



HAL
open science

Draft genome sequence and annotation of the entomopathogenic bacterium *Xenorhabdus nematophila* strain F1

Anne Lanois, Jean-Claude Ogier, Jerome Gouzy, Christine Laroui, Zoé Rouy, Alain Givaudan, Sophie Gaudriault

► To cite this version:

Anne Lanois, Jean-Claude Ogier, Jerome Gouzy, Christine Laroui, Zoé Rouy, et al.. Draft genome sequence and annotation of the entomopathogenic bacterium *Xenorhabdus nematophila* strain F1. *Genome Announcements*, 2013, 1 (3), 10.1128/genomeA.00342-13 . hal-01837259

HAL Id: hal-01837259

<https://hal.science/hal-01837259>

Submitted on 9 Jun 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

Draft Genome Sequence and Annotation of the Entomopathogenic Bacterium *Xenorhabdus nematophila* Strain F1

Anne Lanois,^{a,b} Jean-Claude Ogier,^{a,b} Jérôme Gouzy,^c Christine Laroui,^{a,b} Zoé Rouy,^d Alain Givaudan,^{a,b} Sophie Gaudriault^{a,b}

Diversité, Génomique et Interactions Microorganismes-Insectes (DGIMI) Institut National de la Recherche Agronomique, Montpellier, France^a; Diversité, Génomique et Interactions Microorganismes-Insectes (DGIMI), Université Montpellier 2, Montpellier, France^b; Laboratoire des Interactions Plantes Microorganismes (LIPM)–UMR441/2954 Institut National de la Recherche Agronomique, Centre National de la Recherche Scientifique, Castanet Tolosan, France^c; CEA, Genoscope, CNRS-UMR 8030, Laboratoire d'Analyse Bioinformatique en Génomique et Métabolisme, Evry, France^d

We report the 4.3-Mb genome sequence of *Xenorhabdus nematophila* strain F1, a Gram-negative bacterium that is a symbiont of the entomopathogenic nematode *Steinernema carpocapsae* and pathogenic by direct injection for a wide variety of insects.

Received 26 April 2013 Accepted 8 May 2013 Published 20 June 2013

Citation Lanois A, Ogier J-C, Gouzy J, Laroui C, Rouy Z, Givaudan A, Gaudriault S. 2013. Draft genome sequence and annotation of the entomopathogenic bacterium *Xenorhabdus nematophila* strain F1. *Genome Announc.* 1(3):e00342-13. doi:10.1128/genomeA.00342-13.

Copyright © 2013 Lanois 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 Sophie Gaudriault, sgaudriault@univ-montp2.fr.

The *Xenorhabdus* genus belongs to the *Enterobacteriaceae* family (1). It contains species that are symbionts of nematodes of the family *Steinernematidae*, pathogenic for a wide variety of insects. The entomopathogenic nematodes are used as effective biological control agents for soil-inhabiting insects and they have been commercially available since the 1970s (2). Bacteria alone may also be pathogenic for insects. The entomopathogenic bacteria are good models for deciphering both pathogenic and mutualistic interaction with invertebrates. The studies of the molecular mechanisms governing host-bacterium interactions are mainly achieved in the *Xenorhabdus nematophila* species (1, 3). The genome of the type strain *X. nematophila* ATCC 19061, isolated from an American (United States) nematode *Steinernema carpocapsae*, has been recently sequenced and analyzed (4–6). The *X. nematophila* strain F1, isolated from the nematode *Steinernema carpocapsae* “Plou-gastel” from Brittany, France, was also highly genetically documented (for example, see references 7–17), but no genomic data were available. Therefore, we sequenced the genome of this highly studied strain.

