

# Complete Genome Sequence of *Lelliottia* Podophage phD2B

Grzegorz Nowicki, Jakub Barylski, Natalia Kujawa, Anna Goździcka-Józefiak

Department of Molecular Virology, Institute of Experimental Biology, Adam Mickiewicz University, Poznań, Poland

The genus *Lelliottia* was recently created from the group of environmental gammaproteobacteria previously included in the genus *Enterobacter*. Here, we report the complete genome sequence of phD2B, the first (according to our current knowledge) known phage that infects bacterium from the taxon.

Received 8 September 2014 Accepted 17 October 2014 Published 26 November 2014

Citation Nowicki G, Barylski J, Kujawa N, Goździcka-Józefiak A. 2014. Complete genome sequence of *Lelliottia* podophage phD2B. *Genome Announc.* 2(6):e01046-14. doi:10.1128/genomeA.01046-14.

Copyright © 2014 Nowicki et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Jakub Barylski, jakub.barylski@gmail.com.

The genus *Lelliottia* was proposed by Brady and coworkers in 2013. It currently comprises two species: *L. amnigena* and *L. nimipressuralis* (1). These motile, facultatively anaerobic rods were isolated from water, food products, and plant tissues (*L. nimipressuralis* is notable for causing wetwood disease of trees) (2, 3). Neither *L. amnigena* nor *L. nimipressuralis* is considered pathogenic for mammals, but a few cases of human infections were reported (4, 5). In this report, we describe the complete genome of the first-known phage that infects *Lelliottia* sp.

Bacteriophage phD2B was isolated from a sediment sample from Lake Góreckie, an eutrophic reservoir located in Wielkopolski National Park, Poland. It infects strain GL2 isolated from the same reservoir and was identified as *Lelliottia* sp. (based on complete sequences of 16S rDNA as well as genes encoding hsp 60 GroEL chaperonin,  $\beta$ -subunits of RNA polymerase, and DNA gyrase).

The genome was sequenced using the 454 method in Genomed SA (Warsaw, Poland) and assembled using Newbler version 2.5.3 (454 Life Sciences) and Geneious version 6.1 (6) (64.98-fold coverage). Protein coding genes were predicted using GeneMarkS (7) and Prodigal version 2.60 (8). Their functional annotation was performed based on BLASTx hits against the UniprotKB viruses database (9). To search for tRNA genes we used tRNAscan-SE version 1.21 (10). Mapping of pyrosequencing reads that allows determination of genome ends was performed with the Pause pipeline (<https://cpt.tamu.edu/computer-resources/pause/>).

phD2B is an SP6-like podophage. The complete genome of the phage is 44,366 bp in length with a G+C content of 51% and ends with direct repeats (262 bp). We identified 49 coding sequences, all on one strand.

The arrangement of the modules seems to roughly reflect the order of expression. The left end of the genome contains a group of genes involved in the takeover of a host metabolism (*S*-adenosyl-L-methionine hydrolase and RNA polymerase) followed by a cluster of CDSs associated with replication and recombination (HNH endonuclease, primase/helicase, DNA polymerase, exonuclease, homing nuclease, and ligase). The right half is occupied mostly by a morphogenesis module. The last 4 to 5 kb of the genome encode proteins involved in DNA packaging and lysis of the host cell (terminase subunits, holin, and M15 family lytic pep-

tidase). Surprisingly, the gene for the large terminase subunit is split into two open reading frames, which together encode the full-length protein. This suggests that we deal with exons of the single gene (separated by the intron that contains gene for homing endonuclease). A similar layout is rather uncommon for *Autographivirinae* (we found it only in the genome of phage K1E) but was observed in unrelated phages, including myoviruses (11–13) and siphoviruses (14–17).

**Nucleotide sequence accession numbers.** The complete sequence of phD2B genome is available from GenBank under the accession number [KM370384](https://www.ncbi.nlm.nih.gov/nuccore/KM370384). Sequences from the host bacterium are stored in records [KM458060](https://www.ncbi.nlm.nih.gov/nuccore/KM458060), [KM458061](https://www.ncbi.nlm.nih.gov/nuccore/KM458061), [KM458062](https://www.ncbi.nlm.nih.gov/nuccore/KM458062), and [KM458063](https://www.ncbi.nlm.nih.gov/nuccore/KM458063).

## ACKNOWLEDGMENTS

The work was financed using internal funds of Department of Molecular Virology of Adam Mickiewicz University in Poznań.

We thank Eric Rasche from the Center for Phage Technology at Texas A&M University for comprehensive and intelligible guidance with PAUSE.

