

# Computerized identification of species of the genus *Radopholus* (Tylenchida: Pratylenchidae)

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**Summary.** A polytomous identification key for 24 species of *Radopholus* was constructed using the computer software packages EXCEL 5.0., spreadsheets and BIKEY 7 (©Lobanov & Dianov, 1994). Specimen identification is based on the principle that the initial set of taxa can be investigated interactively and reduced by different filters (i.e. character states) in several steps of identification. Quantitative characters are best utilised by EXCEL which can filter, using "Autofilter", "Advanced Filter" or "Sort", initial assemblages of taxa by a set of several characters at each step. Conversely, BIKEY has preferences to utilise qualitative characters and uses images during selection of character states, with text explanations providing only an auxiliary aid. This package provides a list of characters, arranged in descending order depending on their diagnostic value (not at random). In constructing the identification key for *Radopholus* it was determined that 20 characters are sufficient to identify the 24 species, with an average identification path of only 5.196 steps. The most important characters are: number of incisures from phasmid to tail terminus, sperm shape, tail terminus shape, tail terminus annulation, relative width of the central band in lateral field, number of cephalic annules, number of incisures in lateral field, and difference in size between the anterior and posterior spermatheca.

**Key words:** *Radopholus*, computerized key, pictorial key, taxonomy.

Rapid and reliable identification of nematode species can be achieved utilising user-friendly computerized keys. Polytomous identification keys are the most effective, and can be relatively easily developed for use as a computerized identification system. Several computerized identification systems have been developed for use in nematology (Boag & Smith, 1983; Fortuner, 1983; Fortuner & Wong, 1984; Rey *et al.*, 1988; Viscardi & Brzeski, 1993, 1996; Robbins & Brown, 1995; Decraemer & Baujard, 1997). The most simple keys utilise the software packages LOTUS and EXCEL 5.0 Spreadsheets (Brown & Robbins, 1995, Decraemer & Baujard, 1997).

Two different approaches were used to construct computerized identification keys for the 24 species in the genus *Radopholus*. These two systems were developed using i) the EXCEL 5.0. Spreadsheet and ii) the BIKEY 7 package (©Lobanov & Dianov, 1994), and both keys are described here.

## Identification in EXCEL 5.0.

The EXCEL 5.0. Spreadsheet system most effectively uses quantitative characters. Here it is proposed to use the "Filter" command for identification of

species. Initially, datasheets are constructed containing morphological/morphometrical data obtained for each species. These are combined to form a data matrix, where the species are rows and the characters are columns. Each character, for each species, has two numerical values, the minimum and maximum.

This provides two columns in the data matrix for each character. These data are readily obtained for quantitative characters, e.g., morphometrics, number of structures, ratios and indices. For qualitative characters, such as shape, it has to be constructed as a row with one direction: e.g., shape of tail terminus can be presented as follows - 1) mucronate, 2) acute, 3) conical, 4) conically rounded, 5) rounded, 6) broadly rounded, 7) hemispherical, 8) truncate. The values of the one-direction row (here, in the tail terminus shape, from 1 to 8) are then used to fill the minimum and maximum columns of the qualitative character for each species.

Data collected from the unidentified specimens, with the name X, are entered into the data matrix. It is not necessary to provide data for all characters as initial identification may be achieved using only part of the key. The identification can continue using

only the characters known for your material. However, the more complete the data set entered for the unidentified specimens the more reliable will be the resultant identification.

When the data are entered the command "Auto-filter" is used (command path: Data-Filter-Auto-filter). Arrows appear at the left side of the columns near the name of each character. The character considered most appropriate for the first step in the identification process is chosen.

The value ranges of the unidentified specimens and those of the most similar valid species may overlap only partially or even only correspond in their minimum (for one species) and maximum (for other species) values. To restrict the group of species, to which the unidentified X-specimens may correspond, two conditions to select valid species from the datasheet can be used:

1) Character minimum  $\leq$  maximum of the same character of the unidentified X-specimens.

2) Character maximum  $\geq$  minimum of the same character of the unidentified X-specimens.

To order the conditions mentioned above, click the arrow of the column with the minimum values of the character. Choose "Custom" line. A frame labelled "Custom AutoFilter" appears. The example shown has the stylet length 12-15  $\mu\text{m}$  for the unidentified specimens. In the upper left window of the frame choose a symbol " $\leq$ ". In the upper right window insert the maximum value for the unidentified specimens, i.e., 15, and click OK. "Filter" produces a set of species that only correspond to this condition.

