

University of New Hampshire  
University of New Hampshire Scholars' Repository

---

Molecular, Cellular and Biomedical Sciences  
Scholarship

Molecular, Cellular and Biomedical Sciences

---

3-1-2014

# Draft Genome Sequence of *Photorhabdus luminescens* Strain BA1, an Entomopathogenic Bacterium Isolated from Nematodes Found in Egypt

Shimaa M. Ghazal

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

Sheldon G. Hurst IV

*University of New Hampshire, Durham*

Krystalynne Morris

*University of New Hampshire, Durham*

Feseha Abebe-Akele

*University of New Hampshire, Durham*

W. Kelley Thomas

*University of New Hampshire, Durham, Kelley.Thomas@unh.edu*

*See next page for additional authors*

Follow this and additional works at: [https://scholars.unh.edu/mcbs\\_facpub](https://scholars.unh.edu/mcbs_facpub)

---

## Recommended Citation

Ghazal, S., S.G. Hurst IV, 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 luminescens* strain BA1, an Entomopathogenic Bacterium Isolated from Nematodes Found in Egypt. *Genome Announc.* 2(3):e00396-14. doi:10.1128/genomeA.00396-14.

This Article is brought to you for free and open access by the Molecular, Cellular and Biomedical Sciences at University of New Hampshire Scholars' Repository. It has been accepted for inclusion in Molecular, Cellular and Biomedical Sciences Scholarship by an authorized administrator of University of New Hampshire Scholars' Repository. For more information, please contact [nicole.hentz@unh.edu](mailto:nicole.hentz@unh.edu).

---

**Authors**

Shimaa M. Ghazal, Sheldon G. Hurst IV, Krystalynne Morris, 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 luminescens* Strain BA1, an Entomopathogenic Bacterium Isolated from Nematodes Found in Egypt

Shimaa Ghazal,<sup>a,b</sup> Sheldon G. Hurst IV,<sup>a</sup> Krystalynne Morris,<sup>a</sup> Feseha Abebe-Akele,<sup>a</sup> W. Kelley Thomas,<sup>a</sup> Usama M. Badr,<sup>b</sup> Mona A. Hussein,<sup>c</sup> Mohamed A. AbouZaied,<sup>d</sup> Kamal M. Khalil,<sup>b</sup> Louis S. Tisa<sup>a</sup>

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

***Photorhabdus luminescens* strain BA1 is an entomopathogenic bacterium that forms a symbiotic association with *Heterorhabditis* nematodes. We report here a 5.0-Mbp draft genome sequence for *P. luminescens* strain BA1, with a G+C content of 42.46% and 4,250 candidate protein-coding genes.**

Received 8 April 2014 Accepted 14 April 2014 Published 1 May 2014

**Citation** Ghazal S, Hurst SG, IV, Morris K, Abebe-Akele F, Thomas WK, Badr UM, Hussein MA, AbouZaied MA, Khalil KM, Tisa LS. 2014. Draft genome sequence of *Photorhabdus luminescens* strain BA1, an entomopathogenic bacterium isolated from nematodes found in Egypt. *Genome Announc*. 2(2):e00396-14. doi:10.1128/genomeA.00396-14.

**Copyright** © 2014 Ghazal 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 Louis S. Tisa, louis.tisa@unh.edu.

Members of the genus *Photorhabdus* are Gram-negative motile bioluminescent bacteria that maintain two distinct lifestyles as insect pathogens and as symbionts with 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 nonfeeding third-instar infective stage nematode retains a monoculture of *Photorhabdus* within the anterior region of the intestine (8, 9). The nematodes actively seek and infect insect hosts by entering through natural openings or by burrowing directly through the insect cuticle. Once inside the insect, the nematodes regurgitate the bacteria into the hemolymph (8). The bacteria release highly virulent toxins (10, 11), which results in insect death in <48 h. As the bacteria enter the stationary phase of their growth cycle, they secrete extracellular enzymes that aid in breaking down insect tissue, thereby providing nutrients for both the bacteria and nematodes. The bacteria also generate essential growth factors for nematode growth and development. The growth and development of *Heterorhabditis* nematodes have an obligate requirement for their specific bacterial symbiont (12). The bacteria also release antibiotics to prevent secondary invasion and putrefaction of the insect carcass (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 *Photorhabdus* genus is divided into three bacterial species: *Photorhabdus luminescens*, *Photorhabdus temperata*, and *Photorhabdus asymbiotica* (15, 16). Our understanding of these bacteria has been greatly enhanced by the genome sequencing of two of the three established species: *P. luminescens* TT01 (17) and *P. asymbiotica* ATCC 43949 (18, 19). Recently, draft genomes have been available for *P. asymbiotica*

Kingcliff (20) and *P. temperata* M121 (21). Here, we present a draft genome sequence for *P. luminescens* strain BA1, which was isolated from *Heterorhabditis bacteriophora* (BA1) nematodes found in Egypt (22, 23).

