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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Celeribacter* Bacteriophage P12053L

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The *Roseobacter* clade has been recognized as one of the abundant bacterial lineages in marine environments, which makes the characterization of bacteriophages infecting members of the clade important. Here we report the complete genome sequence of bacteriophage P12053L, which infects *Celeribacter* sp. strain IMCC12053, a member of the *Roseobacter* clade.

Bacteriophages are the most abundant biological entities in marine environments, exceeding the number of bacterioplankton by an order of magnitude (4, 15), and contain a myriad of genetic diversity, as revealed by recent metagenomic studies (2, 14). Bacteriophages have influences on the dynamics of bacterial assemblages (9, 11, 12), consequently affecting material cycle and energy flow (5, 6). The marine *Roseobacter* clade is one of the major marine bacterial lineages. Genome analysis of more than 30 strains in the *Roseobacter* clade have shown that its members are equipped with various metabolic potentials, including photoheterotrophy and methylotrophy (13). Compared to the number of genome sequences of bacterial strains in the *Roseobacter* clade, however, only a few genome sequences of roseophages (currently there are four roseophages), bacteriophages infecting the *Roseobacter* clade of bacteria, are publicly available (1, 8, 17). Here we announce the complete genome sequence of bacteriophage P12053L, which infects *Celeribacter* sp. strain IMCC12053, a marine member of the *Roseobacter* clade.

Host bacterial strain IMCC12053 was isolated from seawater collected off the coast of the Yellow Sea, South Korea. The host strain was affiliated with the genus *Celeribacter* of the *Roseobacter* clade, showing 97.4% 16S rRNA gene sequence similarity to *Celeribacter baekdonensis* L-6^T (10). Bacteriophage P12053L was isolated from a seawater sample collected at the same station using the standard plaque assay after being enriched with host bacteria. We tentatively classified bacteriophage P12053L as belonging to the order *Caudovirales*, since the phage contained double-stranded DNA, had isometric capsids, and was chloroform resistant.

Genome sequencing of P12053L was performed by Illumina sequencing with 36-bp single-read runs using a DNA sample extracted from phage concentrates. Initial assembly by Velvet 1.0 (16) produced 3 contigs having more than 1,300-fold coverage. Gaps between contigs were filled by combinatorial PCR and sequencing, resulting in a single contig that was finalized using Consed (7). Gene prediction and initial annotation were performed using the RAST server (3). BLASTP analysis against the NCBI nonredundant database, a Pfam search, and the InterProScan service were used to check and improve the initial annotation.

The genome sequence of bacteriophage P12053L had a length of 35,889 bp and a G+C content of 46.1 mol%. The RAST server predicted 56 open reading frames (ORFs) in the genome, with no tRNA genes. We could assign protein functions to 15 ORFs, the majority of which (7 of 15) were found to encode proteins related to DNA metabolism and replication, including a thymidine synthase, a DNA primase/helicase, a T7-like DNA polymerase, 2 endonucleases, MazG nucleotide pyrophosphohydrolase, and a ribonucleotide reductase. Four ORFs were predicted to encode proteins involved in the structure and assembly of virions, such as a coat protein, a head-to-tail connecting protein, a tail fiber protein, and the large subunit of terminase. Genes encoding the phosphate starvation-inducible PhoH protein, a glutaredoxin, and a GCN5-related *N*-acetyltransferase were also predicted. A preliminary comparative analysis indicated that the genome sequence of bacteriophage P12053L is most similar to that of roseophage SIO1, which infects *Roseobacter* strain SIO67, among the publicly available phage genomes (1).

Nucleotide sequence accession number. The complete genome sequence of P12053L was deposited in the GenBank database under accession number JQ809650.

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