

## Radobase – A Database on Burrowing Nematodes Infesting Tropical and Subtropical Crops

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**ABSTRACT:** Burrowing nematodes (*Radopholus* spp.) are endo-parasitic nematodes attacking several commercially important crops in tropics and sub-tropics. They probably are the most important economic nematode pest in the tropics. The objective of the present study was to assemble information on morphology, host range, molecular data and relevant literature pertaining to different species of the genus *Radopholus*, which will be quite helpful to researchers and developmental officials around the world. Details about 26 species of *Radopholus*, presently considered valid, are made available in this database. Features like morphometric comparison and Radoblast will be helpful in comparing and identifying new specimens obtained. This database will help in comparison of different species of *Radopholus* by providing all available resources under a single platform, thus making studies on various species of *Radopholus* simple and easy. The database is freely available on <http://220.227.138.213/radobase/>.

**Keywords:** Burrowing nematodes, Database, Plant parasitic nematodes, *Radopholus similis*

Burrowing nematodes constitute an important group of migratory endoparasitic nematodes infecting more than 365 plant species including banana, coconut, arecanut, tea, ginger, pepper, betel vine, turmeric, avocado, coffee, ornamentals, sugarcane and citrus (CABI, 2016). The major species of the genus is *Radopholus similis* with two host races that differ in their parasitism of citrus. Infection by burrowing nematode causes several diseases like toppling-over disease in banana, yellows disease in pepper and spreading decline in citrus. Because of the damage it causes worldwide, it is on the list of quarantined pests in many countries.

*R. similis* is found worldwide in tropical and subtropical areas of Africa, Asia, Australia, North and South America and many island regions (Sekora and Crow, 2002), and is considered one of the 10 most damaging plant-parasitic nematodes worldwide (Sasser and Freckman, 1987; Jones et al., 2013). The widespread distribution of this nematode is mainly due to its dissemination with propagative plant materials like infected banana/corns/rhizome/suckers. Besides, management of this nematode is a difficult task as they infect mainly

perennial crops. Of late several new species of this nematode are being reported (Stanton et al., 2001; Nguyen et al., 2003; Trinh et al., 2004). Therefore the detection, description and identification of this economically important nematode group is highly relevant to both practical nematology and quarantine departments around the world.

*Radopholus* at present encompasses 51 original descriptions but the number of valid species varies according to different authors since some species have been synonymised or transferred to other taxa after their discovery (Duncan and Moens, 2006). Besides information on this species is at present scattered across various resources and repositories, making research on the genus immensely difficult. Therefore, the main aim of the present study was to assemble scattered information on the genus *Radopholus*, such as morphology, host preference, existing sequence data and accessible literatures under a single platform. This interactive, searchable database will also help in diagnosing different species of *Radopholus* by comparing their/morphological or molecular features.

## MATERIALS AND METHODS

Morphology of all the valid species was collected by scanning published literature. Host status of various plants was compiled from literature as well as Goodey (1965). The molecular data was downloaded from NCBI's GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>). The collected information was organized as an online relational database and a web application,

which helps users to quickly access the desired information using an interactive web-based user interface. The front end is developed using Hypertext Markup Language (HTML), cascading style sheets (CSS), JavaScript and jQuery. At the backend PHP 5.2.11 (<http://www.php.net/>) is used for server side scripting and MySQL (<http://www.mysql.com/>) is used as the Database Management System (DBMS). The database schema of Radobase is shown in Fig. 1.

