

# WORKING GROUP ON INTEGRATED MORPHOLOGICAL AND MOLECULAR TAXONOMY (WGIMT)

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## WORKING GROUP ON INTEGRATED MORPHOLOGICAL AND MOLECULAR TAXONOMY (WGIMT)

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## i Executive summary

The ICES Working Group on Integrated Morphological and Molecular Taxonomy (WGIMT) met online 09 June 2022. The meeting was chaired by Elaine Fileman (UK) and Jasmin Renz (Germany) and was attended by 22 scientists representing 11 countries. During the meeting, WGIMT members reviewed progress on multi-annual ToRs, reports, and recommendations, evaluated progress on existing ToRs and sought opportunities for partnerships in the ICES science community. WGIMT membership currently totals 63 members from 19 countries; new members were added again this year, continuing the steady increase in membership numbers each year since 2013. This trend is consistent with WGIMT goals to enhance our capacity for developing and using morphological and molecular approaches to taxonomic analysis of zooplankton.

Extensive progress has been made in the identification of challenging zooplankton taxa in the ICES area (including hidden diversity associated with cryptic, rare, and invasive species and species delimitation) by performing a meta-analysis in cooperation with the Working Group on Zooplankton Ecology (WGZE) on the most abundant taxa from 19 monitoring stations based on expert knowledge from the respective sites (ToR A). A review that aims to provide condensed up to date information on these important taxa, pinpoints important species complexes as well as the identification issues for these key taxa, and evaluates the relevance of potentially hidden diversity or non-accessible diversity for ecosystem and time-series studies is planned for autumn 2022.

The WGIMT web platform has been updated (ToR B), it will continue to be expanded as WGIMT continues into the future. In strong partnership with SCOR WG 157 (MetaZooGene), the WGIMT/MetaZooGene Barcode Atlas and Database was launched and a link implemented into the platform. This Atlas summarizes the geographic distribution and barcoding status of zooplankton species in the ICES North Atlantic subregion, the Baltic Sea, and the Mediterranean Sea.

WGIMT continued to initiate and support provision of standards, preparation of training materials, and organization of formal workshops (ToR C) and made lectures given during the first Advanced Zooplankton Course (Stazione Zoologica Anton Dohrn, MOTax, October 2018) on morphological and molecular taxonomy of copepods available on the WGIMT portal.

WGIMT promoted and encouraged the continuing integration of molecular and morphological taxonomy by organizing special sessions at national and international conferences, including the ASLO 2021 Aquatic Sciences Meeting and the 13th International Conference on Copepoda. During 2020–2022, WGIMT members published at least 9 relevant peer-reviewed articles directly related to the core mission and goals of the EG. A special journal issue in the ICES Journal of Marine Science entitled: Patterns of biodiversity of marine zooplankton based on molecular analysis, was organized by member Ann Bucklin and colleagues, who also wrote an overview and introduction for the special issue. In all, 15 manuscripts were included in the special issue ([https://academic.oup.com/icesjms/pages/themed\\_sets](https://academic.oup.com/icesjms/pages/themed_sets)), of which 4 were co-authored by WGIMT members.

WGIMT has a strong partnership with SCOR WG 157 (MetaZooGene) and collaborated closely with WGZE, the Working Group on Phytoplankton and Microbial Ecology (WGPME) and the Working Group entitled Towards a European Observatory of the non-indigenous calanoid copepod *Pseudodiaptomus marinus* (WGEUROBUS) on joint session proposals and a ToR to expand the WGIMT/ MetaZooGene Barcode Atlas to include genetic information on Phyto- and Microzooplankton.

## ii Expert group information

<b>Expert group name</b>	Working Group on Integrated Morphological and Molecular Taxonomy (WGIMT)
<b>Expert group cycle</b>	Multiannual
<b>Year cycle started</b>	2020
<b>Reporting year in cycle</b>	3/3
<b>Chairs</b>	Elaine Fileman (UK)
	Jasmin Renz (Germany)
<b>Meeting venue and dates</b>	27 March 2020, online (25 participants)
	1 October 2020, online (27 participants)
	26 February 2021, online (27 participants)
	27 September 2021 online (17participants)
	9 June 2022 online (22 participants)

# 1 Introduction

The main focus of the ICES Working Group on Integrated Morphological and Molecular Taxonomy (WGIMT) is to promote and provide new tools for species-level taxonomic analysis of the pelagic ecosystem. WGIMT works towards these objectives with a particular focus on species recognition, discrimination, and identification of marine metazoan zooplankton species and communities. Closely allied with this are more specific goals, including the detection of cryptic species and determination of the evolutionary/systematic relationships between pelagic metazoan species.

