

Complete Genome Sequence of Phytopathogenic *Pectobacterium atrosepticum* Bacteriophage Peat1

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Pectobacterium atrosepticum is a common phytopathogen causing significant economic losses worldwide. To develop a biocontrol strategy for this blackleg pathogen of solanaceous plants, *P. atrosepticum* bacteriophage Peat1 was isolated and its genome completely sequenced. Interestingly, morphological and sequence analyses of the 45,633-bp genome revealed that phage Peat1 is a member of the family *Podoviridae* and most closely resembles the *Klebsiella pneumoniae* bacteriophage KP34. This is the first published complete genome sequence of a phytopathogenic *P. atrosepticum* bacteriophage, and details provide important information for the development of biocontrol by advancing our understanding of phage-phytopathogen interactions.

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The phytopathogenic Gram-negative bacterium *Pectobacterium atrosepticum* (syn. *Erwinia atrosepticum*) causes blackleg in a wide range of solanaceous plants, resulting in severe economic losses (1). Bacteriophage treatments provide an alternative strategy to control various diseases caused by bacteria. Several phages from species of *Pectobacterium* have been isolated, and a few of these have been sequenced (2–4), but a genomic sequence of a phytopathogenic *P. atrosepticum* phage has not been published. In this study, we isolated a *P. atrosepticum* phage and sequenced the entire genome of Peat1, which most closely resembles the *Klebsiella pneumoniae* KP34 phage (5).

Genomic DNA of *P. atrosepticum* phage Peat1 was isolated using density-gradient centrifugation with DNase I and EDTA proteinase K extractions (6). The genomic DNA was fragmented by ultrasonication, and library preparation was performed using the Illumina TruSeq DNA sample preparation kit. Paired-end sequencing was performed on an Illumina HiSeq 2000. Sequences were filtered for low-quality readings using the Dynamic Trim Perl script within SolexaQA. Short reads were assembled using SOAPdenovo (<http://soap.genomics.org.cn>). The high-throughput platform produced 50 Mb of sequence, providing >500-fold coverage (CD Genomics, Shirley, NY). Prediction of open reading frames (ORFs) and their confirmation were obtained with Glimmer version 3.02 (7) and the Conserved Domain Database (8). Analyses of conserved protein domains were performed using BLASTp (9), and tRNAs were predicted with the use of the tRNAscan-SE software (10).

The complete double-stranded DNA genome of *P. atrosepticum* phage Peat1 consists of 45,633 bp, with a G+C content of 48.9%, 61 predicted open reading frames (ORFs), and no tRNAs. The genomic sequences of Peat1 showed little similarity to those of previously reported *Pectobacterium* phages. Consequently, 29 of the 61 ORFs encode hypothetical proteins, and the others appear to encode proteins with conserved domains or similarity to intracellular trafficking and secretion proteins, DNA/RNA polymerases, phage-related lysozyme, a DNA-binding domain in tran-

scriptional regulators, an endo- and exonuclease, acetylornithine deacetylase, subtilisin-like serine proteases, Zn peptidases, a tail spike protein, a phage capsid domain, and phage-related proteins whose functions remain unknown.

Nucleotide sequence accession number. The entire genome sequence of *P. atrosepticum* phage Peat1 has been deposited in GenBank under the accession no. [KR604693](https://www.ncbi.nlm.nih.gov/nuccore/KR604693).

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REFERENCES

- De Boer SH, Li X, Ward LJ. 2012. *Pectobacterium* spp. associated with bacterial stem rot syndrome of potato in Canada. *Phytopathology* 102: 937–947. <http://dx.doi.org/10.1094/PHYTO-04-12-0083-R>.
- Lee DH, Lee JH, Shin H, Ji S, Roh E, Jung K, Ryu S, Choi J, Heu S. 2012. Complete genome sequence of *Pectobacterium carotovorum* subsp. *carotovorum* bacteriophage My1. *J Virol* 86:11410–11411. <http://dx.doi.org/10.1128/JVI.01987-12>.
- Lee JH, Shin H, Ji S, Malhotra S, Kumar M, Ryu S, Heu S. 2012. Complete genome sequence of phytopathogenic *Pectobacterium carotovorum* subsp. *carotovorum* bacteriophage PP1. *J Virol* 86:8899–8900. <http://dx.doi.org/10.1128/JVI.01283-12>.
- Lim JA, Shin H, Lee DH, Han SW, Lee JH, Ryu S, Heu S. 2014. Complete genome sequence of the *Pectobacterium carotovorum* subsp. *carotovorum* virulent bacteriophage PM1. *Arch Virol* 159:2185–2187. <http://dx.doi.org/10.1007/s00705-014-2005-7>.
- Drulis-Kawa Z, Mackiewicz P, Kęsik-Szeloch A, Maciaszczyk-Dziubinska E, Weber-Dąbrowska B, Dorotkiewicz-Jach A, Augustyniak D, Majkowska-Skrobek G, Bocor T, Empel J, Kropinski AM. 2011. Isolation and characterisation of KP34—a novel ϕ KMV-like bacteriophage for *Klebsiella pneumoniae*. *Appl Microbiol Biotechnol* 90:1333–1345. <http://dx.doi.org/10.1007/s00253-011-3149-y>.
- Gill JJ, Svircev AM, Smith R, Castle AJ. 2003. Bacteriophages of *Erwinia amylovora*. *Appl Environ Microbiol* 69:2133–2138. <http://dx.doi.org/10.1128/AEM.69.4.2133-2138.2003>.
- Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved

- microbial gene identification with Glimmer. *Nucleic Acids Res* 27: 4636–4641. <http://dx.doi.org/10.1093/nar/27.23.4636>.
8. Marchler-Bauer A, Derbyshire MK, Gonzales NR, Lu S, Chitsaz F, Geer LY, Geer RC, He J, Gwadz M, Hurwitz DJ, Lanczycki CJ, Lu F, Marchler GH, Song JS, Thanki N, Wang Z, Yamashita RA, Zhang D, Zheng C, Bryant SH. 2015. CDD: NCBI's Conserved Domain Database. *Nucleic Acids Res* 43:D222–D226. <http://dx.doi.org/10.1093/nar/gku1221>.
 9. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:3389–3402. <http://dx.doi.org/10.1093/nar/25.17.3389>.
 10. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* 25: 955–964. <http://dx.doi.org/10.1093/nar/25.5.0955>.