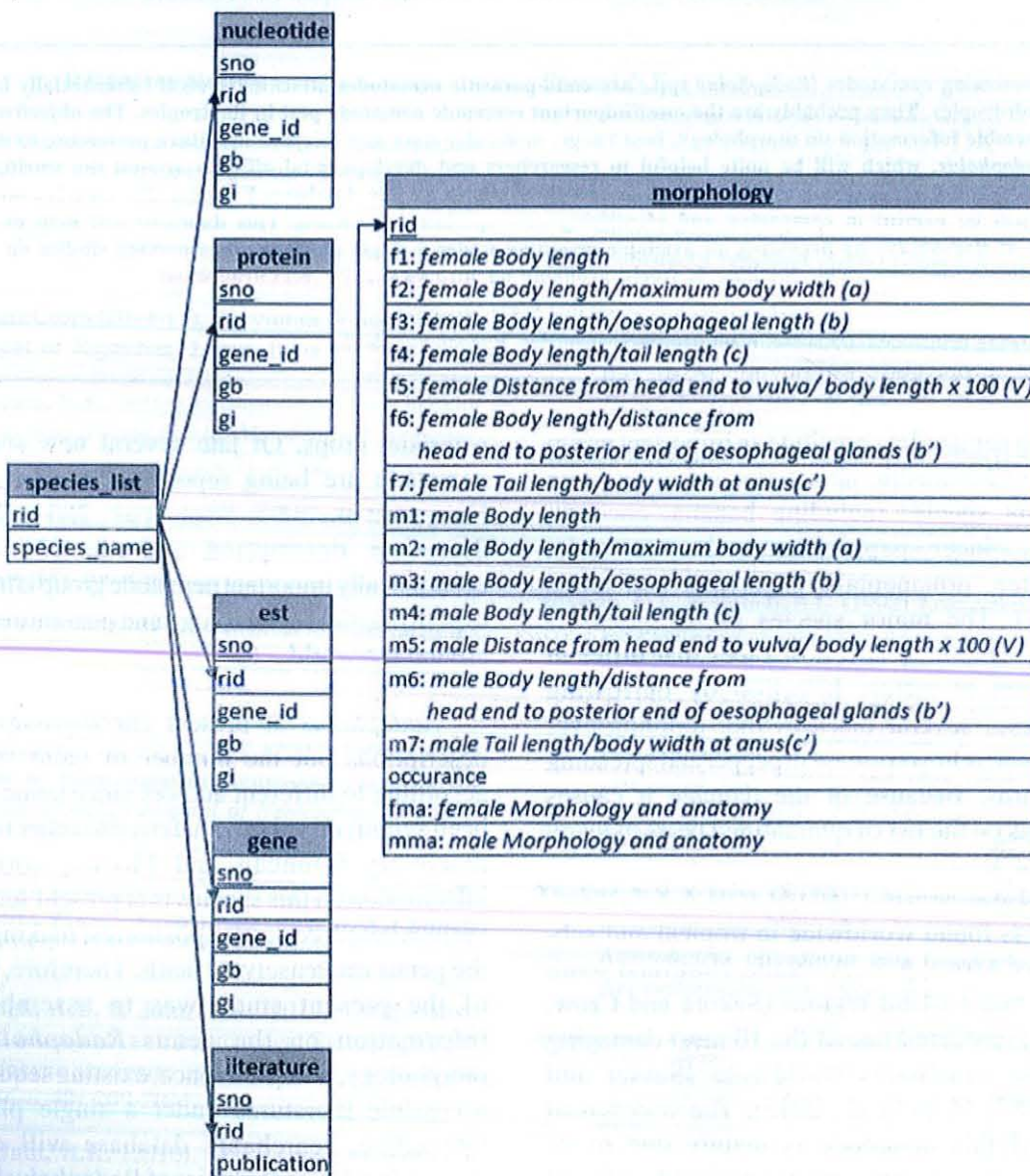


Fig. 1. Database schema of Radobase. Underlined attribute denotes the primary key of particular table and arrow shows relationship between primary key and foreign key

The application integrates standalone blast – blast-2.2.31+, from NCBI, as an additional feature, for easy sequence comparison. Blast comparison is locally performed with default parameters. The blast performs its similarity search with the available sequences of the genus *Radopholus* stored as a backend database in Radobase. The output obtained will be in tabular format and contains information about the sequences against which match is found, like the sequence ID, percentage of identity, length of matched sequence, mismatch, gap opening score, query start, query end, sequence start, sequence end, e-value and bit scores.

## RESULTS AND DISCUSSION

Radobase provides an interactive user interface which is quite user friendly (Fig. 2). The home page contains a brief introduction about the database and a

search option which helps the user to search about various *Radopholus* species using the species name. The navigation bar in the database helps the user to browse between various pages. ‘Species available’ link provides the list of available *Radopholus* species and from this, the user can select a particular *Radopholus* species which in turn provides its details like morphology, sequences (EST, Protein, Nucleotide, Gene Segments), host range and various literature. Sequence details are available in GenBank and FASTA formats. ‘Morphometric Comparison’ feature helps the user to compare the morphological characteristics of a minimum of any two species or more. The morphometric comparison would help in quickly identifying and distinguishing new specimens based on morphological features. ‘Nematology @ IISR’ briefly tells about various research activities on *Radopholus* species which are being conducted in ICAR-IISR.

