

2021 Annual SCOR Working Group Report

1. Name of group

SCOR WG157 MetaZooGene: Toward a new global view of marine zooplankton biodiversity based on DNA metabarcoding and reference DNA sequence databases

2. Activities since previous report to SCOR (e.g., virtual or in-person meetings, email discussions, special sessions). Limit 1000 words

Virtual Meetings and Email Discussions for Creation of MetaZooGene Barcode Atlas & Database

Planning and cooperation among WG157 members was carried out through email, virtual meetings, and shared website workspaces to allow completion of the MetaZooGene Barcode Atlas & Database (MZGdb, <https://metazoogene.org/database>). The effort was led by WG157 member Todd O'Brien (NOAA, USA). Email and virtual meetings also resulted in a multi-authored review paper linked to the MZGdb were led by Ann Bucklin (University of Connecticut, USA). Additional information is provided below (Section #4, ToR 1).

Special Session at (virtual) ASLO 2021 Aquatic Sciences Meeting (23 June 2021)

MetaZooGene members chaired SS32 – “Name that species: Toward a new global view of species diversity of marine zooplankton” at ASLO 2021 on June 23, 2021. Chairs: Silke Laakmann* (Helmholtz Institute for Functional Marine Biodiversity at the University of Oldenburg, DE), Leocadio Blanco-Bercial* (Bermuda Institute of Ocean Science, BM), Katja Peijnenburg* (Naturalis Biodiversity Center and University of Amsterdam, NL), and Ann Bucklin* (University of Connecticut, USA). Several WG157 members were among the presenters, indicated by asterisk (*); early career co-authors are also indicated (EC).

1. Cornils, A.* - Why do we need integrative methods in marine zooplankton species identification?
2. O'Brien, T.D.* - Exploring marine zooplankton with the MetaZooGene Barcode Atlas and database: What we know, where we know it, and what we still need to discover.
3. Govender, A.^{EC}, Singh, S., Groeneveld, J., Willows-Munro, S. - Metabarcoding of zooplankton enhances analyses of connectivity in marine pelagic environments.
4. Martell, L., Soto-Àngel, J., Hosia, A.* - Diversity assessment of hydromedusae and siphonophores: lessons from the Norwegian Taxonomy Initiative.
5. Choo, L.Q.^{EC}, Choquet, C.^{EC}, Goetze, E.*, Hoarau, G., Peijnenburg, K.C.T.A.* - Genome-wide phylogeography of a circumpolar planktonic calcifier
6. Smith, S.^{EC}, Santoferrara, L., Katz, L., McManus, G., - Navigating cryptic species boundaries in marine ciliates using single-cell 'omics.
7. Beckmann, L., Hosia, A.*, Martell, L. - Linking zooplankton and benthos: an integrative approach to identify the diversity of hydromedusae
8. Ohnesorge, A.^{EC}, Taudien, S., John, U., Neuhaus, S., Laakmann, S.* - Evaluation of multi-taxa identification of the zooplankton community in dynamic temperate waters. Poster

- Documents published since previous report to SCOR (e.g., peer-reviewed journal articles, reports, Web pages) and should be limited to publications that resulted directly from WG activities and which acknowledge SCOR support

Bucklin, A., Peijnenburg, K.T.C.A., Kosobokova, K.N., O'Brien, T.D., Blanco-Bercial, L., Cornils, A., Falkenhaus, T., Hopcroft, R.R., Hosia A., Laakmann, S., Li, C., Martell, L., Questel, J.M.^{EC}, Wall-Palmer, D.^{EC}, Wang, M., Wiebe, P.H., Weydmann-Zwolicka, A. (2021) Toward a global reference database of COI barcodes for marine zooplankton. *Marine Biology* 168 (78). <https://doi.org/10.1007/s00227-021-03887-y>

Machida, R., Kurihara, H., Nakajima, R., Sakamaki, T., Lin, Y.-Y., Furusawa, K. (2021) Comparative analysis of zooplankton diversities and compositions estimated from complement DNA and genomic DNA amplicons, metatranscriptomics, and morphological identifications. *ICES Journal of Marine Science*, fsab084. <https://doi.org/10.1093/icesjms/fsab084>

Parry, H., Atkinson, A., Somefield, P., Lindeque, P. (2021) What does conventional plankton monitoring miss? A metabarcoding comparison of taxonomic richness, composition and density between the water column and the benthic boundary layer. *ICES Journal of Marine Science* <https://doi.org/10.1093/icesjms/fsaa228/6042356>

- Progress toward achieving group's terms of reference. List each term of reference separately and describe progress on each one. Limit 1000 words

ToR 1) Create an open-access web portal for DNA barcodes for marine zooplankton

The MetaZooGene Barcode Atlas & Database (MZGdb, <https://metazoogene.org/database>) is now online and open access to all users. The release of the MZGdb was announced and introduced by a multi-authored review paper published in *Marine Biology* <https://doi.org/10.1007/s00227-021-03887-y>. The MZGdb is a reference database and valuable resource for DNA barcoding and metabarcoding of marine zooplankton and fish, with advanced search functions by ocean region and taxonomic group. The MZGdb now includes ~186,000 barcodes, and is updated regularly from GenBank and BOLD.

