Genome Sequence of Gordonia Phage Yvonnetastic

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Gordonia bacteriophage Yvonnetastic was isolated from soil in Pittsburgh, PA, using Gordonia terrae 3612 as a host. Yvonnetastic has siphoviral morphology and a genome of 98,136 bp, with 198 predicted protein-coding genes and five tRNA genes. Yvonnetastic does not share substantial sequence similarity with other sequenced bacteriophage genomes.

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REFERENCES

1. De los Reyes FL, III, Raskin L. 2002. Role of filamentous microorganisms in activated sludge foaming: relationship of mycolata levels to foaming initiation and stability. Water Res 36:445–459. http://dx.doi.org/10.1016/S0043-1354(01)00227-5.
2. De los Reyes FL, III, Rothauszky D, Raskin L. 2002. Microbial community structures in foaming and nonfoaming full-scale wastewater treatment plants. Water Environ Res 74:437–449. http://dx.doi.org/10.2175/106143002X140233.
3. Petrovski S, Seviour RJ, Tillett D. 2011. Prevention of Gordonia and...
Nocardia stabilized foam formation by using bacteriophage GTE7. Appl Environ Microbiol 77:7864–7867. http://dx.doi.org/10.1128/AEM.05692-11.
4. Blaschke AJ, Bender J, Byington CL, Korgenski K, Daly J, Petti CA, Pavia AT,ampofo K. 2007. Gordonia species: emerging pathogens in pediatric patients that are identified by 16S ribosomal RNA gene sequences. Clin Infect Dis 45:483–486. http://dx.doi.org/10.1086/500018.
5. Grisdold AJ, Roll P, Hoenigl M, Feierl G, Vicenzi-Moser R, Martth E. 2007. Isolation of Gordonia terrae from a patient with catheter-related bacteraemia. J Med Microbiol 56:1687–1688. http://dx.doi.org/10.1099/jmm.0.47388-0.
6. 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 biocontrol. PLoS One 10:e0134512. http://dx.doi.org/10.1371/journal.pone.0134512.
7. Liu M, Gill J, Young R, Summer EJ. 2015. Bacteriophages of wastewater foaming-associated filamentous Gordonia reduce host levels in raw activated sludge. Sci Rep 5:13754. http://dx.doi.org/10.1038/srep13754.
8. Petrovski S, Seviour RJ, Tillett D. 2011. Characterization of the genome of the polyvalent lytic bacteriophage GTE2, which has potential for bio-control of Gordonia-, Rhodococcus-, and Nocardia-stabilized foams in activated sludge plants. Appl Environ Microbiol 77:3923–3929. http://dx.doi.org/10.1128/AEM.00025-11.
9. Petrovski S, Tillett D, Seviour RJ. 2012. Genome sequences and characterization of the related Gordonia phages GTE5 and GRU1 and their use as potential biocontrol agents. Appl Environ Microbiol 78:42–47. http://dx.doi.org/10.1128/AEM.00584-11.
10. Jacobs-Sera D, Marinelli LJ, Bowman C, Broussard GW, Guerrero Bustamante MA, Petrova ZO, Dedrick RM, Pope WH. Science Education Alliance-Phage Hunters Advancing Genomics, Evolutionary Science Sea-phages Program, Modlin RL, Hendrix RW, Hatfull GF. 2012. On the nature of mycobacteriophage diversity and host preference. Virology 418:187–201.
11. Mageeney C, Pope WH, Harrison M, Moran D, Cross T, Jacobs-Sera D, Hendrix RW, Dunbar D, Hatfull GF. 2012. Mycobacteriophage Marvin: a new single phage with an unusual genome organization. J Virol 86:4762–4775. http://dx.doi.org/10.1128/JVI.00073-12.
12. Pope WH, Anders KR, Baird M, Bowman CA, Boyle MM, Broussard GW, Chow T, Clase KL, Cooper S, Cornely KA, Dejong RJ, Delesalle VA, Deng L, Dunbar D, Edgington NP, Ferreira CM, Weston Hafer K, Hartzog GA, Hatherill JR, Hughes LE, Iapalo K, Krukonis GP, Meier CG, Monti DL, Oml MR, Page ST, Peebles CL, Rinehart CA, Rubin MR, Russell DA, Sanders ER, Schoer M, Shaffer CD, Wherley J, Vazquez E, Yuan H, Zhang D, Cresawn SG, Jacobs-Sera D, Hendrix RW, Hatfull GF. 2014. Cluster M mycobacteriophages Bongo, PegLeg, and Rey with unusually large repertoires of tRNA isotypes. J Virol 88:2461–2480. http://dx.doi.org/10.1128/JVI.00336-13.