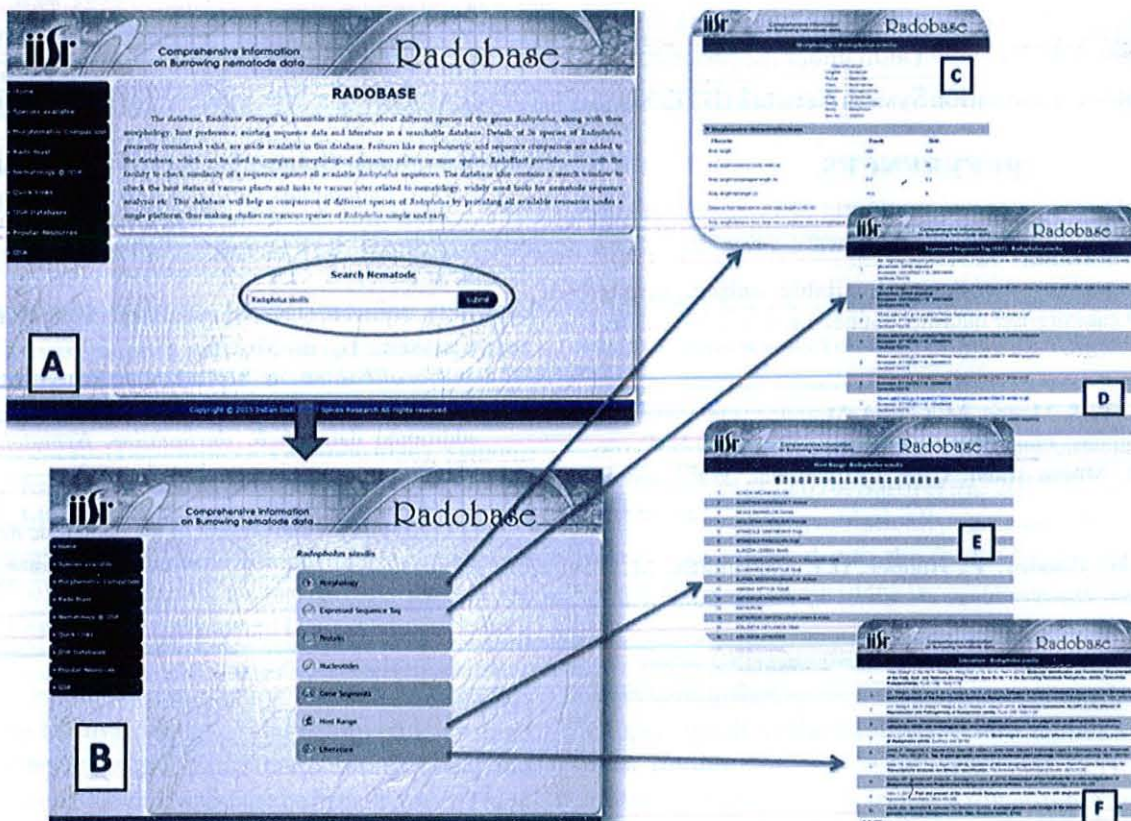


Fig. 2. Radobase web interface. (A) Radobase home page, contains a search option. By typing the species name e.g. *Radopholus similis* the user is presented (B) with a list of features such as information on morphology, host preference, existing sequence data and literature. Each of the feature can be opened into a new window that provides additional details, explaining them further (C, D, E, F).

Local BLAST is incorporated with the name Radoblast to calculate the sequence similarity of a given sequence to all the available *Radopholus* sequences available in Radobase. 'Quick Links' and 'Popular resources' provides a list of useful websites and tools which are related to this database.

This database will help to compare of different species of *Radopholus* by providing all available resources under a single platform, thus making studies on various species of *Radopholus* simple and easy. The database is freely available on <http://220.227.138.213/radobase/>. Any additional information on this nematode and suggestions for improvement can be sent to [disc@spices.res.in](mailto:disc@spices.res.in).

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