PPNEMA: a database of the RNA cistron from Plant Parasitic nematodes.

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Motivation

Plant parasitic nematodes are an important pest of crop plants world wide and among the most difficult animals to identify [1,2]. Currently, their identification based on sequences of the nuclear ribosomal DNA (rDNA) cistron (18S, 28S and 5.8S RNA genes, and the Internal Transcribed Spacers (ITS1 and ITS2)) is becoming a popular tool. Each rDNA repeating cistron [3] is arranged as follows: an external non coding region (ETS), a small ribosomal subunit (18S gene), an internal transcribed spacer 1 (ITS1), the 5.8S gene, a another internal transcribed spacer 2 (ITS2), a large ribosomal subunit (28S gene) and finally an intergenic spacer region (IGS).

The sequences from the cistron are now used to classify the identity of isolates from different hosts by applying molecular approaches and to unravel the relationships of cryptic and complex species that suffer from confused published taxonomy.

Furthermore, the availability of RNA sequences allows phylogenetic relationships between nematodes to be studied - a study oriented not only toward taxonomy, but also toward a more complete understanding of their biology as agricultural pests.

Here we present the PPNEMA database storing the Ribosomal Cistron sequences from different species of plant parasitic nematodes grouped according to nematode genera.

Methods

PPNEMA is a bioinformatic platform allowing the storage, query and analysis of phytoparasites rDNA sequences. It is available on the web at http://www.ppnema.uniba.it. Each sequence in the PPNEMA database related to a fragment of one of the ribosomal RNA genes for a single isolate within a nematode species is identified by a code defining species and function. The sequences derived from the different nematode species are multi-aligned within each nematode genus.

However, since not all the sequences span the entire rDNA array, separate multi-alignments of the sequences have been produced for single rRNA genes or for portions of the same gene separately, depending upon the availability of the sequences. Thus, each entry in the database is related to a species-specific functional element. More entries are associated in a group. More groups are available for the same genus and the same functional element. Phylogenetic data and dating are not reported at present in the PPNEMA database since paleontologic information is missing and the only functional element that remains constant indifferent genera is 18S [4], for which the feasibility of construction of phylogenetic trees will be evaluated. The database is physically based on the SQLite DBMS, while the web application is based on an application framework written in Python. At present PPNEMA reports 2409 entries for a total of 26 genera and 405 species grouped in 208 multialignments.

Results

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Availability: http://www.ppnema.uniba.it
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