13. Pope WH, Bowman CA, Russell DA, Jacobs-Sera D, Asai DJ, Cresawn SG, Jacobs WR, Hendrix RW, Lawrence JG, Hatfull GF, Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science, Phage Hunters Integrating Research and Education, Mycobacteriogenetics Course. 2015. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. Elife 4:e06416.
14. Pope WH, Ferreira CM, Jacobs-Sera D, Benjamin RC, Davis AJ, Delong RJ, Elgin SC, Guifoille FR, Forsyth MH, Harris AD, Harvey SE, Hughes LE, Hynes PM, Jackson AS, Jalal MD, MacMurray EA, Manley CM, McDonough MJ, Mossier JL, Osterbann LJ, Rabinowitz HS, Ryhan CN, Russell DA, Saha MS, Shaffer CD, Simon SE, Sims EF, Tovar IG, Weisser EG, Wertz JT, Weston-Hafer KA, Williamson KE, Zhang B, Cresawn SG, Jain P, Piuri M, Jacobs WR Jr, Hendrix RW, Hatfull GF. 2011. Cluster K mycobacteriophages: insights into the evolutionary origins of mycobacteriophage TM4. PLoS One 6:e26750. http://dx.doi.org/10.1371/journal.pone.0026750.
15. Pope WH, Jacobs-Sera D, Russell DA, Peebles CL, Al-Attrache Z, Alcoser TA, Alexander LM, Alfano MB, Alford ST, Amy NE, Anderson MD, Anderson AG, Ang AA, Ares M Jr, Barber AJ, Barker LP, Barrett JM, Barshop WD, Bauerle CM, Bayles IM, Belfield KL, Best AA, Borjon A Jr, Bowman CA, Boyer CA, Bradley KW, Bradley VA, Broadway LN, Budwai K, Busby KN, Campbell IW, Campbell AM, Carey A, Caruso SM, Chew RD, Cockburn CL, Cohen LB, Corajoud JM, Cresawn SG, Davis KR, Deng L, Denver DR, Dixon BR, Ekram S, Elgin SC, Engelsen AE, English BE, Erb ML, Estrada C, Fillionz LG. 2015. Expanding the diversity of mycobacteriophages: insights into genome architecture and evolution. PLoS One 6:e16329. http://dx.doi.org/10.1371/journal.pone.0016329.
16. Jordan TG, Burnett SH, Carson S, Caruso SM, Clase K, Delong RJ, Denneby JJ, Denver DR, Dunbar D, Elgin SC, Findley AM, Gissendanner CR, Golebiewska UP, Guild N, Hartzog GA, Grillo WH, Holowell GP, Hughes LE, Johnson A, King RA, Lewis LO, Li W, Rosenweig F, Rubin MR, Saha MS, Sandoz J, Shaffer CD, Taylor B, Temple L, Vazquez E, Ware VC, Barker LP, Bradley KW, Jacobs-Sera D, Pope WH, Russell DA, Cresawn SG, Lopatto D, Bailey CP, Hatfull GF. 2014. A broadly implementable research course in phage discovery and genomics for first-year undergraduate students. mBio 5:e01051-13. http://dx.doi.org/10.1128/mBio.01051-13.
17. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiotic DNA with Glimmer. Bioinformatics 23:673–679. http://dx.doi.org/10.1093/bioinformatics/btm009.
18. Besemer J, Borodovsky M. 2005. GeneMark: Web software for gene finding in prokaryotes, eukaryotes and viruses. Nucleic Acids Res 33:W451–W454. http://dx.doi.org/10.1093/nar/gkj487.
19. Cresawn SG, Bogel M, Day N, Jacobs-Sera D, Hendrix RW, Hatfull GF. 2011. Phamerator: a bioinformatic tool for comparative bacteriophage genomics. BMC Bioinformatics 12:395. http://dx.doi.org/10.1186/1471-2105-12-395.
20. Laslett D, Canback B. 2004. ARAGORN, a program to detect tRNA genes in nucleotide sequences. Nucleic Acids Res 32:W451–W454. http://dx.doi.org/10.1093/nar/gkj487.
21. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol 215:403–408. http://dx.doi.org/10.1016/S0022-2836(05)80360-2.
22. Söding J, Biegert A, Lupas AN. 2005. The HHpred interactive server for protein homology detection and structure prediction. Nucleic Acids Res 33:W244–W248. http://dx.doi.org/10.1093/nar/gki408.