An interactive identification key to species of Echinoderidae (Kinorhyncha)

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ABSTRACT

An interactive, continuously updated identification key to species of the large kinorhynch family Echinoderidae has been made available online. The key is based on the DELTA format (DEscription Language for TAxonomy), and provides, with a multiple entry approach, an intuitive and user friendly tool to identify more than 145 echinoderid species. The present short note describes software requirements, how to access the database and keep it updated, and how to use the identification tools.

1. Introduction

Kinorhyncha currently includes around 300 valid species, distributed on eleven families. However, nearly half of the species are accommodated in a single family, Echinoderidae Zelinka, 1894. The family is characterized by species with trunk segment 1 always forming a closed ring, segment 2 showing variation in its plate composition, and segments 3 to 10 consisting of a tergal and two sternal plates. Middorsal spines are, if present at all, restricted to appear on segments 4 to 8, and a midterminal spine is never present in adults. Five genera, *Echinoderes* Claparède, 1863, *Cephalorhyncha* Adrianov, 1999 in Adrianov & Malakhov (1999), *Fissuroderes* Neuhaus & Blasche, 2006, *Meristoderes* Herranz et al., 2012 and *Polacanthoderes* Sørensen, 2008, are currently recognized within the family. The latter four genera are rather small and accommodate one to nine species only, whereas a vast majority of the diversity is contained in the *Echinoderes*, that holds more than 100 species. Globally *Echinoderes* is also the most diverse, abundant and commonly encountered of all kinorhynch genera.

The last identification key to species of *Echinoderes* was published by Adrianov et al. (2002), and among the smaller genera an identification key is only available for *Meristoderes* (see Sørensen et al. 2013). However, the number of described *Echinoderes* species has more than doubled since 2002 and it is still increasing in recent years. Also, since 2002 our understanding of taxonomically important structures have improved significantly, and currently many species are recognised by characters that previously have been neglected (see, e.g., Sørensen et al. 2012). In addition, recent taxonomic studies have pointed out several previously overlooked structures in species from older species descriptions (e.g., Grzelak & Sørensen 2018; Yamasaki & Dal Zotto 2019). Considering these advances in the taxonomy of the family, the need for a modern and continuously updated key is obvious. Thus, we would like to share a key prepared with DELTA software (DEscription Language for TAxonomy) (Dallwitz, 1974, 1980; Dallwitz et al., 1999) that together with the required freeware offers easy identification of all identifiable members of the Family Echinoderidae. The key also includes 7 unnamed species of which morphological information has been made available in previous studies. We hope that this tool will be used broadly by kinorhynch taxonomists, as well as meiofauna systematicians and ecologists in general. The following protocol only provides simple instructions necessary to use the Echinoderidae key. For further information on additional functions of the program see Dallwitz et al. (1999).

2. Materials and methods

2.1. Software requirements

Before implementing the database, users should install the Intkey program, which is a part of the DELTA package for interactive identification and information retrieval. The installation file (intkey.zip) can be downloaded from https://www.delta-intkey.com/www/programs.htm following the installation instructions provided on the website. Please note that this software works on Windows platforms only.

2.2. Downloading the identification key

A download link to the updated database, containing the actual identification key, can be found at Hiroshi Yamasaki's website – a website about Scalidophora systematics and taxonomy managed by the first author: https://sites.google.com/a/meiobenthos.com/laboratory/database/kinorhyncha-identification-key

Installation can be done following these steps:

1. Download the intkey starter file (Echinoderidae.ink) with the link provided above
2. Click the downloaded file to let the program start downloading the newest version of the Echinoderidae database from our server
3. After downloading, the interactive key will open automatically.

2.3. Using the interactive key

The opening screen will be divided into four quadrant or boxes, the characters of the multiple entry key will show to the upper left (box "Best Characters"), and a list of potential species identities to the upper right (box "Remaining Taxa").

A character can be selected for coding with a single click. When clicked, a window will open and either just show the available coding states, or the available coding states together with graphics providing a more detailed explanation of the character. The chosen character state can be coded either by single clicking the selected state followed by pressing the enter button (or clicking "OK") or by double clicking the correct state. The character state will now appear in the lower left quadrant of the window (box "Used Characters"), while species not showing the selected trait will disappear from the list of "Remaining Taxa", and instead appear to the lower right under "Eliminated Taxa". As more characters are coded, the list with potential species identities will gradually shorten until a final identification is reached. If a character or a state was selected by mistake, it can be changed by clicking the character in the box "Used Characters", deselecting the correct state, followed by clicking "OK" button.

When the list of potential species has been narrowed down to a single, or only a few species, it might be helpful to double click a species name in the list of "Remaining Taxa". This will open a new box with additional information about the species. To the right side the box will have links to graphic files that, when clicked, shows light microscopical images of the species (file name: [species name]+LM.gif) (eventually scanning electron microscopical in the few cases where no LM images were available), and a map showing the distribution of the species (file name: [species name]+GEO.gif). A list to the left side has links to descriptions of the species. The 'Full description' provides a text file from the authors, with a more complete species diagnosis and hints about how to distinguish the species from others. The 'Diagnostic description' is generated by the software, and provides a list of characters that, when coded, will lead to full identification of the species.

Tips and hints when using the key: (1) The characters in the box "Best Characters" are ordered by its contribution for species-identification as well as character's observability, thus, it is recommended to code from upper characters in the box. (2) Coding of 'absent' states might be just as useful as the coding of presence. If a species has middorsal spines on segment 4 only, this should obviously be coded as present, and a fast elimination of potential species will subsequently happen when middorsal spines on the following four segments are coded as absent. (3) Users should also keep in mind that the condition of some character states might be unknown for certain species – especially species of older descriptions that have been unavailable for re-examination. Such species might be more difficult to eliminate from the list of potential identities, because many of their character states would be "either absent or present". Hence, if a user narrows the list of potential identities down to, e.g., one well-described species and three poorly described ones, it might be worthwhile to check the graphic presentations of the latter. This would often lead to fast elimination of some of the species. (4) Finally, it should be kept in mind that numerous (+40) species from museum collections in Berlin, Copenhagen and Washington DC were examined in order to check and confirm the nature of the different characters. This revealed several new findings that differed from the original descriptions (these results will be published in

a series of revisions that got prompted by the present studies). The characters in the database are based on these observations, meaning that the character states in the key might deviate from the information provided with the original descriptions.

2.4. Closing the program – and keeping it updated

When the software is closed, it will ask users whether or not to save the downloaded data. In order to use the key off-line, for instance during a field trip, please click "Yes" and select the saving folder. With the saved ink file, users can start the program without downloading anything. If users click "No", the downloaded database (except for the starter file) will be deleted from the computer. If users wish to download the newest database, please start the program with the original file downloaded from "Hiroshi Yamasaki's website" (see above).

The webpage also informs about the latest updates of the database. By contacting the first author by email, the user can furthermore sign up for a mailing service that will provide a notification when a new version is available.

2.5. Appropriate Citation

We would like to suggest all users to cite the present contribution when publishing studies where the interactive key has been used to identify parts of the studied material.

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