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Species limits in Swedish oligochaetes

Abstract

In this project we have resolved species limits of a number of Swedish oligochaetes. We have analysed genetic data (DNA sequences) within nominal morpho-species, i.e., named and described taxa that can be recognized by their morphological features. The aim has been to test whether each of these taxa is a panmictic metapopulation, or whether some of them contain different separately evolving lineages which would be better regarded as different species, i.e. lineages among which gene flow has totally, or at least to a great extent, ceased.

Recent systematic studies have shown that these so called cryptic species are common among invertebrate groups, and not the least among segmented worms. Contemporarily, ideas of DNA barcoding (for animals, comparing sequences of the mitochondrial COI gene) have been developed, to be used for the identification of species in general, and of cryptic species in particular.

In our project, and with reference to barcoding, we have demonstrated two important, but somewhat paradoxical results. First, with complementary studies of nuclear markers (ITS and Histone 3 = H3), we have shown that sometimes there is indeed ITS/H3 support for the clusters of individuals that are clearly delimited by the COI barcoding gene. We have often found minor morphological differences that are congruent with this conclusion – the individuals of the different clusters do look a bit different after all.

In the case of many oligochaetes, such differences have earlier been regarded as annoying intraspecific variation, but now the explanation is clear: a number or more or less cryptic species have been hiding under one and the same taxon name.

However, in two of our published studies we have reached another conclusion. In these, we found distinct COI clusters, which in a DNA barcoding context could be interpreted as different species, but which in our ITS/H3 gene trees are broken up into completely different groups of individuals.

The take-home message of these results is that COI barcoding, with an *a priori* threshold value for species delimitation, would not work in any universal way, not even within one and the same animal group. All species and species complexes first have to be studied separately, in a perspective where morphological, mitochondrial and nuclear patterns are integrated with each other. Only when this has been done, COI barcoding will become the powerful tool it is been meant to be. To correctly describe the species diversity of Swedish oligochaetes, this insight is pivotal.

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