



Conference Abstract

Artificial Reef Monitoring Structures (ARMS) providing insights on hard substrate biodiversity and community structure of the Eastern Mediterranean Sea

Christina Pavludi[‡], Eleni Ioanna Yperifanou[§], Jon Bent Kristoffersen[‡], Thanos Dailianis[‡], Vasilis Gerovasileiou[‡]

[‡] Hellenic Centre for Marine Research (HCMR), Institute of Marine Biology, Biotechnology and Aquaculture (IMBBC), Heraklion, Crete, Greece

[§] School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece

Corresponding author: Christina Pavludi (cpavloud@hcmr.gr)

Received: 21 Feb 2021 | Published: 04 Mar 2021

Citation: Pavludi C, Yperifanou EI, Kristoffersen JB, Dailianis T, Gerovasileiou V (2021) Artificial Reef Monitoring Structures (ARMS) providing insights on hard substrate biodiversity and community structure of the Eastern Mediterranean Sea. ARPHA Conference Abstracts 4: e64760. <https://doi.org/10.3897/aca.4.e64760>

Abstract

Monitoring marine biodiversity in hard-bottom habitats is challenging as it typically involves resource-intensive, non-standardized, and often destructive sampling methods that limit its scalability. Differences in monitoring approaches furthermore hinder inter-comparison among monitoring programs. Standardised collectors such as [Artificial Reef Monitoring Structures \(ARMS\)](#) can be used to monitor status and changes of hard substrate communities in coastal environments. In addition, ARMS constitute an early-warning system for marine biological invasions by identifying newly introduced Non-Indigenous Species (NIS) and track the migration patterns of already known NIS in European continental waters.

In the framework of [ASSEMBLE+](#) project and as part of the European ARMS programme ([ARMS-MBON](#)) (Obst et al. 2020), ARMS were deployed in two locations in Greece and, more specifically, in the marina of the Old Venetian Harbour of Heraklion (1HERP) and in

the [Underwater Biotechnological Park](#) of the Hellenic Centre for Marine Research (2UBPC).

The ARMS deployment and retrieval dates are shown in Table 1; deployment and retrieval were done according to the standards and protocols established by the [Smithsonian Institution](#). Upon retrieval, the plates from the ARMS were disassembled, photographed (Fig. 1a) and samples of both the motile and sessile communities were collected for molecular analysis. Each sampling event produced three fractions (sessile, motile 90–500 μm and motile 500 μm –2 mm) as well as a stack of plate and specimen images.

Table 1.

Overview of sample events.

Deployment Date	Collection Date	ARMS-ID
2018-09-28	2019-01-28	1HERP
2018-09-28	2019-01-28	1HERP
2018-09-28	2019-01-28	1HERP
2018-09-28	2019-01-28	1HERP
2018-09-28	2019-01-28	1HERP
2018-09-28	2019-01-28	1HERP
2019-06-12	2019-10-11	1HERP
2019-06-12	2019-10-11	1HERP
2019-06-12	2019-10-11	1HERP
2019-06-12	2020-02-10	1HERP
2019-06-12	2020-02-10	1HERP
2019-06-12	2020-02-10	1HERP
2019-06-12	2020-06-18	1HERP
2019-06-12	2020-06-18	1HERP
2019-06-12	2020-06-18	1HERP
2019-09-24	2020-12-11	2UBPC
2019-09-24	2020-12-11	2UBPC
2019-09-24	2020-12-11	2UBPC
2020-09-03	2021-01-22	1HERP
2020-09-03	2021-01-22	1HERP
2020-09-03	2021-01-22	1HERP

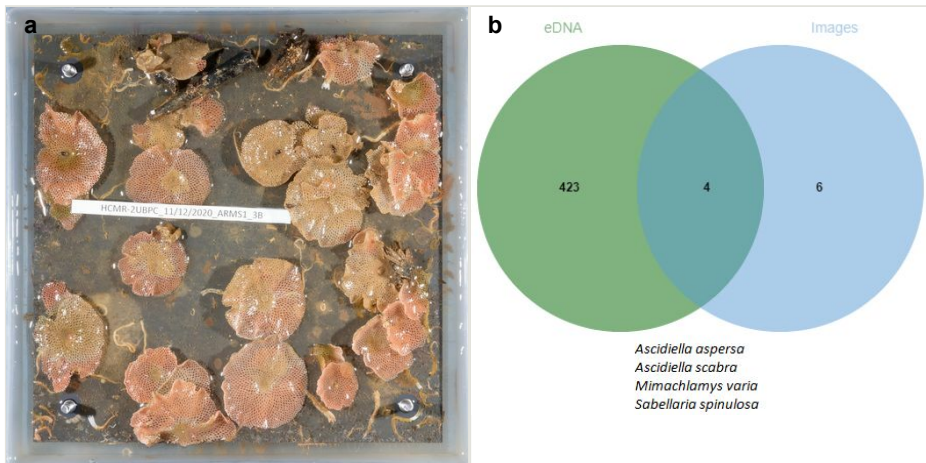


Figure 1.

a. Example of an ARMS plate with bryozoan formations (*Reteporella* sp.) b. Comparison of image-based and eDNA metabarcoding based results, for the taxa identified at the species level, from the ARMS that was retrieved on 2019-01-28.

DNA was extracted from the sampled fractions and amplified by PCR, targeting different molecular markers (18S rRNA, COI and ITS). Resulting amplicons were sequenced using Illumina MiSeq Reagent Kit v3 (2 × 300 bp) and analyzed using PEMA (Zafeiropoulos et al. 2020). All raw sequence files of this study were submitted to the European Nucleotide Archive (ENA) (Harrison et al. 2021) with the study accession number [PRJEB33796](https://www.ebi.ac.uk/ena/record/PRJEB33796).