WGIMT seeks to contribute to efforts to analyse, recognise, and understand changes in community structure, species diversity, and species phenology and productivity. Furthermore, the group contributes to ICES efforts to understand and predict how these characteristics will affect trophic relationships and foodwebs, as well as the transfers and cycles of nutrients, chemical elements, energy, and biological production. In addition to the [ICES-hosted WGIMT brief overview page](#), WGIMT has designed and maintains a web portal (<http://wgimt.net>) to facilitate access to useful websites, materials, and online publications related to morphological, molecular, and optical approaches to species identification of marine zooplankton.

## 2 ToR A - Evaluate the potential of molecular and morphological approaches for understanding zooplankton communities

Molecular methods are widely used for rapid assessment of species diversity and can contribute to improving our understanding of the impacts of climate change and anthropogenic effects on marine ecosystems. Standardized protocols for assessment of pelagic biodiversity are needed to fulfil requirements defined in the Marine Strategy Framework Directive (MSFD). There is a need for intercomparison of results to understand the impact of protocol choice. A range of molecular approaches, e.g. barcoding and metabarcoding, environmental DNA (eDNA), or proteomic approaches can be adopted to help to address some of the key applications of integrative taxonomy.

### **Review the current methods for integrative morphological and molecular taxonomy and evaluate the impacts of choosing different protocols (deliverable 1)**

This deliverable addresses the core competence of the working group as it specifically focuses on the value of integrative studies using molecular and morphological tools. Two highlights of the scientific outputs of the WGIMT group are referenced here in more detail. Laakmann and co-authors discuss past, present and forward-looking perspectives on identifying and recording planktonic diversity in the context of marine biodiversity conservation and management (Laakmann *et al.*, 2020). They specifically focus on the transition from traditional species identification based on morphological diagnostic characters to full molecular genetic identification of marine assemblages. Advantages and drawbacks of each method are evaluated (Table 2.1) and used to assess the strength and usefulness of different integrative approaches to address different research questions. From their meta-analysis comparing morphological and molecular multi-species identification, they conclude that the molecular approach is not yet ready to completely replace morphological analyses. They strongly recommend (1) ground-truthing of metabarcoding by direct comparison to the traditional morphological taxonomic analysis especially for quantification and (2) the implementation of protocol optimization and error minimization into metabarcoding studies followed by a downstream analysis that considers potential and remaining biases. This is even more necessary for metabarcoding of environmental DNA for which there is still an urgent need for best practices ranging from field to laboratory and data processing standards.

More details on specific protocols are covered by the ICES Journal of Marine Science theme session initiated by Ann Bucklin and co-authors (Bucklin *et al.*, 2021). They present a synergistic output from WGIMT and SCOR WG 157 “Metazoogene” activities documenting important advances in molecular protocols and procedures, integration with morphological taxonomic identifications, and quantitative analyses. This collection provides an overview on a variety of applied protocols including different target genes, but also on new developments in ribonucleic acid barcoding, meta-transcriptomics, and population genomics. They identify three major milestones that need to be targeted in future research: (1) taxonomically complete DNA reference databases for different target gene regions, based on morphologically identified species across the broad taxonomic range of marine zooplankton, (2) reference genomes and transcriptomes for species representing all the taxonomic groups of the pelagic assemblage, and (3) development of



transcriptomic resources providing tools to reveal physiological responses and adaptive potential of species, and allowing prediction of future changes in pelagic ecosystems.

