Complete Genome Sequence of Pseudomonas Aeruginosa Phage vB_PaeM_CEB_DP1

The MIT Faculty has made this article openly available. Please share how this access benefits you. Your story matters.

Citation: Pires, Diana P., Sanna Sillankorva, Andrew M. Kropinski, Timothy K. Lu, and Joana Azeredo. “Complete Genome Sequence of Pseudomonas Aeruginosa Phage vB_PaeM_CEB_DP1.” Genome Announc. 3, no. 5 (September 24, 2015): e00918–15.

As Published: http://dx.doi.org/10.1128/genomeA.00918-15

Publisher: American Society for Microbiology

Persistent URL: http://hdl.handle.net/1721.1/99636

Version: Final published version: final published article, as it appeared in a journal, conference proceedings, or other formally published context

Terms of use: Creative Commons Attribution
The lytic bacteriophage vB_PaeM_CEB_DP1 was isolated from hospital sewage in Portugal using Pseudomonas aeruginosa PAO1 as the host strain. Its host range was evaluated using a panel of 30 P. aeruginosa clinical isolates, and this phage was able to infect approximately 57% of them.

The morphological characterization of phage vB_PaeM_CEB_DP1 was performed by transmission electron microscopy, revealing an icosahedral head of ~70 nm in diameter and an ~140-×18-nm contractile tail. Thus, it was possible to determine that this phage belongs to the Myoviridae family of phages. Furthermore, the growth parameters determined by the one-step growth experiment showed that phage vB_PaeM_CEB_DP1 has a latent period of ~50 min, a rise period of ~50 min, and a burst size of ~70 phages per infected cell.

The phage genome was sequenced using Roche 454 sequencing procedures at the Plateforme d’analyses of the Institut de Biologie Integrative et des Systèmes (Laval University, Quebec, QC, Canada). Shotgun reads were assembled using the gsAssembler module of Newbler v 2.5.3.

The complete coding sequences (CDSs) were first annotated using myRAST (1). Sequence similarity searches were performed with the translation of each predicted CDS against the National Center for Biotechnology Information (NCBI) protein database, using BLASTP (2), in order to assign putative protein functions. Promoter sequences were predicted based on their similarity to promoter sequences from other Phunalike phages (3). Predicted terminators were annotated using ARNold (4). The tool tRNAscan-SE (5) was used for tRNA annotation but, similarly to other Phunalike phages (3, 6, 7), no putative genes coding for tRNAs were found in this genome.

The genome of the phage vB_PaeM_CEB_DP1 consists of 66,158 bp of dsDNA with a GC content of 55.6%. The whole genome was scanned for CDSs, resulting in 89 predicted genes ranging from 141 bp to 3,111 bp. Furthermore, 37 of these genes are rightward oriented while 52 are leftward oriented. The initiation codon of 90% of the genes is ATG, while 8% start with TTG and 2% with TTG. According to BLASTP analyses, 68% of the proteins encoded in the genome of vB_PaeM_CEB_DP1 are hypothetical. This study further revealed that this phage has 7 predicted promoters and 12 terminators.

Although controversial, most of the phages belonging to the Phunalike genus are reported to encode linear, nonpermuted genomes (3, 6). In the present study, direct Sanger sequencing of phage DNA was performed to determine the genome ends of phage vB_PaeM_CEB_DP1. However, the ends of the genome were not identified, suggesting that the phage genome has cohesive ends or terminal redundancy as described for phage KPP12 (7).

The genome of phage vB_PaeM_CEB_DP1 shares high nucleotide identity with other P. aeruginosa Phunalike phages: LMA2 (95.6%), KPP12 (94.3%) and vB_PaeM_PA01_Ab27 (93.1%).

**Nucleotide sequence accession number.** The complete genome of the P. aeruginosa phage vB_PaeM_CEB_DP1 was deposited in GenBank under the accession number KR869157.

**ACKNOWLEDGMENTS**

D.P.P. acknowledges the financial support from the Portuguese Foundation for Science and Technology (FCT) through the grant SFRH/BD/76440/2011. S.S. is an investigator (IF/01413/2013). We also thank FCT for the Strategic Project of the UID/BIO/04469/2013 unit, FCT and European Union funds (FEDER/COMPETE) for the project RECI/BBB-EBI/0179/2012 (FCOMP-01-0124-FEDER-027462), and the project “BioHealth—Biotechnology and Bioengineering approaches to improve health quality” (NORTE-07-0124-FEDER-027462) cofunded by the Programa Operacional Regional do Norte (ON.2-O Novo Norte), QREN, and FEDER.

T.K.L. acknowledges support by grants from the Defense Threat Reduction Agency (HDTRA1-14-1-0007), the National Institutes of Health (1DP2OD008435, 1P50GM098792, and 1R01EB01775S), and the U.S. Army Research Laboratory and the U.S. Army Research Office through the Institute for Soldier Nanotechnologies, under contract number W911NF-13-D-0001.

---

**Complete Genome Sequence of Pseudomonas aeruginosa Phage vB_PaeM_CEB_DP1**

Diana P. Pires, a Sanna Sillankorva, a Andrew M. Kropinski, a,b,c Timothy K. Lu, a,e Joana Azeredo a

Centre of Biological Engineering, University of Minho, Braga, Portugal; Public Health Agency of Canada, Laboratory for Foodborne Zoonoses, Guelph, Ontario, Canada; Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada; Department of Electrical Engineering and Computer Science, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA; Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA.

vB_PaeM_CEB_DP1 is a Pseudomonas aeruginosa bacteriophage (phage) belonging to the Phunalike virus genus of the Myoviridae family of phages. It was isolated from hospital sewage. vB_PaeM_CEB_DP1 is a double-stranded DNA (dsDNA) phage, with a genome of 66,158 bp, containing 89 predicted open reading frames.

Received 23 July 2015 Accepted 11 August 2015 Published 24 September 2015


Copyright © 2015 Pires et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Joana Azeredo, jazeredo@deb.uminho.pt.
REFERENCES


