

Genome Sequences of *Pseudomonas oryzihabitans* Phage POR1 and *Pseudomonas aeruginosa* Phage PAE1

Zoe A. Dyson,^a Robert J. Seviour,^b Joseph Tucci,^a Steve Petrovski^b

La Trobe Institute of Molecular Sciences, Bendigo, Victoria, Australia^a; Department of Physiology, Anatomy and Microbiology, La Trobe University, Bundoora, Victoria, Australia^b

We report the genome sequences of two double-stranded DNA siphoviruses, POR1 infective for *Pseudomonas oryzihabitans* and PAE1 infective for *Pseudomonas aeruginosa*. The phage POR1 genome showed no nucleotide sequence homology to any other DNA phage sequence in the GenBank database, while phage PAE1 displayed synteny to *P. aeruginosa* phages M6, MP1412, and YuA.

Received 6 November 2015 Accepted 4 May 2016 Published 16 June 2016

Citation Dyson ZA, Seviour RJ, Tucci J, Petrovski S. 2016. Genome sequences of *Pseudomonas oryzihabitans* phage POR1 and *Pseudomonas aeruginosa* phage PAE1. *Genome Announc* 4(3):e01515-15. doi:10.1128/genomeA.01515-15.

Copyright © 2016 Dyson et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Steve Petrovski, steve.petrovski@latrobe.edu.au.

Pseudomonas aeruginosa and *Pseudomonas oryzihabitans* are opportunistic pathogens that have developed resistance to a wide range of antimicrobials (1–5). Here we describe two phages, PAE1 and POR1 infective for *P. aeruginosa* and *P. oryzihabitans*, respectively.

Phage PAE1 was isolated from a wastewater treatment plant in Bendigo (Victoria, Australia), and formed plaques on *P. aeruginosa* strain PAO9505 lawn cultures (6). It is a member of the family *Siphoviridae* with a B2 capsid morphotype. Its genomic DNA was prepared and sequenced as described previously (7). A minimum sequence coverage of 50 times was obtained. Genomes were assembled using gsAssembler (v2.6) (Roche Applied Science, Indianapolis, IN, USA), and open reading frames (ORFs) were predicted with Glimmer (v3.02) and manual annotations (8). Homology and conserved domain searches were performed using BLASTp (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>), and the presence of tRNA sought with the tRNAscan-SE program (9).

Genomic analysis revealed that the 62,818-bp genome of the *Siphovirus* PAE1 displays between 93% and 97% nucleotide sequence identity to that of phages MP1412 (61,167 bp; accession no. JX131330), M6 (59,446 bp; accession no. DQ163916), and YuA (58,663 bp; accession no. AM749441) over a coverage of 92%, 93%, and 89%, respectively (10–12). DNA sequence comparisons reveal recombination events have most probably occurred leading to DNA deletions and/or insertions, and generating sequence variations seen between PAE1 phage and its closest relatives. A total of 88 open reading frames (ORFs) were detected, and no tRNAs seen. The PAE1 genome has a modular architecture, with regions associated with DNA packaging (*orf1-2*), virion morphogenesis/host lysis (*orf7-orf31*), and DNA replication/maintenance identified (*orf37-orf79*). The presence of a phage integrase (*orf63*) suggests PAE1 might be capable of a lysogenic existence (10, 13). The integrase gene appears highly conserved in PAE1 and its relative phages MP1412, M6, and YuA and together with the high level of sequence similarity to *Pseudomonas aeruginosa* genomes, suggests these phages too are probably temperate.

Phage POR1 was isolated from a sample obtained from the Nambour (QLD, Australia) wastewater treatment plant, and formed plaques on lawn plates of *P. oryzihabitans* strain J81P. Phage POR1 is also a member of the *Siphovirus* family, possessing a B1 capsid morphotype. The POR1 genome was sequenced as described above obtaining a 107 times coverage and revealing the genome size of 55,349 bp, sharing no nucleotide sequence homology with any sequence in GenBank database. Given that many of the predicted gene products shared similarity to those encoded by their bacterial hosts, it is predicted that POR1 is a prophage. Sequencing and restriction endonuclease profiling revealed that both PAE1 and POR1 had circularly permuted genome, but whether terminal repeats or headful packaging is used is unknown.

Nucleotide sequence accession numbers. Genome sequences of phages PAE1 and POR1 have been deposited in GenBank under accession numbers [KT734862](https://www.ncbi.nlm.nih.gov/nuccore/KT734862) and [KT716399](https://www.ncbi.nlm.nih.gov/nuccore/KT716399), respectively.

ACKNOWLEDGMENTS

We thank Robert Glaishier (LIMS) and Glenys Shirley (LIMS) for assistance with transmission electron microscopy, Pierre Faou for assistance with mass spectroscopy, and Daniel Tillett for useful discussions.

Z.A.D. is the recipient of an Australian Postgraduate Award Scholarship.