potentials		drawbacks
morphological identification		
	# information on	# requires taxonomic expertise on diverse groups
	— life stage composition and size class distribution	# incoherent species descriptions
	— traits and hence ecological role/function	# gender- and stage-related diagnostic species characters
	— quantification (abundance, biomass)	# identification depends on condition of the organism
		# subjective nature of diagnostic characters
		# no identification of sibling and cryptic species and populations
		# time intensive
molecular genetic identification		
single species	# species identification of young developmental stages and cryptic/sibling species → higher diversity	# requires prior methodological knowledge
	# identification of populations	
	# standardized identification, automation	
metabarcoding	# simultaneous identification of a multitude of species	# no information on
	# processing of large numbers of samples	— community structure regarding size and stage distribution
	# efficient and cost-effective for analysing bulk samples	— biomass and abundance
	# standardized identification, automation	— ecological role
		# depends on high-quality sequence reference database for different regions and progress in providing sequence reference entries
		# identification of thresholds
		# false positives, false negatives
		# primer and PCR biases (amplicon sequencing)

**Table 2.1. Potentials and drawbacks for the traditional morphological and molecular genetic species identification in biodiversity analyses (modified from Laakmann *et al.*, 2020).**

## Construct an overview of case studies utilizing combined molecular and morphological approaches in zooplankton taxonomy (deliverable 2)

The compilation of case studies on integrated approaches on morphological and molecular taxonomy within the WGIMT community currently comprises 46 case studies providing an overview of WGIMT-related activities in the field of plankton research. The WG established an online table to provide access to the information on applied methods to all members and facilitate discussion on applied methods and knowledge transfer between working group members. Most studies focus either on single groups of crustacean or gelatinous plankton, or on metabarcoding of the whole community.

**Table 2.2 Taxonomic focus of ongoing integrative plankton studies within the WGIMT community using combined molecular and morphological approaches.**

Focus of study	Number of studies
Taxa specific approaches	
Crustacea (Copepoda, Cladocera)	9

Gelatinous (Cnidaria, Appenticularia, Tunicata	5
Other	1
<b>Metabarcoding</b>	
Mesozooplankton community	19
With taxonomic focus	12

The analysis of applied methods revealed that identification based on morphological characters is an essential component in nearly 90% of all studies (Figure 2.1). Classical taxonomy, such as description of new species, is addressed by 15% of the studies. Nearly 70% of studies use multi-species approaches and novel approaches using environmental DNA are applied in nearly one fifth of the studies.

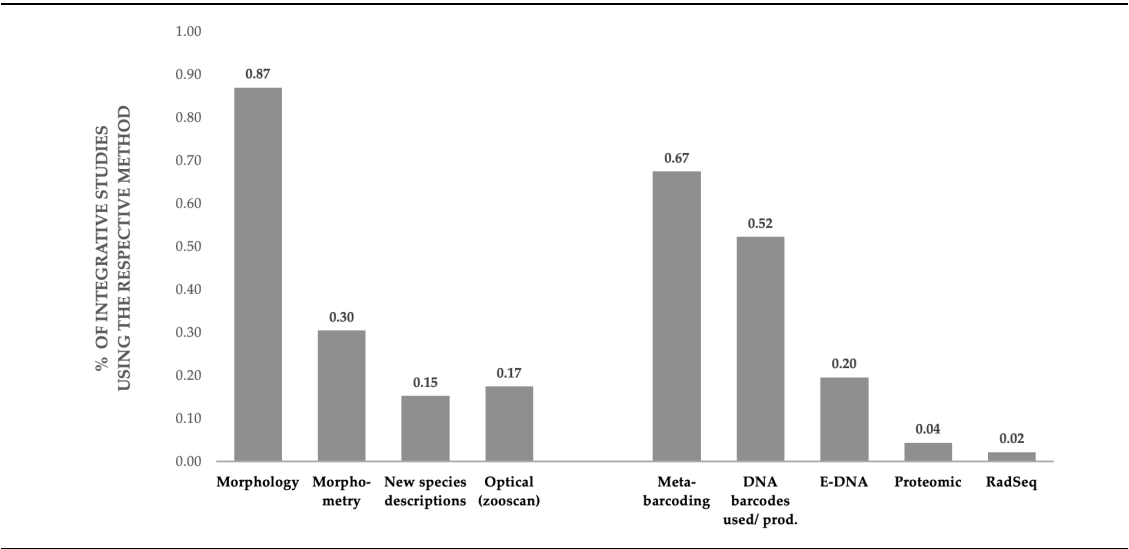


Figure 2.1. Relative importance (% of studies) of a method in integrative studies within the WGIMT group using combined morphological and molecular approaches in zooplankton studies.

