

Inventory completeness and accuracy of taxonomic determination: outcomes of a large scale barcoding effort of echinoderms in Terra Nova Bay (Antarctica, Ross Sea)

Schiaparelli Stefano^{1,2}, Alvaro Maria Chiara², Matteo Cecchetto¹, Bruno Danis³, Giulia Fassio⁴, Alice Guzzi¹, Quentin Jossart³, Maria Vittoria Modica⁴, Camille Moreau³ and Marco Oliverio⁴

¹ Department of Earth, Environmental and Life Sciences (DISTAV), University of Genoa, Corso Europa 26, I-16132 Genoa, Italy

E-mail: stefano.schiaparelli@unige.it

² Italian National Antarctic Museum (MNA) (Section of Genoa), University of Genoa, Genoa, Italy

³ Laboratoire de Biologie Marine, Université Libre de Bruxelles, 50 Av. F.D. Roosevelt, UC5.240, 1050 Bruxelles, Belgium

⁴ Department of Biology and Biotechnologies “Charles Darwin”, University of Rome “La Sapienza”, Zoology – Viale dell’Università 32, 00185 Rome, Italy

In 2010, the Italian National Antarctic Research Program (PNRA) funded a two-years pilot-project named “BAMBi” (Barcoding of Antarctic Marine Biodiversity) with the aim of creating a first data first set of DNA-barcoding COI sequences from the Terra Nova Bay (TNB) area for the highest possible number of invertebrates. This project was followed by others and, after several sampling expeditions, a large amount of samples from a variety of taxa has now been COI sequenced. In this contribution we focus on the results obtained for echinoderms, one of the most important group of invertebrates in the Antarctic benthos both in term of richness and abundance. The group was widely studied in the past in Terra Nova Bay and checklists, based on morphological classifications, are available for Ophiuroidea, Astroidea and Echinoidea. Holothuroidea and Crinoidea, instead, have never been subject of specific studies and determined despite their abundance in benthic samples.

Of the 535 specimens selected for barcoding from the above classes, COI sequences were successfully obtained for 468 of these. The analysis showed the existence of >14 species of Asteroidea, 14 of Ophiuroidea, 12 of Holothuroidea, 6 of Echinoidea and 3 species of Crinoidea. The barcoding approach enabled the recognition of several mistakes in the past classification based on morphology, even in the case of very common species. This has a wide relevance that goes beyond a correct classification since several of these species are also used as model organism in physiological tests. Two new records for the Ross Sea were also found. Several unexpected ‘sister clades’ were evidenced even in common species suggesting that our knowledge of the Terra Nova bay fauna was far to be complete and precise.