A DNA barcode reference library for the superorder Peracarida (Crustacea) from European coasts

Pedro Vieira1,2, Michael Raupach3, Filipe O Costa3*, Henrique Queiroga1

1 Departamento de Biologia and CESAM - Centro de Estudos do Ambiente e do Mar, Universidade de Aveiro, 3810-193 Aveiro, Portugal
2 CBMA - Centro de Biologia Molecular e Ambiental, Departamento de Biologia, Universidade do Minho, 4710-057 Braga, Portugal
3 AG Systematics and Evolutionary Biology, Institute for Biology and Environmental Sciences (IBU), Carl von Ossietzky University Oldenburg, Carl von Ossietzky Str. 9-11, 26111 Oldenburg, Germany

*Corresponding author: foxosta@bio.uniof.de.pt

ABSTRACT

BACKGROUND: The superorder Peracarida is a highly diverse crustacean taxon, comprising numerous prominent members in European coastal areas’ communities and ecosystems. Here we present a core DNA barcode reference library for marine European superorder Peracarida, comprising specimens from Black and Mediterranean Seas and from Northeast Atlantic coasts, ranging from Iberian Peninsula to Scandinavia, including Azores, Iceland and British Islands.

RESULTS: A total of 953 DNA barcodes were compiled in a BOLD dataset, with 220 new DNA barcodes. The dataset included specimens of the orders Amphipoda (67.2%), Cumacea (1.6%), Isopoda (25.3%), Mysida (4.1%), and Tanaidacea (1.8%). In total, 176 peracaridean morphospecies were assigned to 205 BINs, with 163 (92.6%) represented by single BINs, comprising specimens collected from geographically distant populations, up to approximately 3500 km in the most extreme cases (e.g. Idotea baltica granulosa from Azores, Portugal, Iceland, Scotland, North Sea and Norway). The remaining thirteen morphospecies, belonging to Amphipoda and Isopoda, split between two to six BINs each, and had maximum intraspecific genetic distances between 3 to 25%. All multiple intraspecific BINs were allopatric, although the geographic distance between members of each BIN lineage ranged from 60 km up to 3000 km. Major splits were detected between upper north and south regions of the NE Atlantic, between Atlantic and the Mediterranean Sea, or even between countries. The most striking case was revealed for the isopod Janira maculosa, which split into six BINs (maximum intraspecific distance 25.16%).

SIGNIFICANCE: The high percentage of morphospecies matching unique BINs (92.6%) shows the good reliability of our DNA barcode reference library. However, the presence of deeply divergent intraspecific lineages suggests the presence of considerable overlooked taxonomic diversity. These findings indicate the need for a comprehensive revision and DNA barcode-based probation of the peracaridean fauna from the European coasts.

REFERENCES


Funding Sources