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Data in Brief

Genome sequences of *Photorhabdus luminescens* strains isolated from entomopathogenic nematodes from southern India

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ABSTRACT

We report here draft whole genome sequences of three novel strains of *Photorhabdus luminescens* of 5.2–5.3 Mbps in size, and with a G + C content of 42.5% (each). Symbiotic γ-proteobacteria belonging to the genera, Photorhabdus (Family: *Enterobacteriaceae*) with their natural vectors, the entomopathogenic nematodes (EPN) (Phylum: *Nematoda*; Order: *Rhabditida*; Family: *Heterorhabditidae*), have emerged as important biological control agents of insect pests, and are capable of production and delivery of diverse compounds to influence host biology [1–3]. Analysis of these genomes is expected to provide enhanced insight into mechanisms of virulence, insecticidal toxin genetic diversity, antibiotic resistance and monoxenicity. The nucleotide sequence information for the three strains NBAII PLHb105, NBAII HiPL101 and NBAII H75HRPL105 has been deposited in NCBI Nucleotide database and is accessible via AZAB00000000, JTHJ00000000 and JXUR00000000 accession numbers respectively.

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Specifications	
Organism/cell line/tissue	*Photorhabdus luminescens NBAII PLHb105, Photorhabdus luminescens NBAII HiPL101, Photorhabdus luminescens NBAII H75HRPL105*
Sex	*N/A*
Sequencer or array type	*Illumina-MiSeq*
Data format	*Analyzed*
Experimental factors	*Cultures isolated from natural hosts, cultured in Galleria mellonella*
Experimental features	*Whole-genome sequences and variants from existing references*
Consent	*N/A*
Sample source location	*Karnataka, India*

1. Direct link to deposited data

Photorhabdus (Family: *Enterobacteriaceae*) with their natural vectors, the entomopathogenic nematodes (EPN) (Phylum: *Nematoda*; Order: *Rhabditida*; Family: *Heterorhabditidae*), have emerged as important biological control agents of insect pests, and are capable of production and delivery of diverse compounds to influence host biology [1–3].

Table 1
Accession numbers, and direct-link URLs to data in this study.

	Photorhabdus luminescens NBAII H75HRPL105	*Photorhabdus luminescens* NBAII HiPL101	*Photorhabdus luminescens* NBAII PLHb105
NCBI accession numbers	AZAB00000000	JTHJ00000000	JXUR00000000
URL	http://www.ncbi.nlm.nih.gov/assembly/GCF_000826725.1/	http://www.ncbi.nlm.nih.gov/assembly/GCA_000798635.1/	http://www.ncbi.nlm.nih.gov/assembly/GCF_000931955.1/

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Table 2
Total raw reads, sequenced base-pairs, N50 value of WGS assembly and SNPs identified from *P. luminescens* NBAII H75HRPL105, *P. luminescens* NBAII HiPL101, and *P. luminescens* NBAII HbPL105. *Sequenced base pairs calculated after trimming of Illumina adapters following FASTQC analysis. N50 values calculated from WGS de novo assemblies using FASTQC-trimmed reads. **Sequence variants called from reference-guided assemblies with all *P. luminescens* strains mapped against *P. luminescens* subsp. *Laumondii* TT01 reference genome (NCBI accession NC_005126.1). SNPs—single nucleotide polymorphism. MNP—multiple nucleotide polymorphism. Indel—insertion and/or deletion mutations.

	Photorhabdus luminescens NBAII H75HRPL105	*Photorhabdus luminescens* NBAII HiPL101	*Photorhabdus luminescens* NBAII HbPL105
Total reads	2,604,823	2,790,255	2,463,266
Total bp*	189,591,052	203,431,557	214,900,170
GC content	42.5%	42.5%	42.5%
N50	22,874	27,588	20,747
Mean contig length	8430	7454	6677
SNPs, MNPs, indels**	639	2179	6549

Raw sequencing reads, and whole-genome shotgun assemblies for three *P. luminescens* strains have been deposited at DDBJ/EMBL/GenBank under the accession numbers provided in Table 1.

Total raw reads, sequenced base-pairs, N50 value of WGS assembly and SNPs identified from P. luminescens NBAII H75HRPL105, P. luminescens NBAII HiPL101, and P. luminescens NBAII HbPL105 have been summarized in Table 2.

2. Experimental design, materials and methods

Photorhabdus luminescens and *Xenorhabdus* sp. are symbiotic bacteria associated with soil-born *Heterorhabditis* and *Steinernema* species of entomopathogenic nematodes. Bacterial cultures were established from isolation in these natural hosts, then cultured in lab hosts *Galleria mellonella*. Finally, pure monoxenic cultures were then grown in LB media. Genomic DNA was then extracted using the Sigma Bacterial Genomic DNA isolation kit. Purity of these isolations was checked with 16s rRNA gene sequences, before they were used for whole genome sequencing. Isolated genomic DNA was then used for sequencing and library preparation using the Illumina MiSeq platform (at Chromous Biotech Ltd., Bengaluru, 560692, Karnataka, India) with paired-end libraries generated for each of the three bacterial genomes. Reads were processed, analyzed and trimmed according to FASTQC to remove Illumina adapter sequences. Trimmed reads were assembled into contigs to capture whole-genome shotgun sequences (WGS) using de novo and reference-guided methods using CLCBio Genomics Workbench v. 7.5. All *P. luminescens* strains were mapped to the reference genome of *P. luminescens laumondii* strain TT01 (NCBI accession NC_005126.1, for reference-guided genome assemblies) using global alignment, and trimmed where base-call confidence was less than 95%. Sequence variants (SNPs, multiple nucleotide polymorphisms and indels) were identified against the reference genome of *P. luminescens* subsp. *Laumondii* TT01 reference genome (NCBI accession NC_005126.1) in CLCBio Genomics Workbench using the following parameters: minimum variant coverage—50, minimum variant count—9, minimum variant frequency—50%, minimum quality score neighborhood radius—13, minimum variant quality score—30, and minimum neighborhood quality score—25. Broken read pairs were also ignored.

We report draft genome sequences of three bacterial strains from India, viz., *P. luminescens* strain NBAII H75HRPL105, *P. luminescens* strain NBAII HiPL101, and, *P. luminescens* strain NBAII PLHb105 isolated from the entomopathogenic nematodes, *Heterorhabditis species* strain NBAII H75HR, *Heterorhabditis indica strain* NBAIIHi101 and *Heterorhabditis bacteriophora* strain NBAII Hb105, respectively.

Conflicts of interest

The authors declare no conflicts of interest.

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