

12-11-2014

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Sheldon G. Hurst IV
University of New Hampshire, Durham

Shimaa M. Ghazal
University of New Hampshire, Durham, Shimaa.Ghazal@unh.edu

Krystalynne Morris
University of New Hampshire, Durham

Feseha Abebe-Akele
University of New Hampshire, Durham

Feseha Abebe-Akele
University of New Hampshire, Durham

See next page for additional authors

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Recommended Citation

Hurst IV, S. G., S. Ghazal, K. Morris, F. Abebe-Akele, W. K. Thomas, U. M. Badr, M. A. Hussein, M. A. AbouZaied, K. M. Khalil, and L. S. Tisa. 2014. Draft Genome Sequence of *Photorhabdus temperata* strain Meg1, an Entomopathogenic Bacterium Isolated from *Heterorhabditis megidis* Nematodes. *Genome Announc* 2(6) e01273-14. Doi: 10.1128/genomeA01273-14.

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Authors

Sheldon G. Hurst IV, Shima M. Ghazal, Krystalynne Morris, Feseha Abebe-Akele, Feseha Abebe-Akele, W. Kelley Thomas, Usama M. Badr, Mona A. Hussein, Mohamed A. AbouZaied, Kamal M. Khalil, and Louis S. Tisa

Draft Genome Sequence of *Photorhabdus temperata* Strain Meg1, an Entomopathogenic Bacterium Isolated from *Heterorhabditis megidis* Nematodes

Sheldon G. Hurst IV,^a Shima Ghazal,^{a,b} Krystalynne Morris,^a Feseha Abebe-Akele,^a W. Kelley Thomas,^a Usama M. Badr,^b Mona A. Hussein,^c Mohamed A. AbouZaied,^d Kamal M. Khalil,^b Louis S. Tisa^a

University of New Hampshire, Durham, New Hampshire, USA^a; Applied Microbial Genetics Laboratory, Genetics and Cytology Department, Genetic Engineering & Biotechnology Division, National Research Centre, Dokki, Cairo, Egypt^b; Department of Pests and Plant Protection, Agricultural Division, National Research Centre, Dokki, Cairo, Egypt^c; Department of Microbiology, Faculty of Science, University of Ain Shams, Abbassia, Cairo, Egypt^d

***Photorhabdus temperata* strain Meg1 is an entomopathogenic bacterium that forms a symbiotic association with *Heterorhabditis* nematodes. We report here a 4.9-Mbp draft genome sequence for *P. temperata* strain Meg1, with a G+C content of 43.18% and containing 4,340 candidate protein-coding genes.**

Received 26 October 2014 Accepted 29 October 2014 Published 11 December 2014

Citation Hurst SG, IV, Ghazal S, Morris K, Abebe-Akele F, Thomas WK, Badr UM, Hussein MA, AbouZaied MA, Khalil KM, Tisa LS. 2014. Draft genome sequence of *Photorhabdus temperata* strain Meg1, an entomopathogenic bacterium isolated from *Heterorhabditis megidis* nematodes. *Genome Announc.* 2(6):e01273-14. doi:10.1128/genomeA.01273-14.

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Address correspondence to Louis S. Tisa, louis.tisa@unh.edu.

Members of the genus *Photorhabdus* maintain two distinct life styles as insect pathogens and in symbiotic relationship with the entomopathogenic *Heterorhabditis* nematodes (for reviews, see references 1–7). The life cycle of *Photorhabdus* and its nematode host *Heterorhabditis* is best described as a cyclic association that begins and ends with infective juvenile nematodes (IJs). The IJs, which carry a monoculture of *Photorhabdus* within the anterior region of the intestine (8, 9), actively seek and infect insect hosts. Once inside the insect, the nematodes regurgitate the bacteria into the hemolymph (8). The bacteria multiply inside the host and release highly virulent toxins (10, 11), resulting the death of the insect death in <48 h. To provide nutrients for both the bacteria and nematodes, the bacteria secrete extracellular enzymes that aid in breaking down insect tissue and also generate essential growth factors for the growth and development of the nematode. The growth and development of *Heterorhabditis* nematodes have an obligate requirement for their specific bacterial symbiont (12). To prevent secondary invaders and putrefaction of the insect carcass, the bacteria release antibiotics (13, 14). After several days of feeding, the nematodes and bacteria reassociate and leave in search of a new insect host.