## REFERENCES

- Brady C, Cleenwerck I, Venter S, Coutinho T, De Vos P. 2013. Taxonomic evaluation of the genus *Enterobacter* based on multilocus sequence analysis (MLSA): proposal to reclassify *E. nimipressuralis* and *E. amnigena* into *Lelliottia* gen. nov. as *Lelliottia nimipressuralis* comb. nov. and *Lelliottia amnigena* comb. nov., respectively, *E. gergoviae* and *E. pyrinus* into *Pluralibacter* gen. nov. as *Pluralibacter gergoviae* comb. nov. and *Pluralibacter pyrinus* comb. nov., respectively, *E. cowanii*, *E. radincitans*, *E. oryzae* and *E. arachidis* into *Kosakonia* gen. nov. as *Kosakonia cowanii* comb. nov., *Kosakonia radincitans* comb. nov., *Kosakonia oryzae* comb. nov. and *Kosakonia arachidis* comb. nov., respectively, and *E. turicensis*, *E. helveticus* and *E. pulveris* into *Cronobacter* as *Cronobacter zurichensis* nom. nov., *Cronobacter helveticus* comb. nov. and *Cronobacter pulveris* comb. nov., respectively, and emended description of the genera *Enterobacter* and *Cronobacter*. *Syst. Appl. Microbiol.* 36:309–319. <http://dx.doi.org/10.1016/j.syapm.2013.03.005>.
- Batt CA, Tortorello ML. 2014. *Encyclopedia of food microbiology*, 2nd ed., Academic Press, Amsterdam.
- Dworkin M, Falkow S. 2006. *The prokaryotes: a handbook on the biology of bacteria*, 3rd ed., Springer, New York.
- Capdevila JA, Bisbe V, Gasser I, Zuazu J, Olivé T, Fernández F, Pahissa B, Berga A. 1998. *Enterobacter amnigenus*: an unusual human pathogen. *Enferm. Infecc. Microbiol. Clin.* 16:364–366.

5. Kim DM, Jang SJ, Neupane GP, Jang MS, Kwon SH, Kim SW, Kim WY. 2010. *Enterobacter nimipressuralis* as a cause of pseudobacteremia. *BMC Infect. Dis.* 10:315. <http://dx.doi.org/10.1186/1471-2334-10-315>.
6. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics* 28:1647–1649. <http://dx.doi.org/10.1093/bioinformatics/bts199>.
7. Besemer J, Lomsadze A, Borodovsky M. 2001. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. *Nucleic Acids Res.* 29:2607–2618. <http://dx.doi.org/10.1093/nar/29.12.2607>.
8. Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <http://dx.doi.org/10.1186/1471-2105-11-119>.
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. Schattner P, Brooks AN, Lowe TM. 2005. The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids Res.* 33:W686–W689. <http://dx.doi.org/10.1093/nar/gki366>.
11. Zago M, Scaltriti E, Rossetti L, Guffanti A, Armiento A, Fornasari ME, Grolli S, Carminati D, Brini E, Pavan P, Felsani A, D'Urzo A, Moles A, Claude JB, Grandori R, Ramoni R, Giraffa G. 2013. Characterization of the genome of the dairy *Lactobacillus helveticus* bacteriophage ΦAQ113. *Appl. Environ. Microbiol.* 79:4712–4718. <http://dx.doi.org/10.1128/AEM.00620-13>.
12. Barylski J, Nowicki G, Gozdzicka-Jozefiak A. 2014. The discovery of phiAGATE, a novel phage infecting *Bacillus pumilus*, leads to new insights into the phylogeny of the subfamily *Spounavirinae*. *PLoS One* 9:e86632. <http://dx.doi.org/10.1371/journal.pone.0086632>.
13. Sullivan MB, Huang KH, Ignacio-Espinoza JC, Berlin AM, Kelly L, Weigele PR, DeFrancesco AS, Kern SE, Thompson LR, Young S, Yandava C, Fu R, Krastins B, Chase M, Sarracino D, Osburne MS, Henn MR, Chisholm SW. 2010. Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. *Environ. Microbiol.* 12:3035–3056. <http://dx.doi.org/10.1111/j.1462-2920.2010.02280.x>.
14. Aswani VH, Tremblay DM, Moineau S, Shukla SK. 2014. Complete genome sequence of a *Staphylococcus epidermidis* bacteriophage isolated from the anterior nares of humans. *Genome Announc.* 2(4):14. <http://dx.doi.org/10.1128/genomeA.00549-1400549>.
15. Levesque C, Duplessis M, Labonte J, Labrie S, Fremaux C, Tremblay D, Moineau S. 2005. Genomic organization and molecular analysis of virulent bacteriophage 2972 infecting an exopolysaccharide-producing *Streptococcus thermophilus* strain. *Appl. Environ. Microbiol.* 71:4057–4068. <http://dx.doi.org/10.1128/AEM.71.7.4057-4068.2005>.
16. Yasmin A, Kenny JG, Shankar J, Darby AC, Hall N, Edwards C, Horsburgh MJ. 2010. Comparative genomics and transduction potential of *Enterococcus faecalis* temperate bacteriophages. *J. Bacteriol.* 192:1122–1130. <http://dx.doi.org/10.1128/JB.01293-09>.
17. Zhou Y, Lu C, Wu QJ, Wang Y, Sun ZT, Deng JC, Zhang Y. 2008. GISSD: group I intron sequence and structure database. *Nucleic Acids Res.* 36:D31–D37. <http://dx.doi.org/10.1093/nar/gkm766>.