One then clicks the arrow button near the maximum value of the character. The "Custom Autofilter" frame appears. In the upper left window of the frame one chooses the symbol " $\geq$ ". In the upper right window insert the minimum value for X, i.e. 12, the click OK or press the <Enter> button on the keyboard. A restricted set of species is provided with ranges corresponding to the range of the chosen character of the unidentified X population. The first step of identification is completed. To continue with the identification process the same procedure is followed for an other character. After several steps one is left with a single or only a few species which correspond to the unidentified specimens. Final identification can then be confirmed by reference to type specimens and/or to the original species description.

One can also use the "Advanced Filter" command for identification. In this instance one enters the ranges of several, or all, of the characters and then the command "Advanced Filter" is applied which filters the datasheet as one operation for all the

chosen characters. The logic of the ordered conditions is the same as described above. Information of the "Advanced Filter" can be obtained in the HELP facility of the EXCEL package.

### Identification in the BIKEY 7 pictorial identification system

BIKEY is the Pictorial Identification System developed in Russia by Lobanov and Dianov (1994). (Fig. 1). BIKEY has own built-in database to operate the different states of each character. The system has the advantage that it operates using qualitative characters. Images are used as the main tools for identification, and text descriptions of characters are provided only as an auxiliary aid.

The system provides the user with a sequence of characters based on their diagnostic value for identification (Fig. 2). The sequence changes at each step of identification. The user may choose any preferred character. By providing the characters, the system automatically minimizes a number of steps in the identification process. The system requires a mouse to operate the identification procedure. When the mouse pointer is placed on the frame with the name of the character in the left side of the screen, a coloured image of the character appears in the large, right window of the screen. (Fig. 2). By simply changing the position of the mouse pointer to the different characters one obtains the images of the different characters (compare the positions of the mouse pointer and the character image in Figs. 2 & 3). The row of characters continues below the screen. The next frame with the name of the character can be seen in the left lower corner of the screen. To move the character row it is necessary to place the mouse pointer on the last frame with the name of the character. To view the explanation provided for the character one clicks the frame with the name of the character. To see the character states it is necessary to click the image of the character. A second screen then appears with the images of the character states (Fig. 4). To see the text accompanying the character state it is necessary to place the mouse pointer on the image of the state of particular interest (Fig. 4). A movable frame appears opposite the chosen image. One clicks the image corresponding to unidentified specimens. Having completed the first step of identification one returns to the first screen and continues the identification process by moving to the next character and repeating the above mentioned operations. A small frame in the lower right corner shows the number of remaining taxa. At each step one can check a list of species filtered by the previous steps. To see the list of the remaining taxa, click this frame.

KEY: RDPHS  
 AUTHOR: Alexander Y. Ryss

Number of incisures at phasmid to tail terminus

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Sperm in spermatheca

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Terminus shape

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Tail terminus

---

Central band of lateral field

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Lip region

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Number of incisures in lateral field

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Key to RADOPHOLUS Thorne, 1949

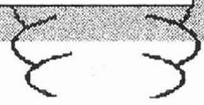
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 Russian Academy of Sciences  
 Zoological Institute, Saint Petersburg

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 Class NEMATODA  
 Order TYLENCHIDA Thorne, 1949  
 Family PRATYLENCHIDAE (Thorne, 1949) Siddiqi, 1963

Genus RADOPHOLUS Thorne, 1949

Thorne, 1949 : 53, - Neoradopholus Khan, Shakil, 1973 : 16-17

Key to 24 valid species of the genus *Radopholus* includes also the closely related *Achlysiella williamsi* (Siddiqi, 1964) Hunt, Bridge et Machon, 1989 (syn. *Radopholus williamsi* Siddiqi, 1964)  
 Closely related *Radopholoides* species are not included in the key.



Remaining taxa: 25

Fig. 1. General information on the pictorial key to *Radopholus*, appearing after clicking in the upper right frame.