**Compile a list of challenging zooplankton taxa which will include a top-ten list of zooplankton species complexes in the ICES area (including hidden diversity associated with cryptic, rare, and invasive species and species delimitation; deliverable 3)**

A meta-analysis from the WGZE provided information to WGIMT on the most abundant taxa from 19 monitoring stations based on expert knowledge from the respective sites (Figure 2.2). In total 60 species groups, or taxon groups, to be of high importance were identified.

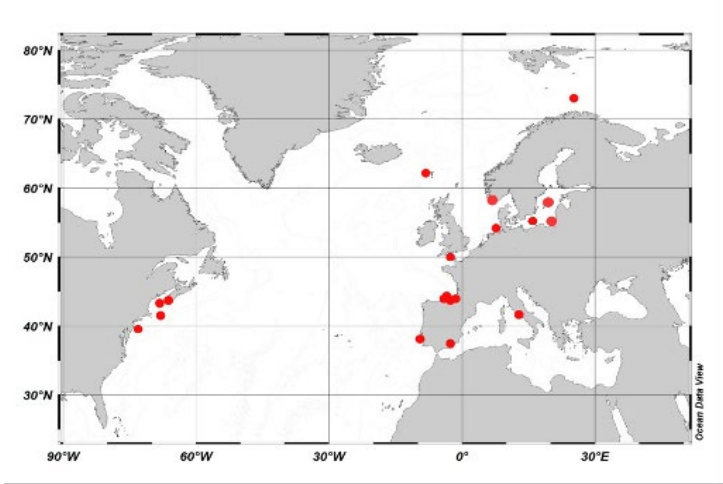


Figure 2.2 Monitoring stations included in the meta-analysis.

Within these species groups, we identified challenging taxa and species complexes and grouped these taxa based on the issues coming along with their identification in species groups (i) considered to be cryptic, (ii) that can only be identified by laborious identification (and sometimes only in a certain planktonic life stage), (iii) that cannot be identified during the whole pelagic phase (but sometimes in the benthic phase), and (iv) that are new to the ecosystem and may have been overlooked in recent years.

cryptic species complexes	laborious identification	no identification	non-indigenous species
<i>Acartia</i> spp.	<i>Oithona</i> spp.	early life stages of holoplankton	<i>Oithona davisae</i>
<i>Oithona</i> spp.	<i>Lucicutia</i> spp.	meroplanktonic larvae	<i>Pseudodiaptomus marinus</i>
<i>Pseudocalanus</i> spp.	<i>Oncaea</i> spp.		<i>Eurytemora carolleeae</i>
<i>Paracalanus</i> spp.	<i>Calanus</i> spp.		<i>Acartia</i> spp.
<i>Eurytemora</i> spp.	<i>Clausocalanus</i> spp.		<i>Mnemiopsis leidyi</i>
<i>Aurelia</i> spp.	<i>Acartia</i> spp.		
	Mesopelagic scyphozoans		
	<i>Cyanea</i> spp.		
	<i>Rhizostoma</i> spp.		
	<i>Beroe</i> spp.		

Table 2.3. List of challenging zooplankton taxa grouped by identification issue

It becomes obvious from this list that taxonomic challenges, such as identification of specimens from cryptic species complexes or species groups with high morphological similarity, is not a minor issue restricted to rare taxa. These challenges exert a significant impact on taxa identification in many zooplankton time-series. The WG therefore decided to extend on this ToR and to produce a review that aims (i) to provide condensed up to date information on the important

taxa from the zooplankton time-series in the North Atlantic and adjacent seas including the Baltic Sea and Mediterranean regions, (ii) to pinpoint important species complexes as well as identification issues for these key taxa, and (iii) to evaluate the relevance of potentially hidden diversity (cryptic species complexes) or non-accessible diversity (identification only on high taxonomic level) for ecosystem and time-series studies. The WGIMT worked extensively via correspondence and via online meetings on the draft and the submission of the manuscript is planned for autumn 2022.

