



Conference Abstract

The small polychaete *Platynereis dumerilii* revealed as a large species complex with fourteen MOTUs in European marine habitats

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Abstract

Recent studies reporting complexes of cryptic or pseudo-cryptic species with narrow geographic distributions have been challenging the cosmopolitan status of a fair number of marine benthic invertebrates. Morphologically similar species are often overlooked but molecular techniques have been extremely effective in signalling potential hidden diversity which, complemented with further detailed examination, might reveal unique morphological and ecological features.

Evidence of morphological stasis, where no clear and stable morphological differences are apparent, can be exemplified by the annelids *Platynereis dumerilii* (Audouin & Milne Edwards, 1833) and *Platynereis massiliensis* (Moquin-Tandon, 1869). These sibling species, usually found among algae in marine intertidal and subtidal habitats, can only be distinguished by their different reproductive strategies and life histories. The former is gonochoric, with a single reproductive event in life (semelparous) transforming into a pelagic epitokous form called heteronereis, has free spawning synchronized by lunar

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periodicity and a larval stage with planktotrophic development; while the latter shows no epitokous transformation and is a protandrous hermaphrodite, characterized by egg brooding and lecithotrophic larval stages with a semi-direct development.

In order to verify the possible existence of additional hidden *Platynereis* species within the *P. dumerilii* morphotype, we used a multi-locus approach to investigate 26 populations along Europe from the NE Atlantic and the Macaronesia islands (Azores, Madeira and Canaries) to the Western and Eastern Mediterranean Sea.

We concatenated the mtDNA COI-5P, rDNA 16S and 28S-D2 sequences and performed a phylogenetic analysis through Bayesian inference (BI). To depict Molecular Operational Taxonomic Units (MOTUs), we applied three delimitation methods (ABGD, bPTP and GYMC) to the concatenated alignment, except for COI where we also applied the Barcode Index Number (BIN), implemented in BOLD, which is exclusive to this locus. Consensus MOTUs were defined based on the majority rule and, in case of draw, the most conservative MOTUs were chosen.

We detected at least 14 MOTUs with 23.1% COI mean K2P distance (6.6 - 32.6%). The BI tree is split into three major clades (Clade A: MOTUs 1-3, Clade B: MOTUs 4-9 and Clade C: MOTUS 10-14), with MOTU 3 appearing to represent *P. dumerilii sensu stricto* and MOTU 9 *P. massiliensis*. This assumption is based on data from the Type locality and a previous study by Wage *et al.* (2017), which combined phylogeographic (COI barcode region), reproductive biology and life-history observations on some selected *Platynereis* populations thriving in the vent areas from the Italian islands of Ischia and Vulcano. Major Cade C seems to be pseudo-cryptic as some visible differences can be found in the specimens, as for example, the size of the tentacular cirri and lack of dorsal pigmentation, in contrast with Clades A and B, where only differences in pigmentation types were found so far.

The Spanish archipelago of the Canary Islands and the whole Mediterranean Sea seem to be a cryptic hotspot. Five MOTUs are unique to the Macaronesia and five sympatric MOTUs are present in the Gran Canaria and La Palma islands alone. Additionally, three lineages were present exclusively in the Mediterranean with four sympatric MOTUs spotted in the southeast of Spain (Calpe) and the Greek island of Crete. Three out of four NE Atlantic MOTUs are shared with the Mediterranean with one exclusive to this part of the continent.

Failure to recognise this hidden biodiversity may compromise the accuracy and the interpretation of biomonitoring data or other relevant ecological studies. Integrative taxonomy is thus essential to solve these uncertainties and to allow naming the involved undescribed species. Otherwise, most molecular data providing enough support for species hypothesis will continue to be unused, and large fractions of biodiversity will persist unnoticed.

Keywords

Annelids, Platynereis, Cryptic species, Phylogeny, DNA barcoding

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