

DNA barcoding echinoderms of the East Coast of South Africa

Yves Samyn, Gontran Sonet, Nathalie Smitz, Kenny Meganck

Abstract

Background: According to the Barcode of Life Data Systems (BOLD, <http://www.boldsystems.org>), approximately a fourth of the described echinoderm species have been already barcoded (more than 2,000, species barcoded out of the about 8,000 species described). However, only less than 300 of the ca. 29,000 echinoderm barcode records available on BOLD are from South Africa, a country with a coastline of more than 2,500 km on both the Atlantic and Indian Oceans. In an effort to explore the echinoderm diversity of South Africa, we barcoded 351 specimens collected during five different campaigns (from 1999 to 2016) in the North and South of the KwaZulu-Natal Province, across two distinct offshore environments. Results: Cross comparison between morphological and molecular identification allowed distinguishing ca. 112 species, including a number of new records for the country and some putative new species. These included Crinoidea (96 specimens and ca. 9 species), Ophiuroidea (95 specimens and ca. 44 species), Asteroidea (48 specimens and ca. 19 species), Echinoidea (27 specimens and ca. 11 species) and Holothuroidea (85 specimens and ca. 29 species). Nonetheless, DNA barcoding revealed unexpected large intraspecific distances (suggesting additional overlooked species) as well as clusters of heterospecific sequences (suggesting either poor marker resolution or the need for further taxonomical consideration). DNA barcodes obtained for more than 40 specimens showed distances of more than 1% with the DNA barcodes currently available in BOLD and GenBank. Significance: This data set will be further investigated using integrative taxonomy and will deliver a valuable addition to the reference library of DNA barcodes for echinoderms.

Introduction

- The DNA barcode DNA sequence (5' end of the cytochrome c oxidase subunit I gene, COI) allows to diagnose species of all five classes of Echinodermata (Layton et al. 2016; Ward et al. 2008).
- Echinoderms from South Africa (SA) have been relatively less intensively barcoded compared to other regions of the world.

Material and Methods

- 351 specimens collected during five different campaigns (from 1999 to 2016) in the North and South of the KwaZulu-Natal Province, across two distinct offshore environments.
- Independent identifications based on morphology (using skeletal elements observed under light stereoscope and SEM) and DNA barcodes (using the Barcode of Life Data System, BOLD).
- Calculation of pairwise uncorrected p-distances and comparison between clusters of DNA barcodes and morphological assignments.

Results and discussion

Overall, we obtained DNA barcodes for ca. 114 species.

Class Ophiuroidea (Fig. 1A)

- 95 specimens and ca. 44 species
- No barcode gap present among the samples analyzed here
- New barcodes for 24 species and 6 new species and records for SA
- 6 species with unexpected small and 3 with large intraspecific distances

Class Holothuroidea (Fig. 1B)

- 85 specimens and ca. 29 species
- No barcode gap present among the samples analyzed here
- 8 species with unexpected small and 3 with large intraspecific distances

Class Echinoidea (Fig. 1C)

- 27 specimens and ca. 11 species
- Barcode gap present among the samples analyzed here
- New barcodes for 4 species and 1 potentially new species

Class Asteroidea (Fig. 1D)

- 48 specimens and ca. 19 species
- Barcode gap present among the samples analyzed here
- New barcodes for 7 species and 2 potentially new species

Class Crinoidea (Fig. 1E)

- 96 specimens and 9 species
- Barcode gap present among the samples analyzed here
- New barcodes for 1 species
- Please read poster ID 426 for more information about this group

