage P12026 seemed to have modular structure, as shown in many other phages (8). ORFs encoding proteins related to phage structure

and assembly, such as terminase, portal protein, prohead protease, major capsid protein, head-tail adaptor, and major tail protein, were clustered together. Genes encoding proteins involved in DNA metabolism and replication, such as DNA methylase, replicative helicase, endonuclease, exonuclease, and RecT protein, were also clustered in another region of the genome. The genome also encoded *N*-acetylmuramoyl-L-alanine amidase, a phage lysin, which was revealed to be highly similar to the same protein predicted in a putative prophage region of the *Marinomonas* sp. strain MED121 genome (12).

Nucleotide sequence accession number. The complete genome sequence of P12026 was deposited in GenBank under accession number [JQ867100](https://doi.org/10.1093/jvi/01328-12).

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