The genomic DNA of *X. nematophila* strain F1 was purified from our laboratory stock according to the method of Brenner et al. (18). Sequencing with the Illumina HiSeq 2000 sequencer resulted in 24,259,054 single-end reads with a length of 36 nucleotides (performed by Montpellier MGX genomics, Montpellier, France) and in 60,622,006 mate-pair reads of a 3-kb insert size library with a length of 50 nucleotides (performed by GATC Biotech AG, Konstanz, Germany). Single-end reads were contiged using SOAPdenovo 1.05 (19), and then contigs were scaffolded with LYNX (J. Gouzy, unpublished data) by utilizing mate-pair information. Final assembly consisted of 61 scaffolds with 351 contigs comprising a total length of 4.3 Mb (4.2 Mb without undetermined bases). The assembly has an N_{50} scaffold size of 401,015 nucleotides and a GC content of 43.64%. Functional annotation was carried out using tools of the MicroScope platform (20), and the annotated genome was implemented in the public *XenorhabduScope* database (<https://www.genoscope.cns.fr/agc/microscope/home/index.php>). The assembly contains 4,325

genomic objects, among which are 4,245 coding sequences, 3 rRNA genes, 47 tRNA genes, and 30 noncoding RNAs.

3,716 coding sequences (CDS) (88% of the whole CDS) of the *X. nematophila* F1 genome are also present in *X. nematophila* ATCC 19061 and are considered the *X. nematophila* species core genome. Among the 529 CDS specific to *X. nematophila* F1, 420, 45, and 3 are annotated as proteins of unknown function, phagic proteins, and transposases, respectively. The remaining CDS are mainly annotated as involved in metabolism, transport, and plasmid mobilization. The genome information provided here will allow for genomic experiments such as RNA-Seq and CHIP-Seq analysis on the *X. nematophila* F1 strain.

Nucleotide sequence accession numbers. This whole-genome sequence of *Xenorhabdus nematophila* strain F1 has been deposited at the European Nucleotide Archive under the accession number [CAVM000000000](https://www.ebi.ac.uk/ena/submit/). The version described is accession no. [CAVM000000000.1](https://www.ebi.ac.uk/ena/submit/).

ACKNOWLEDGMENT

This work was supported by INRA grant number SPE2011_1333_03.

REFERENCES

1. Nielsen-LeRoux C, Gaudriault S, Ramarao N, Lereclus D, Givaudan A. 2012. How the insect pathogen bacteria *Bacillus thuringiensis* and *Xenorhabdus/Photorhabdus* occupy their hosts. *Curr. Opin. Microbiol.* 15: 220–231.
2. Ehlers RU. 2001. Mass production of entomopathogenic nematodes for plant protection. *Appl. Microbiol. Biotechnol.* 56:623–633.
3. Richards GR, Goodrich-Blair H. 2009. Masters of conquest and pillage: *Xenorhabdus nematophila* global regulators control transitions from virulence to nutrient acquisition. *Cell. Microbiol.* 11:1025–1033.
4. Latreille P, Norton S, Goldman BS, Henkhaus J, Miller N, Barbazuk B, Bode HB, Darby C, Du Z, Forst S, Gaudriault S, Goodner B, Goodrich-Blair H, Slater S. 2007. Optical mapping as a routine tool for bacterial genome sequence finishing. *BMC Genomics* 8:321.
5. Ogier J-C, Calteau A, Forst S, Goodrich-Blair H, Roche D, Rouy Z, Suen G, Zumbihl R, Givaudan A, Tailliez P, Médigue C, Gaudriault S. 2010. Units of plasticity in bacterial genomes: new insight from the comparative genomics of two bacteria interacting with invertebrates, *Photorhabdus* and *Xenorhabdus*. *BMC Genomics* 11:568.