KEY: RDPHS  
 AUTHOR: Alexander Y. Ryss

Number of incisures at phasmid to tail terminus

---

Sperm in spermatheca

---

Terminus shape

---

Tail terminus

---

Central band of lateral field

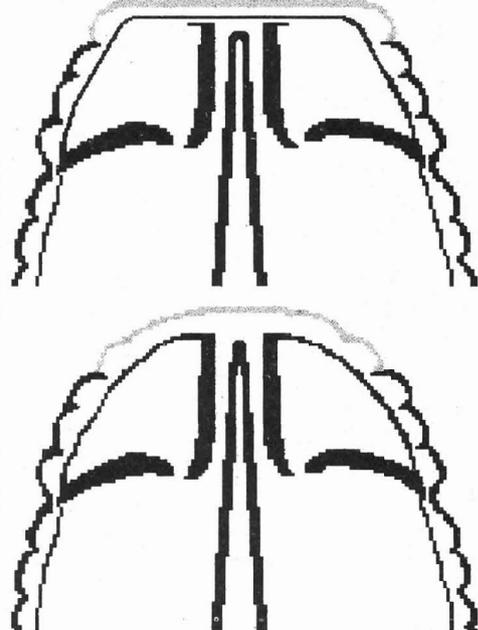
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Lip region

---

Number of incisures in lateral field

---



Remaining taxa: 25

Fig. 2. First screen of the pictorial key to the genus *Radopholus*.

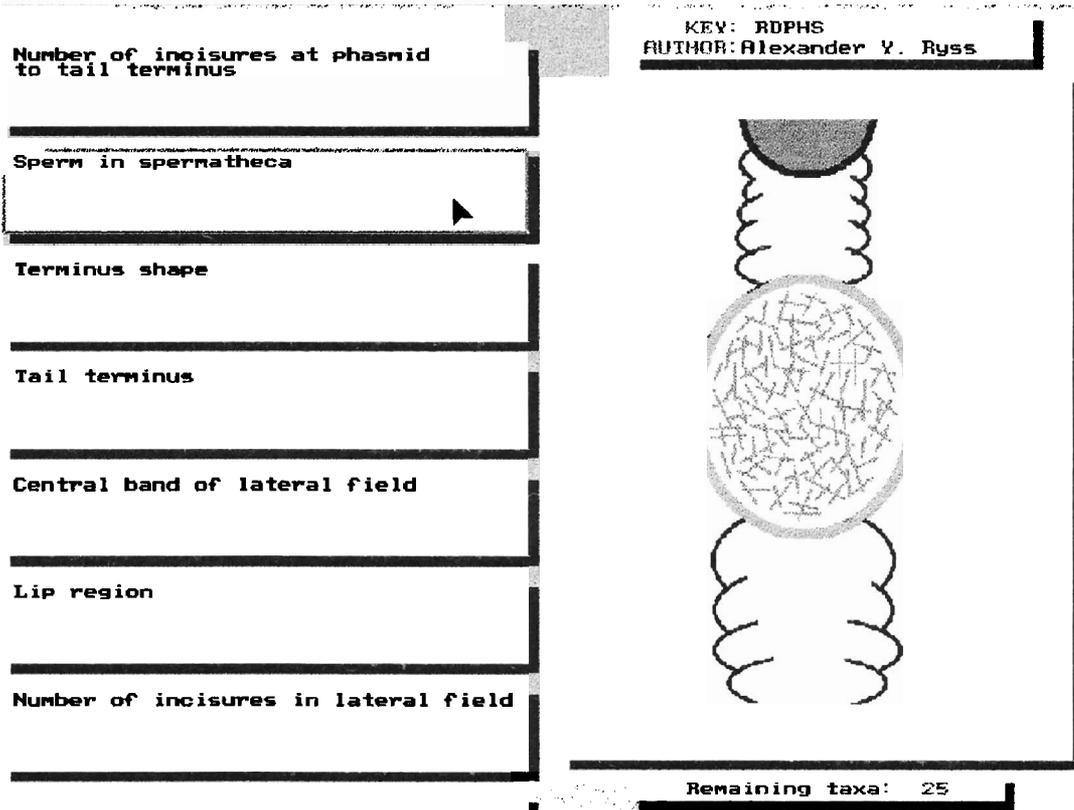


Fig. 3. First screen with an image of the character "Sperm in spermatheca".