### 3 ToR B - Continue development and enhancement of the WGIMT Resource Portal

The development of the WGIMT web portal (<https://wgimt.net>) was continued throughout the 3-year term. In addition to basic maintenance activities such as updating the topic-based literature lists with related publications from 2021 and 2022, the following improvements have been made to the web page: A “WGIMT Terms of Reference” (ToRs) section has been added, summarizing the current (2020–2022) topics and activities being pursued by WGIMT members. A new “Outreach & Training” section has been added, this provides information on WGIMT-related training courses, workshops, conferences, presentations, and publications. The “[WGIMT/Meta-ZooGeneBarcode Atlas](#)” interface and content has been updated. Developed in close collaboration with SCOR WG157 (MetaZooGene), this database now includes a total of 218,299 barcode sequences for cytochrome oxidase I (COI) for 11,356 (25%) of the total 45,345 recognized species of marine zooplankton. The database creator, WGIMT member Todd O’Brien (NOAA Fisheries) has expanded the database to include multiple gene regions used as barcodes and has added fish to the zooplankton focus. Collection records from the OBIS and COPEPOD databases, barcoding coverage, and summary statistics have been generated for > 80 taxonomic groups for multiple ocean basins and regions. The database is a unique and valuable resource for biodiversity researchers and fisheries managers, allowing targeted searches by ocean regions and taxonomic groups, and providing coverage statistics that guide priorities for efforts toward a complete reference database for marine zooplankton.

Work in progress continues on updating the Optical Methods overview page, adding new instruments, and photos, as well as updating associated contacts and relevant publications for each instrument. In addition, a link to current glossaries of molecular terms will be added, e.g. Kahlert *et al.*, (2019) “New molecular methods to assess biodiversity. Potentials and pitfalls of DNA metabarcoding: a workshop report”.

## 4 ToR C - Initiate and support provision of standards, training materials, and taxonomy workshops

During the last three-years (2020-2022), despite the Covid-19 restrictions that severely limited the realization of a series of initiatives and prevented in-person meetings in 2020 and 2021, a number of ToR C activities could still be carried out.

### Provision of training materials via WGIMT resource portal (deliverable 1)

A detailed protocol for zooplankton sample scanning and processing with ZooProcess has been organized and shared by Nerea Valcárcel (IEO-CSIC, Malaga) in the '[Laboratorio de Plancton](#)' blog to provide technical assistance in the identification and/or implementation of the different methods related to zooplankton image analyses.

Seven lectures presented during the first Advanced Zooplankton Course (Stazione Zoologica Anton Dohrn - SZN, MOTax, October 2018) on morphological and molecular taxonomy of copepods have been prepared for the online version by Iole Di Capua and Rosario Balestrieri (SZN, Naples) with the courtesy of the authors G. A. Boxshall, E. L. Markhaseva, A. Cornils, I. Di Capua, M.G. Mazzocchi and R. Böttger-Schnack. These lectures are now available online on the WGIMT portal (<https://wgimt.net/outreach/training>) and on the YouTube channel of SZN. In detail, Geoff Boxshall prepared two introductory lectures on copepod taxonomy and evolution with a comprehensive and updated view of the traditional and most recent approaches including the molecular ones. Elena Markhaseva focused her presentation on calanoid Aetideidae, a common and widespread family in meso- and bathypelagic waters. Taxonomy of the Paracalanidae family was prepared by Astrid Cornils, who presented the most recent research conducted on the morphological and molecular taxonomy of the genus *Paracalanus*. For the family Paracalanidae, a lecture dedicated to the genus *Calocalanus* was prepared by Iole Di Capua. The cyclopoids were the subject of the lectures prepared by Maria Grazia Mazzocchi on *Oithona* species with notes on their biology and ecology, and by Ruth Böttger-Schnack on the very diversified and tricky world of oncaeids, with the explanation of the OncoIdent website for the interactive identification.

In conjunction with WGZE, some members of the WGIMT contributed to the preparation of some of the Plankton ID Leaflets produced by the WGZE (Editors Antonina dos Santos and Lidia Yebra) with updated keys for morphological identification and links to molecular taxonomy on Hydrozoa, Copepoda, Cladocera, Decapoda, which have been regularly published. ID leaflets on the copepods *Temora* (No. 195), *Acartiidae* (No. 194), and *Chaetognatha* (No. 193) are now available on the [ICES website](#), and the publication of *Paracalanus* (Copepoda), *Plagusidae* and *Grapsidae* (Decapoda) are due soon.

