



Draft Genomes of *Heterorhabditis bacteriophora* and its symbiont from Southwestern China

Research Note

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Abstract: *Heterorhabditis* nematodes have been widely exploited as effective biological control agents. Their pathogenicity largely relies on their bacterial symbionts. Here we present the genome assemblies and annotations of *Heterorhabditis bacteriophora* and its symbiotic bacterium *Photorhabdus laumondii*, isolated from Yunnan, China, along with comparative genomic analyses against the type strain TT01 from Australia.

Keywords: Bacterial symbiont • Entomopathogenic nematode • *Heterorhabditis bacteriophora* • *Photorhabdus laumondii*

Entomopathogenic nematodes (EPNs), assisted by their mutualistic bacterial symbionts, are obligate insect pathogens in nature, representing a highly-specified tripartite system for studying bacterium–nematode–insect interactions (Dillman et al., 2012, Dillman and Sternberg, 2012). Additionally, *Heterorhabditis bacteriophora* and its symbiotic bacterium *Photorhabdus* sp. exhibit high genetic diversity (Askary, 2010). However, no genome of *H. bacteriophora* or its symbiont has been reported in China to date, hindering evolutionary studies of nematode–bacterial interactions as well as the development of effective control strategies against insect pests.

A new EPN strain was found from a bayberry orchard soil in Qujing, Yunnan, in 2025. Nematodes were isolated via insect baiting method (Bedding and Akhurst, 1975) and extracted using White trap (White, 1927). Through 18S, ITS, 28S and COI sequences and morphological identification, it was determined to be *Heterorhabditis bacteriophora*, named as strain QJ1. Genomic DNA (gDNA) was extracted from about 100,000 surface-sterilized infective juveniles (IJs) using a Takara genomic DNA extracting kit for whole-genome

sequencing. Symbiotic bacteria were isolated from IJs, identified as *Photorhabdus laumondii* by 16S rRNA sequencing, and gDNA was extracted from bacteria grown on Luria-Bertani (LB) medium.

DNA libraries (350 bp) were constructed and sequenced on an Illumina NextSeq 6000 platform (Novogene, China). The genomes were assembled using SPAdes v3.15.5 (Labroo et al., 2021), and contigs with coverage ≤ 7 and length $\leq 1,000$ bp were subsequently removed. The nematode genome was annotated using BRAKER v3.0.8 (Hoff et al., 2019) with RNAseq data (NCBI accession SRR6294671) as extrinsic evidence, while the bacterial genome was annotated using Prokka v1.12 (Seemann, 2014). The completeness of the nematode genome was evaluated with BUSCO v5.5.0 using the *nematoda_odb10* database, and that of the bacterial genome using the *enterobacterales_odb10* database (Simão et al., 2015). OrthoFinder v1.1.4 (Emms and Kelly, 2019) with default settings was used to identify orthologous groups by clustering the proteome of publicly available *H. bacteriophora* and its symbiont strain TT01 (Duchaud et al., 2003, Bai et al., 2013). Putative natural-product biosynthetic gene clusters (BGCs) of the bacterium were predicted by antiSMASH 8.0 (Blin et al., 2025) with default parameters. The assembled genome of *H. bacteriophora* QJ1 consists of

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Table 1. Genome assembly statistics of *Heterorhabditis bacteriophora* strain QJ1 and its symbiosis bacterium *Photorhabdus laumondii*

Assembly	<i>H. bacteriophora</i>	<i>P. laumondii</i>
Number of contig	13,128	128
BUSCO (%)	75.6	99.5
Length of largest contig (kb)	75	253
Total length (Mb)	65.7	5.1
GC content (%)	33.04	42.51
N50 (kb)	7.6	69.7
Number of protein coding gene	14,574	4,387

13,128 contigs totaling 65.7 Mb and contains 14,574 protein-coding genes. The assembled genome has a 75.6% completeness analyzed using BUSCO (S:74.7%, D:0.9%, F:6.7%; Table 1). Although the BUSCO completeness score of QJ1 is lower than that of the type strain TT01 (C:89.3% [S:49.2%, D:40.1%]), the proportion of duplicated BUSCOs in QJ1 is substantially lower, suggesting reduced assembly redundancy and a more collapsed haploid representation. In addition, compared with TT01, QJ1 contains 2,663 (20.3%) strain-specific genes.

The genome size of *P. laumondii* from QJ1 is 5.1 Mb (GC content = 42.5%) with a BUSCO completeness of 99.5% (S:99.3%, D:0.2%, F:0.2%;), and it encodes 4,387 protein-coding genes (Table 1). Among these, 10.7% of the genes are non-orthologous to *P. laumondii* TT01. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis revealed that both *P. laumondii* QJ1 and TT01 have 36 genes involved in bacterial secretion systems (Type I, II, III and VI), of which two are QJ1-specific. In addition, we found that QJ1 contains 7 strain-specific genes that have domains potentially involved in Type VI secretion systems (T6SS).

A comparative analysis of BGCs was performed between *P. laumondii* QJ1 and TT01. A total of 28 BGCs were identified in QJ1, while 26 BGCs were detected in TT01. The two strains shared 21 core BGC types. Notably, QJ1 possessed three BGC types (azole-containing-RiPP, amglyccycl, and arylpolyene) that are absent in TT01.

The genomic sequencing data, genome assemblies, and annotations of *H. bacteriophora* and *P. laumondii* have been deposited in the NCBI database under BioProject accession number PRJNA1417294.

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Author contributions

Y.M. and Z.W. designed the experiments. All authors performed the experiments. Y.M. analysed the data. Y.M., Z.W., and Z.H. wrote and revised the manuscript.

Conflict of interest

The authors declare no competing interests.

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