

# Draft Genome Sequence and Annotation of the Insect Pathogenic Bacterium *Xenorhabdus nematophila* Strain C2-3, Isolated from Nematode *Steinernema carpocapsae* in the Republic of Korea

Sung-Jun Hong, Ihsan Ullah, Gun-Seok Park, Byung Kwon Jung, JungBae Choi, Abdur Rahim Khan, Min-Chul Kim, Jae-Ho Shin

School of Applied Biosciences, Kyungpook National University, Daegu, Republic of Korea

***Xenorhabdus nematophila* strain C2-3, which belongs to the family *Enterobacteriaceae*, was isolated from entomopathogenic nematodes collected in the Republic of Korea. Herein, we report a 4.38-Mbp draft genome sequence of *X. nematophila* strain C2-3, with a 43.6% G+C content. The RAST annotation analysis revealed 4,994 protein-coding sequences in the draft genome.**

Received 23 December 2014 Accepted 30 December 2014 Published 12 February 2015

**Citation** Hong S-J, Ullah I, Park G-S, Jung BK, Choi J, Khan AR, Kim M-C, Shin J-H. 2015. Draft genome sequence and annotation of the insect pathogenic bacterium *Xenorhabdus nematophila* strain C2-3, isolated from nematode *Steinernema carpocapsae* in the Republic of Korea. *Genome Announc* 3(1):e01521-14. doi:10.1128/genomeA.01521-14.

**Copyright** © 2015 Hong et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Jae-Ho Shin, jhshin@knu.ac.kr.

*Xenorhabdus* spp. are *Enterobacteriaceae*, symbiotic bacteria associated with soil nematodes such as *Steinernematidae* and *Heterorhabditidae* spp. (1). Entomopathogenic bacteria symbiotically associated with nematodes are of great interest as biocontrol agents against insect pests (2, 3). *Xenorhabdus* spp. are virulent pathogens synthesizing proteins and other secondary metabolites, such as benzylidenacetone, iodinine, phenethylamides, xenorhabdins, xenoroxides, and xenocoumamins, involved in pathogenicity against a wide range of insects (4). Previous studies have revealed numerous secondary metabolic activities, e.g., antibacterial activity, antifungal activity, insecticidal activity, and cytotoxicity, investigated in other *Xenorhabdus* strains (5).

In the present study, bacterial strain C2-3 was isolated from nematodes collected in the Republic of Korea. The strain was identified through 16S rRNA sequence comparison, which revealed 99.8% sequence similarity with *Xenorhabdus nematophila* ATCC 19061, and it was therefore named *Xenorhabdus nematophila* strain C2-3. Moreover, the identification was confirmed via average nucleotide identity (ANI) values (6). The whole-genome sequence of the C2-3 strain showed 98.9%, 81.9%, 80.8%, and 79.7% ANI values for *X. nematophila* ATCC 19061 (1), *X. szentirmaii* DSM16338 (7), and *X. bovienii* SS-2004 (1), respectively.

The newly identified strain C2-3 was subjected to draft genome sequencing to investigate the presence of insecticidal toxins, secondary metabolites, and antimicrobial compounds. The genomic DNA from *X. nematophila* C2-3 was extracted using a QIAamp DNA minikit (Qiagen, Hilden, Germany), and the whole genome was sequenced with the Ion Torrent PGM sequencer (Thermo Scientific, Bremen, Germany), using the 316 v2 chip sequencing protocol. A total of 3,310,612 reads were generated, with a mean length 272 bp. The draft genome sequence was assembled *de novo* using MIRA assembler version 4.0, which generated 284 contigs (500 bp or more), with an  $N_{50}$  contig length of 48,919 bp. The draft genome sequence consists of 4,386,383 bp, with 60-fold genome coverage having approximately 43.6% G+C content.

Subsequent to the assembly, the contigs were submitted to the

RAST annotation server (<http://rast.nmpdr.org>) for subsystem classification and functional annotation (8). The annotation results revealed 4,994 predicted coding sequences, including 67 tRNAs, 32 rRNAs, and 4 noncoding RNAs. In addition, there were two complexes, *xptA1/xptB1/xptC1* and *xptA2/xptB1/xptC1* (9, 10). These toxin complexes have 47% to 53% amino acid sequence similarity with that of the toxin complex (TC) protein of *P. luminescens* (11). Moreover, the *xptA1* gene encoding central insecticidal toxin, as well as *xptB1* and *xptC1* genes encoding toxicity enhancer proteins (10), were clustered.

