NEW TOOL TO SUPPORT THE IDENTIFICATION OF *Ditylenchus* SPECIES, BASED ON COMPUTER SCIENCE

Vandor R.V. Rissoli[1]; Túlio O. Santos[2]; Juvenil E. Cares[3]; Vilmar Gonzaga[4] & Renata C.V. Tenente[4]

[1]Universidade Católica de Brasília, vandor@ucb.br
[2]Scholarship of Embrapa tulios@cenargen.embrapa.br
[3]Universidade de Brasília, cares@unb.br
[4] Embrapa Recursos Genéticos e Biotecnologia, renata@cenargen.embrapa.br

INTRODUCTION

The Genus *Ditylenchus compound injurious* species that are of quarantine and economically important to Brazil and other countries (see Figures A and B). This group is quite difficult to identify specially the phytopathogenic species, which are closely related. Therefore, the collaboration work between Embrapa and Brasilia Catholic University aim to do research which would enable a more accurate identification of *Ditylenchus* species.

As there are some difficulties to identify *Ditylenchus* species, both Institutions have been studying to develop a system, which will be used as an identification tool. In this context, computers have been used for identification of species for some **genera**, as cited in the related literature.

Figure A: *Ditylenchus angustus*, symptom in rice; Figure B: *Ditylenchus dipsaci*, anterior part (40 x).

OBJECTIVE

The use of computer resources contributes to accurate and fast systematisation of the nematode identification process and the aim of this work will be to support the nematode identification of *Ditylenchus* species.

MATERIALS AND METHODS

The Computational Systems can give the permission to make simultaneity comparisons of different characters. The *Ditylenchus* genus has one special group of species characters that can be a target of this technique due to their detailed differences, among them the necessary ones for identification based on computational resources. The work started with a bibliographical survey about taxonomy, biology and hosts of the five mainly species of *Ditylenchus*: *D. africanus, D. angustus, D. destructor D. dipsaci* e *D. myceliophagus.*

After morphometric and morphologic informations, obtained through the journals, international database and websites, it was possible to elaborate one dichotomic key. Then, it was made the informatization of this key, where the computer resources were used in development of one capable system that can manipulate one knowledge database with necessary efficacy to identification process.

This **Expert System (ES)** was implemented with using programming language Java, with gives the interested aspects of confidence and robust in this process (See **Figures C and D**) .

RESULTS E DISCUSSION

At present, the **Expert System (ES)** has been access the database of Images of Embrapa Genetic Resources and Biotechnology, offering illustrative morphologic informations, during the necessary interaction of its users. Using this System, it is possible to separate the genus *Ditylenchus* from the others, then if the users have the doubt about the detected genus, this **ES** is capable to give the solution for the question.

The interaction of this **ES** with image database became possible the access approximately, **800 nematode images,** being more than **40 images** of *Ditylenchus* species. In this context, this type of access give the support to **ES** one illustrative and confident base to help its users in a manipulation of system.
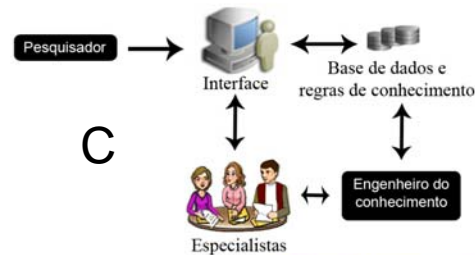

Figure C - Scheme of operation of the Expert System

Figure D - Screens of the system

CONCLUTION

The **Expert System** realizes one planed interference according with the nematologist knowledge that is evolved in the **ES** conception, in direction a correct nematode identification. Therefore, the System can contribute with significant way in the identification of *Ditylenchus* species, being one important tool in support to a difficult purpose.