Complete Genome Sequences of Two *Persicivirga* Bacteriophages, P12024S and P12024L

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The phylum *Bacteroidetes* is one of the major bacterial phyla in marine environments, where bacteriophages are highly abundant. Bacteriophages infecting members of the phylum *Bacteroidetes*, however, have not been well represented in public genome databases. Here we announce the genome sequences of two bacteriophages, P12024S and P12024L, that were isolated from coastal seawater and lytically infect *Persicivirga* sp. IMCC12024, a marine *Bacteroidetes* bacterium.

Members of the phylum *Bacteroidetes* are among the main constituents of marine bacterial assemblages and have been recognized as important players in phytoplankton-bacterium interactions and decomposition of detritus and organic matters (1, 2, 5, 8, 10, 11). Bacteriophages are usually 10 times more abundant than bacteria in marine environments and contribute significantly to bacterial mortality (7, 12). Taken together, it could be deduced that there are an immense number of bacteriophages infecting marine *Bacteroidetes* bacteria. Isolation and characterization of these phages would help in understanding the virus-mediated ecological processes in marine environments. As of now, however, there are only five publicly available genome sequences of marine phages infecting *Bacteroidetes* bacteria, including *Flavobacterium* phage 11b (6) and *Cellulophaga* phages (https://portal.camera.calit2.net). Here we report complete genome sequences of two bacteriophages, P12024S and P12024L, that infect *Persicivirga* sp. IMCC12024, a marine member of the *Bacteroidetes*, isolated from coastal seawater.

Host bacterial strain IMCC12024 was isolated from a surface seawater sample collected off the coast of the Yellow Sea, South Korea. Phylogenetic analysis using 16S rRNA gene sequences showed that strain IMCC12024 was closely related to the genus *Persicivirga* of the family *Flavobacteriaceae* in the *Bacteroidetes* phylum. The genus *Persicivirga* contains bacterial strains able to degrade complex polysaccharides such as xylan and ulvan, usually produced by algae (4, 9), suggesting the close relationship of the genus with marine primary producers. Bacteriophages P12024S and P12024L were isolated together from a seawater sample collected at the same station using the standard plaque assay after being enriched with the host strain. We could classify both phages as belonging to the *Siphoviridae* based on isometric heads and long noncontractile tails observed by transmission electron microscopy.

Genome sequencing was performed by using both pyrosequencing and Illumina sequencing. Assembly of pyrosequencing reads using gsAssembler (version 2.3) resulted in a single contig for each phage. Several errors in homopolymer regions of the single contigs were corrected by comparing them to the contigs assembled from the Illumina sequencing reads. Total coverage ratios were over 1,000 for each genome. Gene prediction and annotation were performed by using the RAST server (3). Searches against the Pfam database, InterProScan service, and BLASTP analysis using the NCBI nr database were employed to check and improve annotation results.

The genome sequences of the two phages were highly similar to each other and showed conserved synteny except for a few short regions unique to each genome. The bacteriophage P12024S genome was 35,700 bp long with a G+C content of 35.5 mol%, while the genome sequence of P12024L had a length of 35,652 bp with 35.9 G+C mol%. Among 59 and 58 open reading frames (ORFs) predicted for P12024S and P12024L, respectively, 47 ORFs were shared between the two genomes, with >90% amino acid identity. Proteins predicted in both genomes included phage portal protein, large subunit of terminase, phage-associated recombination protein, DNA primase, DNA methyltransferase, DNA helicase, and peptidase M15. Most ORFs unique to each genome were predicted to encode hypothetical proteins.

**Nucleotide sequence accession numbers.** The complete genome sequences of P12024S and P12024L were deposited in GenBank under accession numbers JQ823122 and JQ823123, respectively.

**ACKNOWLEDGMENTS**
This work was supported by a National Research Foundation of Korea (NRF) grant funded by the Korean government (MEST) (no. 2010-0014604).

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