REFERENCES

1. Stover CK, Pham XQ, Erwin AL, Mizoguchi SD, Warrenner P, Hickey MJ, Brinkman FSL, Hufnagle WO, Kowalik DJ, Lagrou M, Garber RL, Goltry L, Tolentino E, Westbrock-Wadman S, Yuan Y, Brody LL, Coulter SN, Folger KR, Kas A, Larbig K, Lim R, Smith K, Spencer D, Wong GKS, Wu Z, Paulsen IT, Reizer J, Saier MH, Hancock REW, Lory S, Olson MV. 2000. Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen. *Nature* 406:959–964. [http://dx.doi.org/10.1038/35023079](https://doi.org/10.1038/35023079).
2. Tena D, Fernández C. 2015. *Pseudomonas oryzihabitans*: an unusual cause of skin and soft tissue infection. *Infect Dis* 47:820–824.
3. Woo K-S, Choi J-L, Kim B-R, Kim J-E, Kim K-H, Kim J-M, Han J-Y. 2014. Outbreak of *Pseudomonas oryzihabitans* pseudobacteremia related

- to contaminated equipment in an emergency room of a tertiary hospital in Korea. *Infect Chemother* 46:42–44. <http://dx.doi.org/10.3947/ic.2014.46.1.42>.
4. Lin RD, Hsueh PR, Chang JC, Teng LJ, Chang SC, Ho SW, Hsieh WC, Luh KT. 1997. *Flavimonas oryzihabitans* bacteremia: clinical features and microbiological characteristics of isolates. *Clin Infect Dis* 24:867–873. <http://dx.doi.org/10.1093/clinids/24.5.867>.
 5. Decker CF, Simon GL, Keiser JF. 1991. *Flavimonas oryzihabitans* (*Pseudomonas oryzihabitans*; CDC group Ve-2) bacteremia in the immunocompromised host. *Arch Intern Med* 151:603–604.
 6. Stanisich VA, Bennett PM. 1976. Isolation and characterisation of deletion mutants involving the transfer genes of P-group plasmids in *Pseudomonas aeruginosa*. *Mol Gen Genet* 149:211–216. <http://dx.doi.org/10.1007/BF00332891>.
 7. Petrovski S, Seviour RJ, Tillett D. 2011. Genome sequence and characterization of the *Tsukamurella* bacteriophage TPA2. *Appl Environ Microbiol* 77:1389–1398. <http://dx.doi.org/10.1128/AEM.01938-10>.
 8. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with glimmer. *Bioinformatics* 23:673–679. <http://dx.doi.org/10.1093/bioinformatics/btm009>.
 9. 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>.
 10. Bae H-W, Chung I-Y, Sim N, Cho Y-H. 2012. Complete genomes sequence of *Pseudomonas aeruginosa* siphophage MP1412. *J Virol* 86:9537. <http://dx.doi.org/10.1128/JVI.01403-12>.
 11. Ceyssens PJ, Mesyanzhinov V, Sykilinda N, Briers Y, Roucourt B, Lavigne R, Robben J, Domashin A, Miroshnikov K, Volckaert G, Hertveldt K. 2008. The genome and structural proteome YuA, a new *Pseudomonas aeruginosa* phage resembling M6. *J Bacteriol* 190:1429–1435. <http://dx.doi.org/10.1128/JB.01441-07>.
 12. Kwan T, Liu J, DuBow M, Gros P, Pelletier J. 2006. Comparative genomic analysis of 18 *Pseudomonas aeruginosa* bacteriophages. *J Bacteriol* 188:1184–1187. <http://dx.doi.org/10.1128/JB.188.3.1184-1187.2006>.
 13. Dyson ZA, Tucci J, Seviour RJ, Petrovski S. 2015. Lysis to kill: evaluation of the lytic abilities, and genomics of nine bacteriophages infective for *Gordonia* spp. and their potential use in activated sludge foam biocontrol. *PLoS One* 10:. <http://dx.doi.org/10.1371/journal.pone.0134512>.



Minerva Access is the Institutional Repository of The University of Melbourne

Author/s:

Dyson, ZA; Seviour, RJ; Tucci, J; Petrovski, S

Title:

Genome Sequences of Pseudomonas oryzihabitans Phage POR1 and Pseudomonas aeruginosa Phage PAE1

Date:

2016-05-01

Citation:

Dyson, Z. A., Seviour, R. J., Tucci, J. & Petrovski, S. (2016). Genome Sequences of Pseudomonas oryzihabitans Phage POR1 and Pseudomonas aeruginosa Phage PAE1. MICROBIOLOGY RESOURCE ANNOUNCEMENTS, 4 (3), <https://doi.org/10.1128/genomeA.01515-15>.

Persistent Link:

<http://hdl.handle.net/11343/262457>

File Description:

Published version

License:

CC BY