ToR 2) Design an optimal DNA barcoding pipeline for marine zooplankton

A best practices document describing an optimal pipeline for DNA barcoding of marine zooplankton, including optimal protocols for collection and preservation of samples and specimens, remains an important deliverable for WG157. Despite increasingly frequent use of DNA sequencing of identified specimens by museum collections and major research laboratories, there are no publicly accessible guidelines for DNA barcoding of zooplankton. Given the lack of existing documents, this is a useful and worthwhile WG157 deliverable.

ToR 3) Develop best practices for DNA metabarcoding of marine zooplankton biodiversity

WG157 members are planning to design a metabarcoding inter-calibration experiment, which will entail assigning specific laboratory and bioinformatics protocols and parameters to participating WG157 members, and may include the use of standard samples and mock communities. The inter-calibration analysis will seek to determine which steps in the analytical pipeline have the biggest impacts on the results. Renewed progress on this deliverable is planned for 2021-2022.

5. WG activities planned for the coming year. Limit 500 words

Annual WG157 Meeting @ Ocean Sciences Meeting 2022 (Hawaii; 27 Feb – 4 Mar 2022)

MetaZooGene WG157 will meet in association with OSM 2022, which will be held in Honolulu, Hawaii, USA (27 Feb – 4 Mar 2022); see <https://www.aslo.org/osm2022/>. The meeting will be planned for hybrid (in person and virtual) format, similar to the current planning for OSM 2022.

An OSM 2022 Theme Session proposal, “*Zooplankton diversity through space and time*”, was submitted by MetaZooGene members Katja Peijnenburg* (Naturalis Biodiversity Center, NL) and Erica Goetze* (University of Hawai’i at Manoa, USA), with colleagues Galice Hoarau (Nord University, NO), and Matthew Miller (University of Victoria, CA). The session proposal is directly related to WG157 goals and acknowledges SCOR MetaZooGene.

An important topic for the WG157 2021 meeting will be planning for the inter-calibration experiment to develop best practices for DNA metabarcoding of marine zooplankton biodiversity (ToR 3). A primary first step is to assign specific laboratory and bioinformatics protocols and parameters to participating WG157 members.

Special journal issue in ICES Journal of Marine Science

A Themed Set of the ICES Journal of Marine Science entitled: “*Patterns of biodiversity of marine zooplankton based on molecular analysis*” is now in final production stages. WG157 members Ann Bucklin, Katja Piejnenburg, Ksenia Kosobokova and Ryuji Machida are named as ‘motivators’ and will prepare an overview and introduction for the special issue. Currently, 11 manuscripts are accepted for publication, 2 of which acknowledge SCOR and NSF funding (see https://academic.oup.com/icesjms/pages/themed_sets).

Planning for Capacity Building Workshops

- Hands-on ‘DNA-to-data’ training workshop, organized by Ryuji Machida, Academia Sinica (Taipei, Taiwan). A summer workshop is in (tentative) planning stages. Funding will be requested from SCOR, PICES, and other sources.

- Online bioinformatics workshop for metabarcoding, organized by Ann Bucklin, University of Connecticut (USA). An online training session focused on statistical analysis and bioinformatics of DNA sequencing data for metabarcoding is being planned. UConn computing facilities and expert bioinformatics support staff will provide overviews; Todd O’Brien (NOAA NMFS, USA) will lead demonstrations on use of the MZGdb Atlas and Database.

Support for Early Career Scientists

- Early Career participants have joined every WG157 activity, including meetings, special sessions at conferences, and publications. Individuals are indicated in this report summary by superscript (^{EC}) and are listed in XLS impact summary provided.

Continued Progress on Deliverables

- Progress on Terms of Reference and Deliverables will continue online and via web resources, including project-specific web “work spaces” for WG157 members.

6. Is the group having difficulties expected in achieving terms of reference or meeting original time schedule? If so, why, and what is being done to address the difficulties Limit 200 words

Work toward WG157 deliverables has continued despite the challenges of COVID-19 pandemic, with the exception of activities (e.g., Term of Reference #3) requiring molecular benchwork, due to restrictions by most universities and institutes. Private online work-areas were created for WG157 members, including one for all members and another for specific activities. These areas are linked to the website for the group, <https://metazoogene.org/>, and are valuable tools for collaboration by allowing uploading and sharing of files, which is not possible for all WG157 using other web platforms.

7. Any special comments or requests to SCOR. Limit 100 words.

N/A

Additional information can be submitted and will be included in the background book for the SCOR meeting at the discretion of the SCOR Executive Committee Reporter for the WG and the SCOR Secretariat.