### Taxonomy workshops and laboratory exchanges (deliverable 2)

In person taxonomy workshops and laboratory exchanges were temporarily suspended due to Covid-19 restrictions. The course on "Appendicularian taxonomy" planned by Rade Garić and the "Second Advanced Zooplankton Course" at SZN were postponed. However, once restrictions lifted, a lab exchange was carried out between the German Centre for Marine Biodiversity Research (Hamburg) and the Portuguese Institute of the Sea and the Atmosphere for two

weeks to validate and improve the identification of decapod larvae to establish correct reference libraries for metabarcoding in the North Sea.

In April 2022, an international course on “Diversity, Systematics and Biology of Hydrozoa” was held at the Espegrend Marine Biological Station of the University of Bergen (Norway) ([https://www.forbio.uio.no/events/courses/2022/Hydrozoa Espgrend 2021](https://www.forbio.uio.no/events/courses/2022/Hydrozoa_Espgrend_2021)). This successful 5-day course was taught by seven experts, including WGIMT members, and was attended by ~20 students. The course aimed at providing students with state-of-the-art knowledge of hydrozoan biology and hands-on experience in field and laboratory work, including providing them with taxonomic and methodological skills for sampling and identifying the most common benthic and pelagic species occurring in the North Sea and Eastern Atlantic Ocean.

### **Promotion of best practices for DNA barcoding of zooplankton (deliverable 3)**

WGIMT members take advantage of linking activities, sharing information and collaborating with SCOR Working Group 157 “MetaZooGene” led by WGIMT member Ann Bucklin.

WGIMT member Ann Bucklin and several WGIMT/WG157 members have accepted an invitation from an editor of a planned book focused on molecular protocols. The chapter will be designed to provide guidelines for DNA barcoding of marine zooplankton, including preservation and sequencing of identified specimens, and analysis and interpretation of DNA barcode data. The target audience for the book chapter will include curators of museum collections and researchers focused on diverse topics requiring accurate identification of species.

WGIMT members are involved in a WG157 metabarcoding inter-calibration experiment, which will entail distribution of a set of reference samples among the laboratories of participating WGIMT and WG157 members. The eventual publication will compare results for the reference samples and evaluate the impact and significance of different molecular, bioinformatics, and statistics protocols and parameters used by the research groups. Continued progress is planned for 2022-2023.

## 5 ToR D - Continue to demonstrate leadership in promoting and encouraging use of integrative taxonomic approaches for assessment of pelagic biodiversity

Organize and promote special sessions at national and international conferences: e.g. ICES ASC; ASLO/TOS Ocean Sciences Meetings (deliverable 1)

Members of the working group lead a theme session during the ASLO 2021 Aquatic Sciences Meeting in June 2021 (*Name that species: Toward a new global view of species diversity of marine zooplankton*, conveners: Silke Laakmann, Leocadio Blanco-Bercial, Katja Peijnenburg, Ann Bucklin), were represented in the Steering Committee of the virtual 13th International conference on Copepoda (e-ICOC, July 2022), and led a symposium on '*Marine planktonic copepods: from biodiversity to ecology*' Iole Di Capua, Astrid Cornils) during the conference.

WGIMT members Ann Bucklin, Leocadio Blanco-Bercial and Silke Laakmann, together with additional SCOR MetaZooGene members, have organized and will convene a special MetaZooGene Symposium, New insights into biodiversity, biogeography, ecology, and evolution of marine zooplankton based on molecular approaches, in association with the ICES Annual Science Conference (Hybrid; Dublin, Ireland; September 23, 2022). The program currently includes 26 presentations, of which 14 are by Early Career Scientists (ECS), and 10 WGIMT members are co-authors in various presentations (see: <https://metazoogene.org/planned/symposium2022>).

### **Publish peer-reviewed scientific papers on topics central to the WGIMT mission (deliverable 2)**

WGIMT members have led a number of peer-reviewed publications, which have demonstrated leadership in identifying topics and areas of high priority for new research that use integrated morphological – molecular approaches to characterize pelagic diversity. A review paper that was published by Laakmann *et al.* (2020) illustrated the transition from traditional species identification based on morphological diagnostic characters to full molecular genetic identification of marine assemblages. It highlighted how molecular tools could aid in cases where morphological approaches were insufficient to properly understand species limits, distribution, community composition or even community ecology processes (Laakmann *et al.*, 2020). This article was also presented in the ICES highlights section.