Images were analyzed using photoQuad image processing software (Trygonis and Sini 2012), which is specialised for the analysis of sessile biodiversity on photoquadrats. Cover of sessile taxa was measured by superimposing on every image 100 randomly distributed points. Each point was manually assigned to the corresponding taxon or morpho-functional category based on external morphological characters.

Repeatable workflow procedures for integrated processing of image and sequence data are currently under development as part of the LifeWatch-ERIC [Internal Joint Initiative](#) on NIS. In addition, all ARMS-related data are stored in the [ASSEMBLE Plus data collection](#) of the [Marine Data Archive \(MDA\)](#) using a Darwin Core Archive (DwC-A) format, including the linkages to the images and sequences (Exter et al. 2020).

Comparison of traditional biodiversity assessment methods, such as image-based identifications, complemented by the eDNA metabarcoding results, will shed light on the investigation of marine biodiversity patterns in the Eastern Mediterranean Sea (Fig. 1b). Furthermore, the results will provide crucial information on the importance of ARMS for biodiversity assessment and as an efficient tool to monitor community shifts and invasion events in marine ecosystems undergoing fast change.

Presenting author

Christina Pavloudi

Presented at

1st DNAQUA International Conference (March 9-11, 2021)

Acknowledgements

We would like to thank [Giorgos Chatzigeorgiou](#), [Eva Chatzinikolaou](#), [Kleoniki Keklikoglou](#), Grigoris Skouradakis, [Katerina Vasileiadou](#) and Emmanouela Vernadou and for their help on ARMS deployment and retrieval and [Christos Arvanitidis](#) and [Georgios Kotoulas](#) for promoting the participation in the ARMS-MBON network. This research was supported in part through computational resources provided by IMBBC (Institute of Marine Biology, Biotechnology and Aquaculture) of the HCMR (Hellenic Centre for Marine Research). Funding for establishing the [IMBBC HPC](#) has been received by the MARBIGEN (EU Regpot) project, LifeWatchGreece RI and the CMBR (Centre for the study and sustainable exploitation of Marine Biological Resources) RI.

Funding program

This ARMS-MBON network is funded by the infrastructure programs ASSEMBLE Plus (grant no. 730984) and the European Marine Biological Resource Centre, EMBRC. Both programs establish and maintain the core network and provide services and consultation for deployment, sample processing, sequencing, data management, and analysis. Additional support was provided by the project “Centre for the study and sustainable exploitation of Marine Biological Resources (CMBR)” (MIS 5002670), which is implemented under the Action “Reinforcement of the Research and Innovation Infrastructure,” funded by the Operational Programme “Competitiveness, Entrepreneurship and Innovation” (NSRF 2014–2020) and co-financed by Greece and the EU (European Regional Development Fund).

References

- Exter K, Decruw C, Portier M, Gerovasileiou V, Pavloudi C, Obst M (2020) Genomics Observatory Use-Case: The challenge to standardise image and sequence data to Darwin Core format. *Biodiversity Information Science and Standards* 4 <https://doi.org/10.3897/biss.4.58938>
- Harrison PW, Ahamed A, Aslam R, Alako BTF, Burgin J, Buso N, Courtot M, Fan J, Gupta D, Haseeb M, Holt S, Ibrahim T, Ivanov E, Jayathilaka S, Balavenkataraman Kadhivelu V, Kumar M, Lopez R, Kay S, Leinonen R, Liu X, O’Cathail C, Pakseresht A,

- Park Y, Pesant S, Rahman N, Rajan J, Sokolov A, Vijayaraja S, Waheed Z, Zyoud A, Burdett T, Cochrane G (2021) The European Nucleotide Archive in 2020. *Nucleic acids research* 49 (D1): D82-D85. <https://doi.org/10.1093/nar/gkaa1028>
- Obst M, Exter K, Allcock AL, Arvanitidis C, Axberg A, Bustamante M, Cancio I, Carreira-Flores D, Chatzinikolaou E, Chatzigeorgiou G, Christmas N, Clark M, Comtet T, Dailianis T, Davies N, Deneudt K, de Cerio OD, Fortič A, Gerovasileiou V, Hablützel P, Keklikoglou K, Kotoulas G, Lasota R, Leite B, Loisel S, Lévêque L, Levy L, Malachowicz M, Mavrič B, Meyer C, Mortelmans J, Norkko J, Pade N, Power AM, Ramšak A, Reiss H, Solbakken J, Staehr P, Sundberg P, Thyrring J, Troncoso J, Viard F, Wenne R, Yperifanou EI, Zbawicka M, Pavludi C (2020) A Marine Biodiversity Observation Network for Genetic Monitoring of Hard-Bottom Communities (ARMS-MBON). *Frontiers in Marine Science* 7 <https://doi.org/10.3389/fmars.2020.572680>
 - Trygonis V, Sini M (2012) photoQuad: A dedicated seabed image processing software, and a comparative error analysis of four photoquadrat methods. *Journal of Experimental Marine Biology and Ecology* 99-108. <https://doi.org/10.1016/j.jembe.2012.04.018>
 - Zafeiropoulos H, Viet HQ, Vasileiadou K, Potirakis A, Arvanitidis C, Topalis P, Pavludi C, Pafilis E (2020) PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes. *GigaScience* 9 (3). <https://doi.org/10.1093/gigascience/giaa022>