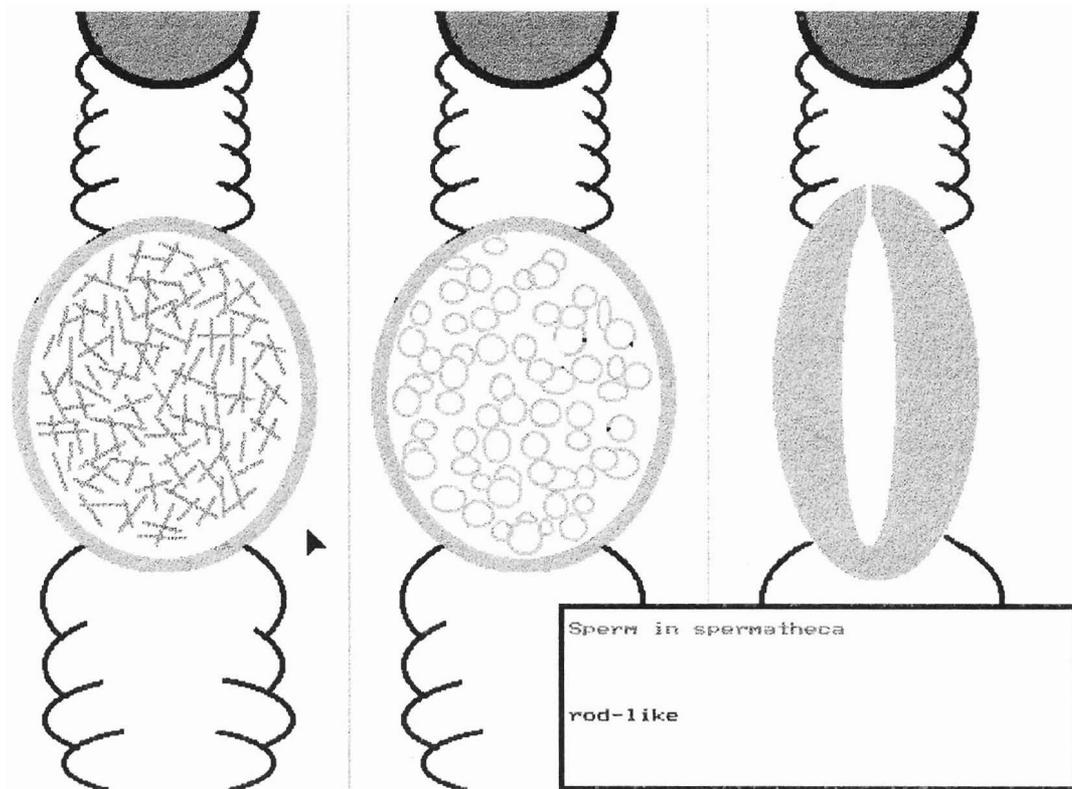


Fig. 4. Second screen with the states of the character "Sperm in spermatheca".

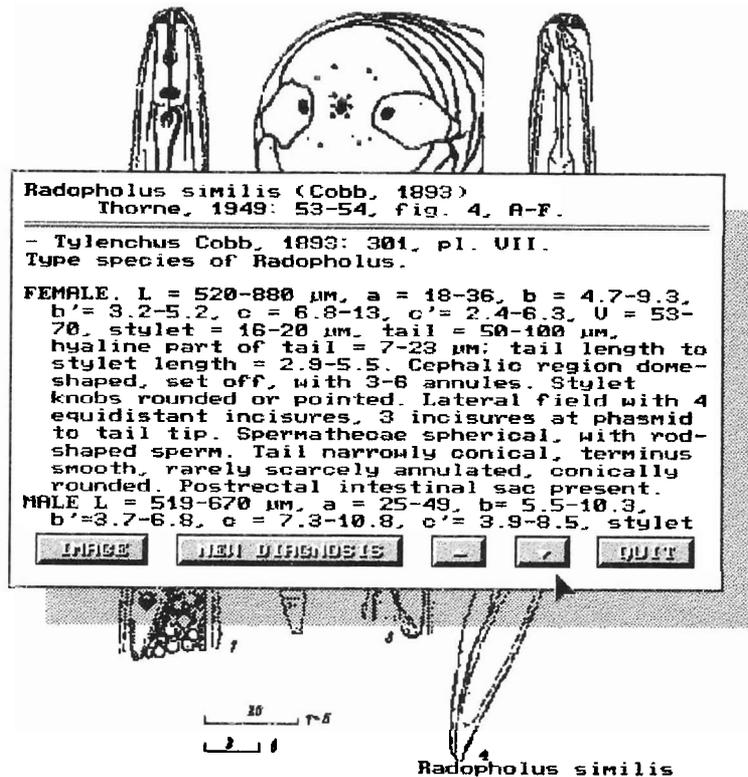


Fig. 5. Finish of identification. Screen with the scrolling description of identified species.