The draft genome of *P. luminescens* BA1 was generated at the Hubbard Genome Center (University of New Hampshire, Durham, NH) using Illumina technology (24) techniques. A standard Illumina shotgun library was constructed and sequenced using the Illumina HiSeq 2000 platform, which generated 41,799,700 reads (260-bp insert size) totaling 4,179.9 Mbp. The Illumina sequence data were assembled using the CLC Genomics Workbench (6.5.1) and AllPaths-LG (version r41043) (25). The final draft assembly contained 114 contigs, with an  $N_{50}$  of 60.9 kb. The total size of the genome is 5.0 Mbp, and the final assembly is based on 3,341 Mb of Illumina draft data, which provided an average  $668.2\times$  coverage of the genome.

The high-quality draft genome of *P. luminescens* strain BA1 was resolved to 114 contigs consisting of 5,004,588 bp, with a G+C content of 42.46%. The assembled *P. luminescens* BA1 genome was annotated via the Integrated Microbial Genomes (IMG) platform developed by the Joint Genome Institute, Walnut Creek, CA, USA (26), and resulted in 4,250 candidate protein-coding genes.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JFGV00000000. The version described in this paper is version JFGV01000000.

## 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.
- 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>.
- Forst S, Neelson K. 1996. Molecular biology of the symbiotic-pathogenic bacteria *Xenorhabdus* spp. and *Photorhabdus* spp. *Microbiol. Rev.* 60: 21–43.
- 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>.
- 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>.
- 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>.
- 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>.
- 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>.
- Endo BY, Nickle WR. 1991. Ultrastructure of the intestinal epithelium, lumen, and associated bacteria in *Heterorhabditis-bacteriophora*. *J. Helminthol. Soc. Wash.* 58:202–212.
- Bowen D, Rocheleau TA, Blackburn M, Andreev O, Golubeva E, Bhartiya R, Ffrench-Constant RH. 1998. Insecticidal toxins from the bacterium *Photorhabdus luminescens*. *Science* 280:2129–2132. <http://dx.doi.org/10.1126/science.280.5372.2129>.
- Ffrench-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>.
- 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>.
- 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.
- 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.
- Fischer-Le Saux M, Viallard 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(Pt 4):1645–1656. <http://dx.doi.org/10.1099/00207713-49-4-1645>.
- 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>.
- Duchaud E, Rusniok C, Frangeul L, Buchrieser C, Givaudan A, Taourit S, Bocs S, Boursaux-Eude C, Chandler M, Charles JF, Dassa E, Derose R, Derzelle S, Freyssinet G, Gaudriault S, Médigue C, Lanois A, Powell K, Siguier P, Vincent R, Wingate V, Zouine M, Glaser P, Boemare N, Danchin A, Kunst F. 2003. The genome sequence of the entomopathogenic bacterium *Photorhabdus luminescens*. *Nat. Biotechnol.* 21: 1307–1313. <http://dx.doi.org/10.1038/nbt886>.
- Wilkinson P, Waterfield NR, Crossman L, Corton C, Sanchez-Contreras M, Vlisidou I, Barron A, Bignell A, Clark L, Ormond D, Maythar M, Mason N, Smith F, Simmonds M, Churcher C, Harris D, Thompson NR, Quail M, Parkhill J, Ffrench-Constant RH. 2009. Comparative genomics of the emerging human pathogen *Photorhabdus asymbiotica* with the insect pathogen *Photorhabdus luminescens*. *BMC Genomics* 10:302. <http://dx.doi.org/10.1186/1471-2164-10-302>.
- Ffrench-Constant R, Waterfield N, Daborn P, Joyce S, Bennett H, Au C, Dowling A, Boundy S, Reynolds S, Clarke D. 2003. *Photorhabdus*: towards a functional genomic analysis of a symbiont and pathogen. *FEMS Microbiol. Rev.* 26:433–456. <http://dx.doi.org/10.1111/j.1574-6976.2003.tb00625.x>.
- Wilkinson P, Paszkiewicz K, Moorhouse A, Szubert JM, Beatson S, Gerrard J, Waterfield NR, Ffrench-Constant RH. 2010. New plasmids and putative virulence factors from the draft genome of an Australian clinical isolate of *Photorhabdus asymbiotica*. *FEMS Microbiol. Lett.* 309: 136–143. <http://dx.doi.org/10.1111/j.1574-6968.2010.02030.x>.
- Park GS, Khan AR, Hong SJ, Jang EK, Ullah I, Jung BK, Choi J, Yoo NK, Park KJ, Shin JH. 2013. Draft genome sequence of entomopathogenic bacterium *Photorhabdus temperata* strain M1021, isolated from nematodes. *Genome Announc.* 1(5):e00747-13. <http://dx.doi.org/10.1128/genomeA.00747-13>.
- Hussein MA, Abou El-Soud AB. 2006. Isolation and characterization of two *Heterorhabditids* and one *Steinernematid* nematodes from Egypt. *Int. J. Nematol.* 16:7–12.
- Hussein MA, Abdel-Aty MA. 2012. Formulation of two native entomopathogenic nematodes at room temperature. *JBiopest.* 5(Suppl): 23–27.
- Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <http://dx.doi.org/10.1517/14622416.5.4.433>.
- 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>.
- 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>.