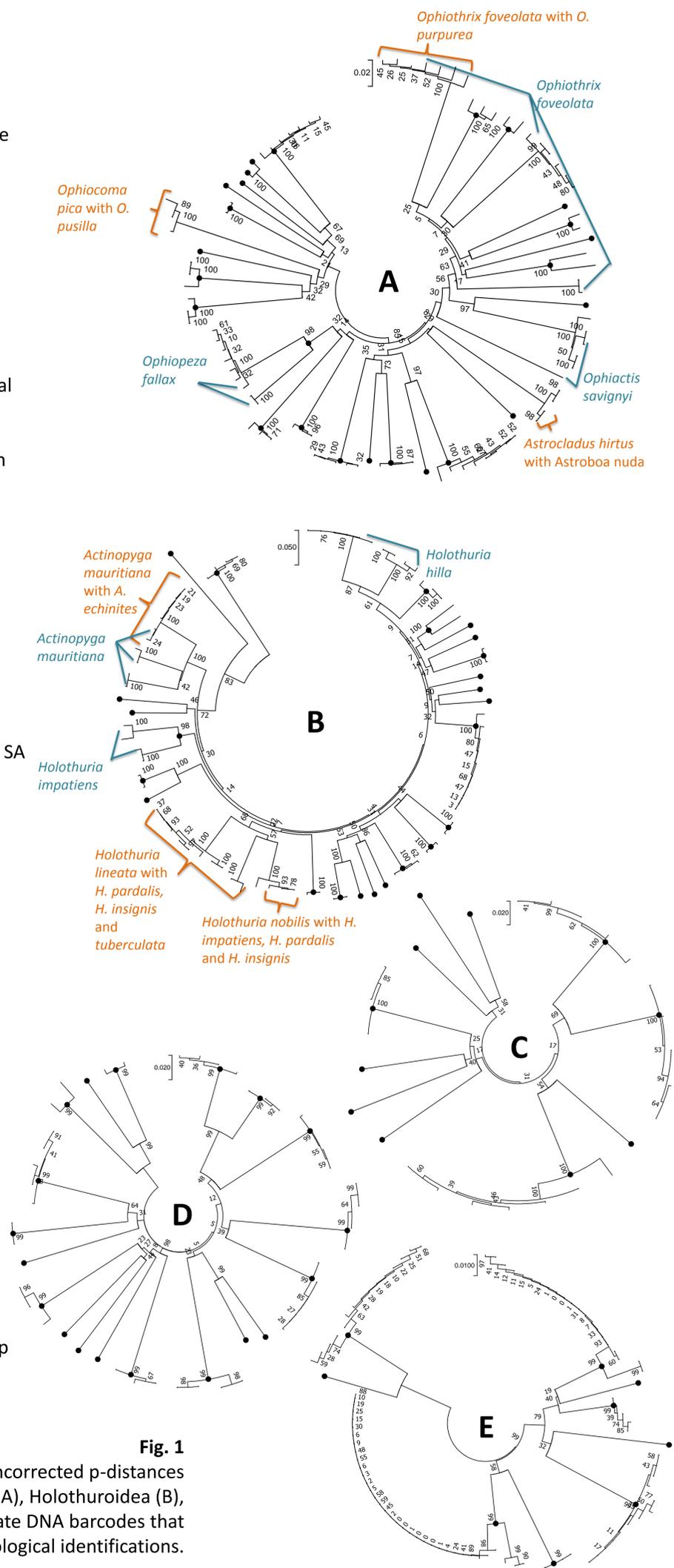


Fig. 1

Neighbour-joining trees (midpoint rooting) constructed with uncorrected p-distances among the COI sequences obtained here for Ophiuroidea (A), Holothuroidea (B), Echinoidea (C), Asteroidea (D) and Crinoidea (E). Black discs indicate DNA barcodes that are clustering in accordance with the morphological identifications.

References

Layton KKS, Corstorphine EA, Hebert PDN. Exploring Canadian Echinoderm Diversity through DNA Barcodes. Cimmaruta R, ed. *PLoS ONE*. 2016;11(11):e0166118. doi:10.1371/journal.pone.0166118. Ward RD, Holmes BH, O'Hara TD. DNA barcoding discriminates echinoderm species. *Mol Ecol Resour*. 2008 Nov;8(6):1202-11. doi: 10.1111/j.1755-0998.2008.02332.x. PubMed PMID: 21586007.

Funding Sources/Acknowledgements

JEMU is founded by BELSPO, the Belgian Science Policy. Funding for this work also came from the Flemish Community (Bilateral (International) Scientific and Technological Cooperation, project numbers BIL98/84 and BIL01/46), the Fund for Scientific Research Flanders, the Research Council of the Free University Brussels (VUB), the Belgian GTI and the King Leopold III Fund for Nature Exploration and Conservation (YS).