



Conference Abstract

CO1 Metabarcoding of Marine Water Samples from the 2nd Turkish Antarctic Expedition (TAE2) Highlights the Deficiencies in the Reference Barcoding Databases for the Continent

Rasit Bilgin[‡], Kübra Karaman[§], Yağmur Tarhana[‡], Ceylan Yücel[‡], Elizabeth Hemond^l, Mehmet Baki Yokeş[¶], Evrim Kalkan[#], Selahattin Ünsal Karhan[‡]

[‡] Institute of Environmental Sciences, Boğaziçi University, Istanbul, Turkey

[§] Institute of Science, Istanbul University, Istanbul, Turkey

^l Molecular Biology & Genetics, Faculty of Engineering and Natural Sciences, Bahçeşehir University, Istanbul, Turkey

[¶] AMBRD Doga Bilimleri, Istanbul, Turkey

[#] Middle East Technical University, Institute of Marine Sciences, Mersin, Turkey

Corresponding author: Mehmet Baki Yokeş (bakiyokes@gmail.com),

Evrim Kalkan (evrimkalkan@ims.metu.edu.tr), Selahattin Ünsal Karhan (unsalkarhan@yahoo.com)

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Abstract

Based on climate projections, the Antarctic Peninsula is one of the regions on the earth expected to be most drastically affected by climate change in the 2nd half of the 21st century. In order to establish baseline levels of marine biodiversity using the environmental DNA approach, we undertook metabarcoding based on the CO1 gene. Samples were collected using 0.22 µm pore-sized Sterivex filters during TAE2 undertaken in 2018, from one site at Deception Island (2 filters), one site at Nansen Island (2 filters), and three sites (one offshore) at Robert Island. A total of 20 taxa were identified (unique hits with BLAST percent identity ≥ 97%) belonging to three kingdoms (Chromista, Plantae, Animalia), nine phyla, 11 classes, 17 orders, 19 families, and 20 genera. Of these, 18 were identified to the species level, one to the genus level, and the other one to the family level. Genetically identified taxa included seven planktonic algae, nine seaweeds, a stalked jellyfish, a

nematode, a planktonic copepod, and a demersal fish. In addition, 129 unique OTUs were detected (unique hits with BLAST percent identity < 97%) as unidentified. These results indicate the high levels of undocumented genetic diversity (without CO1 barcode sequences in GenBank) in the Antarctic Peninsula region and adjacent waters, and the need for more work to complete the reference barcode databases for the continent.

A dendrogram resulting from cluster analysis (Bray-Curtis similarity measure, group-average linkage) based on the presence/absence data of 20 identified species revealed three well-defined sample (*i.e.* filter containing DNA fragments of multiple taxa) groups, which almost coincided with their geographical locations. First group included samples (filters) collected from the coast of Deception Island and the second one from the coast of Robert Island, both in the South Shetland Islands, off the northern tip of the Antarctic Peninsula. The third group included samples from Nansen Island coast (off the west coast of Graham Land, Antarctic Peninsula) together with the only sample collected offshore, off Robert Island. The significance of this clustering, thus the difference among sampling sites with regard to species composition, was confirmed by Analysis of Similarity (ANOSIM) results (Global R = 0.982, $p = 0.001$).

The highest number of identified taxa (per filter) and unidentified OTUs (per filter) were observed offshore off Robert Island. Considering that all of the other sampling sites were by the coasts of islands, this observation indicates i) the offshore waters might contain more DNA-bearing material than coastal sites, and/or ii) a methodological issue where the high phytoplankton and suspended matter concentrations by the coasts created a bottleneck in terms of capturing actual species diversity at the coasts, due to clogging of filters by phytoplankton and fine suspended particles.

Keywords

Antarctica, CO1, marine metabarcoding, barcode references

Presenting author

Raşit Bilgin

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Ethics and security

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Author contributions

RB, MBY, and EK overviewed the study and provided lab materials through grants. KK undertook, labwork and fieldwork for the study. RB, KK, SUH, YT, CY, and EH made the data analyses.

Conflicts of interest

There are no conflicts of interest.