Based on molecular analysis, the genus *Photorhabdus* is divided into three bacterial species: *Photorhabdus luminescens*, *Photorhabdus temperata*, and *Photorhabdus asymbiotica* (15, 16). Here, we present a draft genome sequence for *P. temperata* strain Meg1, which was isolated from *Heterorhabditis megidis* nematodes (17). This bacterial strain is used to propagate axenic nematodes. The *Heterorhabditis bacteriophora* nematodes grow and reproduce normally on Meg1 bacteria, but the resulting surface-sterilized IJ nematodes do not retain Meg1 bacteria and are therefore axenic (18). Because of this property, we chose *P. temperata* strain Meg1 for sequencing to provide an understanding of its symbiotic association.

The draft genome of *P. temperata* subsp. *temperata* strain Meg1 was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH) using Illumina technology (19) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2000 platform, which generated 44,504,248 reads (260-bp insert size) totaling 4,450.4 Mbp. The Illumina sequence data were assembled using CLC Genomics Workbench (version 6.5.1) and AllPaths-LG (version r41043) (20). The final draft assembly contains 127 contigs, with an N_{50} of 86 kb. The total size of the genome is 4.9 Mbp, and the final assembly is based on 3,841 Mb of Illumina draft data, providing an average 778.9× coverage of the genome.

The high-quality draft genome of *P. temperata* strain Meg1 was resolved to 127 contigs consisting of 4,931,142 bp, with a G+C content of 43.18%. The assembled *P. temperata* strain Meg1 genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (21), and resulted in 4,340 candidate protein-coding genes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JGVH000000000](https://www.ncbi.nlm.nih.gov/nuclink/JGVH000000000). The version described in this paper is version JGVH010000000.

ACKNOWLEDGMENTS

This work was supported in part by USDA NIFA grant 2009-35302-05257 and by the College of Life Science and Agriculture at the University of New Hampshire-Durham. S.G. was supported by the Egyptian Cultural and Educational Bureau, Washington, DC.

REFERENCES

- Boemare N, Givaudan A, Brehelin M, Laumond C. 1997. Symbiosis and pathogenicity of nematode-bacterium complexes. *Symbiosis* 22:21–45.