6. 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, Quorollo 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, Gaudriault S, Goodner B, Slater SC, Forst S, Goldman BS, Goodrich-Blair H. 2011. The entomopathogenic bacterial endosymbionts *Xenorhabdus* and *Photorhabdus*: convergent lifestyles from divergent genomes. *PLoS One* 6:e27909.
7. Givaudan A, Lanois A, Boemare N. 1996. Cloning and nucleotide sequence of a flagellin encoding genetic locus from *Xenorhabdus nematophilus*: phase variation leads to differential transcription of two flagellar genes (fliCD). *Gene* 183:243–253.
8. Thaler JO, Duvic B, Givaudan A, Boemare N. 1998. Isolation and entomotoxic properties of the *Xenorhabdus nematophilus* F1 lecithinase. *Appl. Environ. Microbiol.* 64:2367–2373.
9. Givaudan A, Lanois A. 2000. flhDC, the flagellar master operon of *Xenorhabdus nematophilus*: requirement for motility, lipolysis, extracellular hemolysis, and full virulence in insects. *J. Bacteriol.* 182:107–115.
10. Volgyi A, Fodor A, Forst S. 2000. Inactivation of a novel gene produces a phenotypic variant cell and affects the symbiotic behavior of *Xenorhabdus nematophilus*. *Appl. Environ. Microbiol.* 66:1622–1628.
11. Brillard J, Ribeiro C, Boemare N, Brehélin M, Givaudan A. 2001. Two distinct hemolytic activities in *Xenorhabdus nematophila* are active against immunocompetent insect cells. *Appl. Environ. Microbiol.* 67:2515–2525.
12. Sicard M, Brugirard-Ricaud K, Pagès S, Lanois A, Boemare NE, Brehélin M, Givaudan A. 2004. Stages of infection during the tripartite interaction between *Xenorhabdus nematophila*, its nematode vector, and insect hosts. *Appl. Environ. Microbiol.* 70:6473–6480.
13. Goetsch M, Owen H, Goldman B, Forst S. 2006. Analysis of the PixA inclusion body protein of *Xenorhabdus nematophila*. *J. Bacteriol.* 188:2706–2710.
14. Vigneux F, Zumbihl R, Jubelin G, Ribeiro C, Poncet J, Baghdiguian S, Givaudan A, Brehélin M. 2007. The xaxAB genes encoding a new apoptotic toxin from the insect pathogen *Xenorhabdus nematophila* are present in plant and human pathogens. *J. Biol. Chem.* 282:9571–9580.
15. Lanois A, Jubelin G, Givaudan A. 2008. FliZ, a flagellar regulator, is at the crossroads between motility, haemolysin expression and virulence in the insect pathogenic bacterium *Xenorhabdus*. *Mol. Microbiol.* 68:516–533.
16. Gualtieri M, Aumelas A, Thaler J-O. 2009. Identification of a new antimicrobial lysine-rich cyclolipopeptide family from *Xenorhabdus nematophila*. *J. Antibiot.* 62:295–302.
17. Jubelin G, Pagès S, Lanois A, Boyer M-H, Gaudriault S, Ferdy J-B, Givaudan A. 2011. Studies of the dynamic expression of the *Xenorhabdus* FliAZ regulon reveal atypical iron-dependent regulation of the flagellin and haemolysin genes during insect infection. *Environ. Microbiol.* 13:1271–1284.
18. Brenner DJ, McWhorter AC, Knutson JK, Steigerwalt AG. 1982. *Escherichia vulneris*: a new species of *Enterobacteriaceae* associated with human wounds. *J. Clin. Microbiol.* 15:1133–1140.
19. Li R, Zhu H, Ruan J, Qian W, Fang X, Shi Z, Li Y, Li S, Shan G, Kristiansen K, Li S, Yang H, Wang J, Wang J. 2010. De novo assembly of human genomes with massively parallel short read sequencing. *Genome Res.* 20:265–272.
20. Vallenet D, Belda E, Calteau A, Cruveiller S, Engelen S, Lajus A, Le Fèvre F, Longin C, Mornico D, Roche D, Rouy Z, Salvignol G, Scarpelli C, Thil Smith AA, Weiman M, Médigue C. 2013. Microscope—an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. *Nucleic Acids Res.* 41:D636–D647.