

Working Group Report to SCOR (2020)

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

Meetings:

2019 Annual Meeting of MetaZooGene SCOR WG157 was held at the Gothenburg Global Biodiversity Center (GGBC, Gothenburg, Sweden) on Saturday, September 14, 2019, in association with the Annual Science Conference of the International Council for the Exploration of the Sea (ICES). The first annual meeting of WG157 was attended by 15 members (including associate members) and 13 invited guests. WG157 members were encouraged to invite colleagues and collaborators with closely-related interests, with priority given to early career, postdoctoral fellows, and students. Björn Källström (GGBC) and Erik Selander (Dept. Marine Sciences, University of Gothenburg) were our local hosts, who encouraged participation by local researchers and provided outstanding meeting space. Participants presented overviews of their research interests and expertise, expected contributions to MetaZooGene, and summaries of ongoing and future activities.

SCOR Symposium: *Rediscovering pelagic biodiversity: Progress, promise, and challenges of metabarcoding of microbes to mammals*, was held at the Swedish Exhibition & Congress Centre (Gothenburg, Sweden) on September 13, 2019. The Symposium was co-sponsored by ICES, IOC, and other groups. The convenors were Ann Bucklin (University of Connecticut, USA) and Bengt Karlson (Swedish Meteorological and Hydrological Institute, Sweden). The Symposium was organized into three sessions: Diversity of the pelagic assemblage; Data and database resources; and Exploring the potential of metabarcoding. The talks were followed by a discussion session organized and led by Anders Andersson and Katja Peijnenburg. The SCOR Symposium was attended by 50 people (the maximum capacity allowed for the venue), with participants from 20 different countries.

2020 Annual Meeting of MetaZooGene SCOR WG157 was held in association with the Ocean Sciences Meeting (OSM 2020, San Diego, CA USA) on Sunday, February 16, 2020. In all, 14 people joined the meeting, plus one via SKYPE. All members and guests introduced themselves, briefly describing their interests. WG157 members were encouraged to invite guests to the meeting, especially students and early-career scientists with related interests. The meeting began with a review the Agenda (Appendix I) and overview of the MetaZooGene plan of work. SCOR overviews were provided by Ed Urban and Patricia Miloslavich, who summarized what SCOR expects of each WG. In response to questions about SCOR's goals for capacity building, Ed explained that SCOR seeks to reach out to students world-wide, has a committee on capacity building, and a website with suggested approaches (see <https://scor-int.org/work/capacity/>). Recognizing that funds are limited for capacity building, WGs are encouraged to seek additional funds for this effort.

Lunch Meeting at OSM 2020 for WG157 members and guests was held during the Ocean Sciences Meeting on February 20, 2020. Enrique Montes Herrera, new SCOR Reporter for WG157, joined the meeting and described his role as the SCOR Reporter and his research interests.

SCOR Exhibit Booth at OSM 2020 was staffed by WG157 member Todd O'Brien, who demonstrated the MetaZooGene DNA barcode database and atlas. There was considerable interest from visitors to the booth, which provided an opportunity to widen the reach of WG157 and obtain advice and feedback from interested researchers and managers.

3. 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

Laakmann, Silke, Leocadio Blanco-Bercial, and Astrid Cornils (2020, In Press) The crossover from microscopy to genes in marine diversity - from species to assemblages in marine pelagic copepods. *Philos. Trans. Royal Society B*

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

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

The DNA barcode data and metadata have been assembled and posted to an open-access web portal, with deep links to the GenBank records and associated publications (see <https://metazoogene.org/products>). The goal is a comprehensive summary and analysis of COI barcodes available for holopelagic mesozooplankton taxa, organized by ocean region with explicit intent to achieve global coverage. The MetaZooGene barcode atlas now includes maps of global distributions for 20 zooplankton taxonomic groups. The MetaZooGene database (MZGdb) now includes ~186,000 barcodes, and is updated regularly from GenBank and BOLD. The DNA sequence data will be downloadable for use as a reference sequence database for species identification of marine zooplankton from metabarcoding analysis of environmental samples.

2) Design an optimal DNA barcoding pipeline for marine zooplankton

Progress is being made on preparing a best practices document describing an optimal pipeline for DNA barcoding marine zooplankton, including optimal protocols for collection and preservation of samples and specimens. WG157 member Leocadio Blanco-Bercial has searched for existing documents from museum collections and major research laboratories, but could not find any written guidelines for DNA barcoding of zooplankton. Given the lack of existing documents, this will indeed be a useful and worthwhile WG157 deliverable.

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

WG157 members are committed to advancing this topic, and are focusing on designing a metabarcoding inter-calibration experiment, with allocation of alternative laboratory and bioinformatics protocols and parameters to the laboratories of participating WG157 members. The inter-calibration analysis would then be able to determine which steps in the analytical pipeline have

the biggest impacts on the results. The use of “standard samples” and “mock communities” was discussed. Next steps are to agree upon the logistical organization and coordination of the people and labs involved, and to design the experiment to ensure eventual publication. Ann agreed to prepare a draft list of the critical metabarcoding protocol steps and distribute to WG157 members to identify their interest, willingness, and ability to carry out testing of particular protocol steps.

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

Special journal issue in ICES Journal of Marine Science

Ann Bucklin, Katja Piejnenburg, Ksenia Kosobokova and Ryuji Machida are named as ‘motivators’ for a special issue on “Patterns of biodiversity of marine zooplankton based on molecular analysis” in the ICES Journal of Marine Science. Currently, 12 manuscripts have been promised from WG157 member authors. The call for papers is public and has attracted additional manuscripts that will increase attention for the subject and impact of the WG157 contributions. See https://academic.oup.com/icesjms/pages/themed_sets

Review paper: DNA Barcoding of Marine Zooplankton (Ann Bucklin, Katja Peijnenburg, et al.)

Work is ongoing for a manuscript for submission to Marine Biology Reviews: *Toward a global reference database of COI barcodes for marine zooplankton*. The WG157 co-authors have agreed to provide sections either by taxonomic group or ocean regions. A primary goal of the review paper is to answer the question of completeness of the barcode database for zooplankton. Next step is for authors to submit any unpublished barcode data; these will be added to the MZGdb and included in the review paper.

Planning for Capacity Building Workshops

- Hands-on ‘DNA-to-data’ training workshop, organized by Ryuji Machida, Academia Sinica (Taipei, Taiwan). A workshop is tentatively planned for Summer 2021. 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 and atlas. Continue 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 has slowed somewhat due to the challenges of COVID-19 pandemic. Research laboratories in most universities and institutes have been closed for ~2 months. Working from home reduced productivity and progress for many WG157 members, especially those with family responsibilities.

In response, private online work-areas were created for WG157 members, including one for all members and another for co-authors of the Review Paper. 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.