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

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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.

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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 Single-end reads were contiged using SOAPdenovo 1.05 (19), and then contigs were scaffolded with LYNX (J. Gouzy, unpublished data) by utilizing mate-pair information.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/record/CAVM000000000). The version described is accession no. [CAVM000000000.1](https://www.ebi.ac.uk/ena/record/CAVM000000000).

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