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A draft genome for the entomopathogenic nematode *Heterorhabditis indica*

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Introduction

Heterorhabditis indica is the most prevalent strain of the genus in India and is predominantly found in soils of the tropical regions of the world.

It is also one of the most available commercial entomopathogenic nematodes.

The genome of *H. indica* was sequenced to create a genomic resource to facilitate comparative and functional genomics.

Methodology

H. indica genome sequencing pipeline

Inbred line of *H. indica*, strain H-V
(Inbred for 20 generations)
↓
High molecular weight gDNA (Phenol-Chloroform method)
↓
Genomic libraries: 300 bp, 600 bp, and 5 kb mate pair library
↓
Illumina paired end sequencing
↓
160 Million raw reads→155 Million high quality reads
↓
Assembly and annotation

Results

H. indica genome assembly statistics

Final assembly size	**91.26 Mb**
Genes predicted	**10,974**
Number of scaffolds	**3,538**
N50	**587,367 bp**
Min sequence length	500 bp
Max sequence length	2,409,384 bp
Average sequence length	25,795.12 bp
(A + T)s	57.35%
(G + C)s	35.31%
Ns	7.33%
Complete BUSCOs	**266 (87%)**
Fragmented BUSCOs	15 (4.9%)
Missing BUSCOs	15 (4.9%)

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession JAJAVP000000000. The version described in this paper is version JAJAVP010000000.

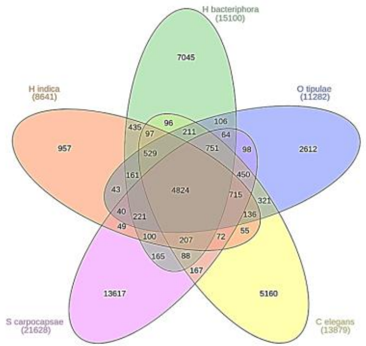

Figure 1. 8,641 orthologous groups were detected in the *H. indica* genome as compared to four other nematode genomes.

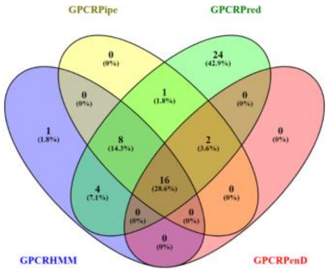

Figure 2. 56 GPCRs were identified in H. indica genome, out of which Rhodopsin-like: 52, Frizzled: 2, Glutamate-like: 1, and Secretin-like: 1

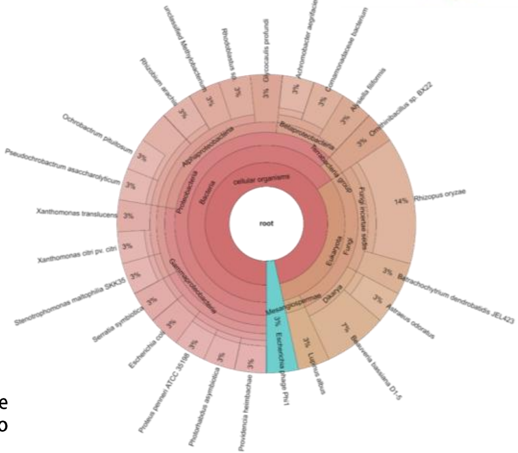

Figure 3. 21 cases of likely HGT were detected in *H. indica* genome by Alienness tool.

In addition, 370 putative secreted proteins, 631 ncRNA, 38 peptidases (1 Aspartic, 2 Threonine, 6 Serine, 7 Cysteine, 18 Metallo peptidases, and 4 peptidase of unknown catalytic type), 31 peptidase inhibitors, 2954 SSRs were also identified in the draft genome of *H. indica*.

Conclusions

High quality draft genome sequence for the entomopathogenic nematode *Heterorhabditis indica* was generated. This will be useful for functional and comparative genomics.

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