2. Forst S, Dowds B, Boemare N, Stackebrandt E. 1997. *Xenorhabdus* and *Photorhabdus* spp.: bugs that kill bugs. *Annu. Rev. Microbiol.* 51:47–72. <http://dx.doi.org/10.1146/annurev.micro.51.1.47>.
3. Forst S, Neelson K. 1996. Molecular biology of the symbiotic pathogenic bacteria *Xenorhabdus* spp. and *Photorhabdus* spp. *Microbiol. Rev.* 60: 21–43.
4. Goodrich-Blair H, Clarke DJ. 2007. Mutualism and pathogenesis in *Xenorhabdus* and *Photorhabdus*: two roads to the same destination. *Mol. Microbiol.* 64:260–268. <http://dx.doi.org/10.1111/j.1365-2958.2007.05671.x>.
5. Clarke DJ. 2008. *Photorhabdus*: a model for the analysis of pathogenicity and mutualism. *Cell. Microbiol.* 10:2159–2167. <http://dx.doi.org/10.1111/j.1462-5822.2008.01209.x>.
6. Waterfield NR, Ciche T, Clarke D. 2009. *Photorhabdus* and a host of hosts. *Annu. Rev. Microbiol.* 63:557–574. <http://dx.doi.org/10.1146/annurev.micro.091208.073507>.
7. Burnell AM, Stock SP. 2000. *Heterorhabditis*, *Steinernema* and their bacterial symbionts—lethal pathogens of insects. *Nematology* 2:31–42. <http://dx.doi.org/10.1163/156854100508872>.
8. Ciche TA, Ensign JC. 2003. For the insect pathogen *Photorhabdus luminescens*, which end of a nematode is out? *Appl. Environ. Microbiol.* 69: 1890–1897. <http://dx.doi.org/10.1128/AEM.69.4.1890-1897.2003>.
9. Endo BY, Nickle WR. 1991. Ultrastructure of the intestinal epithelium, lumen, and associated bacteria in *Heterorhabditis-bacteriophora*. *J. Helminthol. Soc. Wash.* 58:202–212.
10. Bowen D, Rocheleau TA, Blackburn M, Andreev O, Golubeva E, Bhartiya R, French-Constant RH. 1998. Insecticidal toxins from the bacterium *Photorhabdus luminescens*. *Science* 280:2129–2132. <http://dx.doi.org/10.1126/science.280.5372.2129>.
11. French-Constant RH, Bowen DJ. 2000. Novel insecticidal toxins from nematode-symbiotic bacteria. *Cell. Mol. Life Sci.* 57:828–833. <http://dx.doi.org/10.1007/s000180050044>.
12. Thomas GM, Poinar GO. 1979. *Xenorhabdus* gen. nov., a genus of entomopathogenic, nematophilic bacteria of the family *Enterobacteriaceae*. *Int. J. Syst. Bacteriol.* 29:352–360. <http://dx.doi.org/10.1099/00207713-29-4-352>.
13. Akhurst RJ. 1982. Antibiotic activity of *Xenorhabdus* spp., bacteria symbiotically associated with insect pathogenic nematodes of the families *Heterorhabditidae* and *Steinernematidae*. *J. Gen. Microbiol.* 128:3061–3065.
14. Richardson WH, Schmidt TM, Neelson KH. 1988. Identification of an anthraquinone pigment and a hydroxystilbene antibiotic from *Xenorhabdus luminescens*. *Appl. Environ. Microbiol.* 54:1602–1605.
15. Fischer-Le Saux M, Viillard V, Brunel B, Normand P, Boemare NE. 1999. Polyphasic classification of the genus *Photorhabdus* and proposal of new taxa: *P. luminescens* subsp. *luminescens* subsp. nov., *P. luminescens* subsp. *akhurstii* subsp. nov., *P. luminescens* subsp. *laumondii* subsp. nov., *P. temperata* sp. nov., *P. temperata* subsp. *temperata* subsp. nov. and *P. asymbiotica* sp. nov. *Int. J. Syst. Bacteriol.* 49:1645–1656. <http://dx.doi.org/10.1099/00207713-49-4-1645>.
16. Boemare N. 2002. Interactions between the partners of the entomopathogenic bacterium nematode complexes, *Steinernema-Xenorhabdus* and *Heterorhabditis-Photorhabdus*. *Nematology* 4:601–603. <http://dx.doi.org/10.1163/15685410260438863>.
17. Poinar GO, Jackson T, Klein M. 1987. *Heterorhabditis megidis* sp. n. (*Heterorhabditidae: Rhabditida*), parasitic on Japanese beetle, *Popillia japonica* (*Scarabaeidae: Coleoptera*) in Ohio. *Proc. Helminthol. Soc. Wash.* 54:53–59.
18. Hans RC, Ehlers RU. 1987. Cultivation of axenic *Heterorhabditis* spp. dauer juveniles and their response to non-specific *Photorhabdus luminescens* food signals. *Nematologica* 44:425–435.
19. Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
20. Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Burton JN, Walker BJ, Sharpe T, Hall G, Shea TP, Sykes S, Berlin AM, Aird D, Costello M, Daza R, Williams L, Nicol R, Gnirke A, Nusbaum C, Lander ES, Jaffe DB. 2011. High-quality draft assemblies of mammalian genomes from massively parallel sequence data. *Proc. Natl. Acad. Sci. U. S. A.* 108: 1513–1518. <http://dx.doi.org/10.1073/pnas.1017351108>.
21. Markowitz VM, Korzeniewski F, Palaniappan K, Szeto E, Werner G, Padki A, Zhao XL, Dubchak I, Hugenholtz P, Anderson I, Lykidis A, Mavromatis K, Ivanova N, Kyrpides NC. 2006. The integrated microbial genomes (IMG) system. *Nucleic Acids Res.* 34:D344–D348. <http://dx.doi.org/10.1093/nar/gkj024>.