Members of the working group also successfully published several articles in the ICES JMS Themed Set '*Patterns of biodiversity of marine zooplankton based on molecular analysis*' with an article on 'New insights into biodiversity, biogeography, ecology, and evolution of marine zooplankton based on molecular approaches' (Bucklin *et al.*, 2021), the introduction to the cooperative WGIMT/MetaZooGene (SCOR 157) database '*Toward a global reference database of COI barcodes for marine zooplankton*' (Bucklin *et al.*, 2021, contribution of 9 WGIMT members, Marine Biology) and an article focusing on '*From phenotypes to genotypes and back: Toward an integrated evaluation of biodiversity in calanoid copepods*' (Di Capua *et al.*, 2022, Frontiers in Marine Science).

A topical collection titled '*Discovering the water column: integrated taxonomic approaches for measuring marine pelagic biodiversity*' in the journal Marine Biodiversity with WGIMT



members Elaine Fileman, Agata Weydman-Zwolicka and Jasmin Renz is currently underway, the deadline for submission is 1 December 2022.

The following peer-reviewed publications that acknowledge WGIMT contribution have been published in the last 3 years:

- Bucklin, A., Batta-Lona, P.G., Questel, J.M., Wiebe, P.H., Richardson, D.E., Copley, N.J., O'Brien, T.D. 2022. COI metabarcoding of zooplankton species diversity for time-series monitoring of the NW Atlantic continental shelf. *Frontiers in Marine Science* 9:867893. <https://doi.org/10.3389/fmars.2022.867893>.
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## Annex 1: List of participants

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## Annex 2: Resolutions

### Working Group on Integrated Morphological and Molecular Taxonomy (WGIMT)

**2019/FT/EPDSG01** The **Working Group on Integrated Morphological and Molecular Taxonomy** (WGIMT), chaired by Elaine Fileman, UK, and Jasmin Renz, Germany, will work on ToRs and generate deliverables as listed in the Table below.

	MEETING DATES	VENUE	REPORTING DETAILS	COMMENTS (CHANGE IN CHAIR, ETC.)
Year 2020	27 March	by corresp/ webex		physical meeting cancelled - remote work
Year 2021	26 February	Online meeting		
Year 2022	9 June	Online meeting	Final report by September to SCICOM	

### ToR descriptors

TO R	DESCRIPTION	BACKGROUND	<a href="#">SCIENCE PLAN CODES</a>	DURATION	EXPECTED DELIVERABLES
a	Evaluate the potential of molecular and morphological approaches for understanding zooplankton communities	Molecular methods are widely used for rapid assessment of species diversity, and can contribute to improving our understanding of the impacts of climate change and anthropogenic effects on marine ecosystems. Standardized protocols for assessment of pelagic biodiversity are needed to fulfil requirements defined in the Marine Strategy Framework Directive (MSFD). There is a need for inter-comparison of results to understand the impact of protocol choice. A range of molecular approaches, e.g., barcoding and metabarcoding, environmental DNA (eDNA), or proteomic approaches can be adopted to help to address some of the key applications of integrative taxonomy.	1.6; 1.7	year 1,2,3  Year 2  Year 1,2,3	Review the current methods for integrative morphological and molecular taxonomy and evaluate the impacts of choosing different protocols.  Construct an overview of case studies utilizing combined molecular and morphological approaches in zooplankton taxonomy.  Compile a list of challenging zooplankton taxa which will include a top-ten list of zooplankton species complexes in the ICES area (including hidden diversity associated with cryptic, rare, and invasive species and species delimitation).
b	Continue development and enhancement of the	Locating and accessing	1.6; 1.7	Year 1	Create a glossary of

