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Complete Genome Sequence of *Pectobacterium carotovorum* subsp. *carotovorum* Bacteriophage My1

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Pectobacterium carotovorum subsp. *carotovorum*, a member of the *Enterobacteriaceae* family, is an important plant-pathogenic bacterium causing significant economic losses worldwide. *P. carotovorum* subsp. *carotovorum* bacteriophage My1 was isolated from a soil sample. Its genome was completely sequenced and analyzed for the development of an effective biological control agent. Sequence and morphological analyses revealed that phage My1 is a T5-like bacteriophage and belongs to the family *Siphoviridae*. To date, there is no report of a *Pectobacterium*-targeting siphovirus genome sequence. Here, we announce the complete genome sequence of phage My1 and report the results of our analysis.

The plant-pathogenic bacterium *Pectobacterium carotovorum* subsp. *carotovorum* (formerly known as *Erwinia carotovora* subsp. *carotovora*) produces numerous plant cell wall-degrading enzymes to cause soft rot diseases in diverse plants (5, 6, 13, 19) and, consequently, causes severe economic losses. Bacteriophages have been considered novel natural biocontrol agents for bacterial plant diseases (8, 14). Several phages infecting *Erwinia carotovora* subsp. *carotovora* (14, 18) or other *Erwinia* spp. have been isolated (4, 11, 12), and a few of these species have been sequenced. Although we have announced the complete sequence of *P. carotovorum* subsp. *carotovorum* *Podoviridae* phage PP1 (10), a genome sequence of a *Pectobacterium*-targeting phage belonging to the *Siphoviridae* family has not been reported to date. In this study, we isolated the *P. carotovorum* subsp. *carotovorum*-targeting *Siphoviridae* named My1 and completely sequenced its genome.

Genomic DNA extraction of bacteriophage My1 was carried out using SDS-proteinase K and phenol-chloroform extraction methods (15, 21). Purified DNA was sequenced using a Genome Sequencer FLX (GS-FLX) Titanium by Macrogen Inc. (Seoul, Republic of Korea), with 52-fold coverage. Quality filtered reads were assembled using a 454 Newbler 2.3 assembler. The open reading frames (ORFs) were predicted using the Glimmer v3.02 (3), GeneMarkS (2), and FgenesB (Softberry, Inc., Mount Kisco, NY) and then confirmed by the RBSfinder (17). Transfer RNAs were predicted using the tRNAscan-SE program (16). Functional analysis of ORFs was conducted using the BLASTP (1) and InterProScan (22) programs.

In silico complete genome sequence analysis of bacteriophage My1 revealed that it consists of 122,024 bp in length, with an average GC content of 40.61%, 149 ORFs, and 20 tRNA genes. The predicted ORFs were highly homologous to those of T5 (20) or T5-like phages (7, 9) in the *Siphoviridae* family. Interestingly, this genome contains redundant 12,854-bp terminal repeats at both ends.

Of the 149 predicted ORFs, 51 (34.23%) have been annotated and categorized into five functional groups as follows: phage structure and packaging (portal protein, prohead protease, tail protein, terminase large subunit), DNA replication/modification (DNA helicase, DNA primase, DNA polymerase, endonuclease,

NAD-dependent DNA ligase, RNase H), signal transduction and regulatory functions (PhoH-like protein, serine/threonine protein phosphatase, single-stranded DNA [ssDNA]-binding transcriptional regulator), nucleotide metabolism (thymidylate synthase, dihydrofolate reductase, thioredoxin), and host lysis (endolysin, holin, cell wall hydrolase). However, lysogeny-related genes were not detected. Two lysis proteins and no detection of lysogeny-related genes suggest that this phage could be a useful biocontrol agent. YadA domain-containing protein showed high similarity to the L-shaped tail fiber protein among T5 phage genes but low coverage, suggesting that it probably contributes to host-phage-specific interaction. The others were annotated as hypothetical proteins, probably due to insufficient information about *Pectobacterium* phage genes.

This first report of the complete genome sequence of *Pectobacterium carotovorum* subsp. *carotovorum* bacteriophage My1 will extend our knowledge about the interaction between the *Pectobacterium* host and its phages and provide a novel potential as a biocontrol agent to prevent plant diseases caused by *Pectobacterium*.

Nucleotide sequence accession number. The complete genome sequence of *P. carotovorum* subsp. *carotovorum* bacteriophage My1 has been deposited in GenBank under the accession number [JX195166](#).

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