
Reflections on species-level taxonomy of oligochaetes in the 21st century

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Abstract

Nowadays, oligochaete taxonomy is increasingly using DNA sequence data, additional to morphological characters. Both methods are dependant on each other, but in different ways. Considering the amount of data, the richness of analytical tools, and the depth of resolution, DNA sequences outdo morphological characters by orders of magnitude. In cases of conflict, it is therefore the DNA sequence data that take the lead. On the other hand, the species identity of DNA sequences is still largely based on morphological characters of the underlying specimens.

DNA data have, in general, confirmed, the outer limits of species taxa, but questioned the inner limits of taxa through the detection and delimitation of cryptic species. It is important to name these cryptic species, but the former morpho-species should not remain unnamed, especially when the cluster of cryptic species is a monophyletic group.

DNA sequencing technology is developing at high speed, and new data are becoming increasingly available. Yet it is paramount to agree on a specific type of data. New data do not help when they are unknown in similar species. Therefore extension should be favoured over intension when it comes to research programmes. DNA sequences of currently established markers should be generated for as many known species as possible, and for specimens of a morpho-species that cover its distribution range.

Morphological identification will probably be replaced increasingly by molecular identification. Such identification can be carried out by non-experts, which will increase greatly the body of knowledge about the species. Paramount here is the quality of the reference databases.

For those who take delight in observing oligochaete worms, their liberation from the taxonomic tunnel vision may open new ways to study these worms, towards lifestyle, body functioning, or any other aspect of their biology.

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