	WGIMT Resource Portal	morphological and molecular taxonomic information can be difficult: classical taxonomic references are often out-of-print or in a non-digital format; many molecular data are not released prior to publication; and a broad variety of methodologies and approaches exist, possibly overwhelming potential new comers to the field. The WGIMT Resource Portal will provide informational overviews and links to relevant literature and web pages, with a special focus on the use of molecular technologies (and morphological verification) for the integrative taxonomy of zooplankton.		Year 1,2,3	molecular taxonomy terms. Review and update the online WGIMT overview materials and resource links.
				Year 2	Create an overview summary and reference-links to meta-barcoding primer protocols.
				Year 3	Update the WGIMT literature library, adding keywords indices.
c	Initiate and support provision of standards, training materials, and taxonomy workshops	Lab exchanges and workshops, including ICES Taxonomy Workshops, are very effective in engaging target audiences and ensuring trained technicians and researchers for applications in fisheries and ecosystem management. Co-sponsored workshops and meetings with other SCICOM EGs will increase impact and likelihood of adoption for advisory applications.	1.6; 1.8	Year 1,2,3	Ensure provision of training materials through the WGIMT resource portal, linking to ToR b)
				Year 2,3	Design, organize and offer lab exchanges and integrative taxonomy workshops
				Year 1,2,3	Promote best practices for DNA barcoding and metabarcoding of zooplankton
D	Continue to demonstrate leadership in promoting and encouraging use of integrative taxonomic approaches for assessment of pelagic biodiversity	Integrative taxonomy is a developing field; uses and applications for fisheries and ecosystem management should be explained in high-visibility settings in ICES and other organisations through special sessions. It is important to maintain a strong	1.6; 1.7; 1.8	Year 1,2,3	Organize & promote special sessions at national and international conferences: e.g. ICES ASC; ASLO/TOS Ocean Sciences Meetings.
				Year 1,2,3	Publish peer-reviewed scientific papers on topics central to the WGIMT

foundation and visibility in primary research literature in order to validate metagenetic approaches for analysis of zooplankton diversity. Publication in peer-reviewed scientific journals will demonstrate validity of data, protocols, and results, and allow dissemination and new applications in ecosystem management.	mission  Publish peer-reviewed scientific papers on topics central to the WGIMT mission. To include two targeted review papers on 1) The crossover from microscopy to genes in marine diversity, illustrating the transition from traditional morphological species identification using an integrated approach to full molecular genetic identification of marine plankton communities, demonstrated on marine pelagic copepods as model taxa; 2) Zooplankton biodiversity assessment by molecular methods.
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### Summary of the Work Plan

Year 1	Review and evaluate protocols available to promote and accelerate use of state-of-the-art molecular approaches for biodiversity assessment and applications for management and assessment goals (ToR a). Review and update all areas of web portal (ToR b).
Year 2	Carry out collaborative activities with other SCICOM EGs to promote integrative taxonomy and publish peer reviewed scientific articles on topics central to the WGIMT mission (ToR c).
Year 3	Recommend, encourage, and enable use of integrated morphological and molecular taxonomic analysis of zooplankton in integrated ecosystem assessments in ICES area seas (ToRs a, b,).

### Supporting information

Priority	The activities of this Working Group will assist ICES and its Expert Groups with issues related to the development, dissemination and application of taxonomic knowledge and skills in support of Integrated Ecosystem Understanding. Accurate identification of species and characterization of species-level diversity are and will remain foundations of integrated ecosystem assessments of function and state. Integrated taxonomic approaches – including morphological, molecular, optical, and other – may enhance and accelerate progress toward rapid, automatable, and near real-time identification of species for fisheries and integrated ecosystem assessments; detecting the impacts of climate change on species diversity, distribution, abundance; and understanding alterations in food web structure and function, and associated biogeochemical cycles. The availability of and need for new technology and techniques in taxonomic analysis make WGIMT's goals and activities important and high priority
Resource requirements	No additional resources are requested or required for planned activities.
Participants	This Expert Group now includes 50 members from 17 countries, and has a balanced representation among experts in morphological and molecular taxonomic approaches and covering a good range of taxonomic groups and ICES geographic regions. The group's annual meeting is normally attended by some 17-20 members and guests. New members are welcome.

Secretariat facilities	None.
Financial	No financial implications.
Linkages to ACOM and groups under ACOM	There are no obvious direct linkages.
Linkages to other committees or groups	WGIMT arose as a Study Group from the WGZE in response to perceived need, meeting in association with WGZE during 2012 and 2013. WGIMT will remain in close partnership with WGZE and is pursuing additional partnerships (e.g., WGPME), while promoting and supporting integrated morphological and molecular taxonomy science for the benefit of the ICES science and advisory communities as a whole.
Linkages to other organizations	The work of this group relates to and is connected to a diversity of other projects and organisations, e.g. SCOR WG157 MetaZooGene, BONUS BIO-C3 project, NOAA COPEPOD and COPEPODITE, GOBI, and others.