At the end of identification user sees the the black-and-white image and also the species description which can be scrolled (Fig. 5). The frame with the description contains a button "Image" which when selected will provide a coloured image of the identified species. By clicking the "New Diagnosis" button one can initiate a new identification process.

To see the general information for the key, it is necessary to click the small frame with the name of the author in the upper left corner of the first screen (Fig. 1). To invoke the general "HELP", press F1 at the each step of the identification procedure.

BIKEY automatically generates the dichotomous keys for publications. For such keys the system defines the character relative weight for each character which can be altered by the user. The number of variants of a dichotomous key is determined by the number of combinations of the relative weights of characters corrected by the user. Thus, as many or as few variants of a dichotomous key as desired can be generated by the user. The dichotomous key generation program DIAKEY is included in the full version of the BIKEY package (Lobanov & Dianov, 1994; Lobanov *et al.*, 1996.).

### Main parameters of identification keys constructed in BIKEY 7

Twenty characters are sufficient to identify the 24

*Radopholus* species using the identification key developed in the BIKEY 7 software package. The average identification path was 5.196 steps, and the most important characters are: number of incisures from phasmid to tail terminus, sperm shape, tail terminus shape, tail terminus annulation, relative width of central band in lateral field, number of cephalic annules, number of incisures in lateral field, and difference in size between the anterior and posterior spermatheca.

## DISCUSSION

In the EXCEL and BIKEY 7 identification systems, an identification is based on the principle that the initial set of taxa can be investigated interactively and reduced by different filters (i.e. character states) in several steps of identification. EXCEL has preferences to operate quantitative characters and can filter initial assemblage of taxa by a set of several characters at each step (commands "Sort" and "Filter"). BIKEY has preferences to operate qualitative characters, uses images during selection of character states (text explanations serve as auxiliary means only) and proposes the characters in descending sequence, depending on their diagnostic value.

In previous identification keys using LOTUS and EXCEL spreadsheet software nematode identification was based on the "Sort" command (Robbins &

Brown, 1995; Decraemer & Baujard, 1997). Sorting of the species (i.e. rows on the spreadsheet) was done using the minimum values of the character range for each species, e.g., for stylet length with a range 12-18 µm only 12 µm was used for sorting the species. Use of the "Filter" modes ("AutoFilter" and "Advanced Filter") described here, have the advantage of using the complete range for each character, which appears more effective than using only the minimum values.

## ACKNOWLEDGEMENTS

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**Рысс А. Ю.** Компьютерное определение видов рода *Radopholus* (Tylenchida: Pratylenchidae).  
**Резюме.** Предлагается полиномический ключ для определения 24 видов рода *Radopholus*, созданный с использованием компьютерных таблиц EXCEL 5.0, а также пакета программ BIKEY 7 (©Лобанов и Дианов, 1994). Определение основывается на принципе первоначального набора таксонов, которые можно интерактивно исследовать, из числа которых, при помощи различных фильтров (т.е. по состоянию отдельных признаков) в последовательных шагах определения могут отбрасываться как не соответствующие образцу. Количественные признаки лучше всего оцениваются в программе EXCEL, в которой первоначальный набор возможных таксонов анализируется на соответствие нескольким признакам при помощи команд "Autofilter", "Advanced Filter" или "Sort". Напротив, BIKEY более пригоден для использования качественных признаков и использования графических образов в процессе анализа состояний признаков. При этом текстовые объяснения выполняют лишь вспомогательную функцию. Этот пакет представляет список признаков, расположенных в нисходящем порядке в зависимости от их таксономической значимости (не в случайном порядке). При создании ключа для *Radopholus* оказалось, что 20 признаков достаточно для определения 24 видов. При этом в среднем последовательность проводимого определения включала лишь 5,196 шагов. Наиболее значимые в таксономическом отношении признаки - число инцизур на участке от фазмид до терминуса хвоста, форма сперматозоидов, форма терминуса хвоста, характер кольчатости на терминусе хвоста, относительная ширина срединной части латерального поля, число колец кутикулы в головном отделе, число инцизур в латеральном поле, различие в размерах между передней и задней сперматекой.

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