In addition, an antimicrobial gene cluster identified as *xcnA-N* and related to xenocoumamin production (12) was also revealed. Based on the annotation results, we presume that the genome sequence of *X. nematophila* strain C2-3 will lead to the discovery of useful genes and gene products for environmentally friendly agriculture applications.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JRJV000000000](https://www.ncbi.nlm.nih.gov/nuclot/JRJV000000000). The version described in this paper is version JRJV01000000.

## ACKNOWLEDGMENT

This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF), funded by the Ministry of Education (NRF-2013R1A1A2010298).

## REFERENCES

1. Chaston JM, Suen G, Tucker SL, Andersen AW, Bhasin A, Bode E, Bode HB, Brachmann AO, Cowles CE, Cowles KN, Darby C, de Léon L, Drace K, Du Z, Givaudan A, Herbert Tran EE, Jewell KA, Knack JJ, Krasomil-Osterfeld KC, Kukor R, Lanois A, Latreille P, Leimgruber NK, Lipke CM, Liu R, Lu X, Martens EC, Marri PR, Médigue C, Menard ML, Miller NM, Morales-Soto N, Norton S, Ogier J-C, Orchard SS, Park D, Park Y, Qurollo BA, Sugar DR, Richards GR, Rouy Z, Slominski B, Slominski K, Snyder H, Tjaden BC, van der Hoeven R, Welch RD, Wheeler C, Xiang B, Barbazuk B. 2011. The entomopathogenic bacterial endosymbionts *Xenorhabdus* and *Photorhabdus*: conver-

- gent lifestyles from divergent genomes. PLoS One 6:e27909. <http://dx.doi.org/10.1371/journal.pone.0027909>.
2. Kaya HK, Gaugler R. 1993. Entomopathogenic nematodes. Annu Rev Entomol 38:181–206. <http://dx.doi.org/10.1146/annurev.en.38.010193.001145>.
  3. Ehlers R-U. 2001. Mass production of entomopathogenic nematodes for plant protection. Appl Microbiol Biotechnol 56:623–633. <http://dx.doi.org/10.1007/s002530100711>.
  4. Bode HB. 2009. Entomopathogenic bacteria as a source of secondary metabolites. Curr Opin Chem Biol 13:224–230. <http://dx.doi.org/10.1016/j.cbpa.2009.02.037>.
  5. Brachmann AO, Bode HB. 2013. Identification and bioanalysis of natural products from insect symbionts and pathogens. Adv Biochem Eng Biotechnol 135:123–155. [http://dx.doi.org/10.1007/10\\_2013\\_192](http://dx.doi.org/10.1007/10_2013_192).
  6. Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. Int J Syst Evol Microbiol 57: 81–91. <http://dx.doi.org/10.1099/ijs.0.64483-0>.
  7. Gualtieri M, Ogier J-C, Pagès S, Givaudan A, Gaudriault S. 2014. Draft genome sequence and annotation of the entomopathogenic bacterium *Xenorhabdus szentirmaii* strain dsm16338. Genome Announc 2(2): e00190–14. <http://dx.doi.org/10.1128/genomeA.00190-14>.
  8. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
  9. Morgan JAW, Sergeant M, Ellis D, Ousley M, Jarrett P. 2001. Sequence analysis of insecticidal genes from *Xenorhabdus nematophilus* PMFI296. Appl Environ Microbiol 67:2062–2069. <http://dx.doi.org/10.1128/AEM.67.5.2062-2069.2001>.
  10. Sergeant M, Jarrett P, Ousley M, Morgan JA. 2003. Interactions of insecticidal toxin gene products from *Xenorhabdus nematophilus* PMFI296. Appl Environ Microbiol 69:3344–3349. <http://dx.doi.org/10.1128/AEM.69.6.3344-3349.2003>.
  11. Duchaud E, Rusniok C, Frangeul L, Buchrieser C, Givaudan A, Taourit S, Bocs S, Boursaux-Eude C, Chandler M, Charles J-F, Dassa E, Deroose R, Derzelle S, Freyssinet G, Gaudriault S, Médigue C, Lanois A, Powell K, Siguier P, Vincent R. 2003. The genome sequence of the entomopathogenic bacterium *Photorhabdus luminescens*. Nat Biotechnol 21: 1307–1313. <http://dx.doi.org/10.1038/nbt886>.
  12. Park D, Ciezki K, van der Hoeven R, Singh S, Reimer D, Bode HB, Forst S. 2009. Genetic analysis of xenocoumacin antibiotic production in the mutualistic bacterium *Xenorhabdus nematophila*. Mol Microbiol 73: 938–949. <http://dx.doi.org/10.1111/j.1365-2958.2009.06817.x>.