

## Toward a new global view of marine zooplankton biodiversity based on DNA metabarcoding and reference DNA sequence databases

MBON/GOOS/OBPS/OBIS/OceanObsRCN/SCOR Webinar

Presenter: Ann Bucklin

University of Connecticut (USA) July 22, 2020



Hauling in the MOCNESS (P.H. Wiebe, WHOI)

[metazoogene.org/](http://metazoogene.org/) and [scor-int.org/group/157](http://scor-int.org/group/157)

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## MBON/GOOS/OBIS/OBPS/OceanObsRCN/SCOR Webinar July 22, 2020

### Presenter

- Ann Bucklin (WG157 Chair)  
University of Connecticut (USA)



### Panelists for Q&A

- Katja Peijnenburg (WG157 Co-Vice-Chair)  
Naturalis Biodiversity Center and  
University of Amsterdam (Netherlands)
- Todd O'Brien, Marine Ecosystems Division  
COPEPOD, NOAA Fisheries (USA)
- Leocadio Blanco-Bercial  
Bermuda Institute of Ocean Sciences (Bermuda)

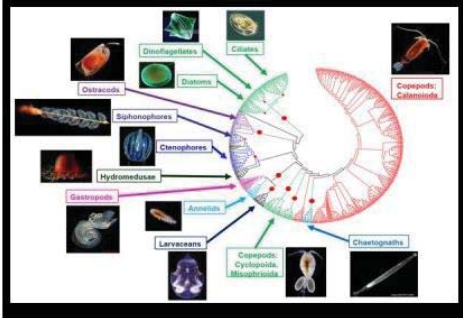


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# MetaZooGene

Toward a new global view of marine zooplankton biodiversity based on DNA metabarcoding and reference DNA sequence databases.

Main Menu	
<ul style="list-style-type: none"> <li>★ <b>MetaZooGene Overview</b> <ul style="list-style-type: none"> <li>* aka "SCOR WG157"</li> <li>* Members &amp; Participants</li> <li>* Original WG157 Proposal</li> </ul> </li> <li>★ <b>Call for Papers</b> <ul style="list-style-type: none"> <li>ICES J. of Marine Science</li> </ul> </li> <li>★ <b>MetaZooGene Products</b> <ul style="list-style-type: none"> <li>MZG Barcoding Atlas</li> <li>MZG Reference Database</li> </ul> </li> <li>★ <b>What is Metabarcoding</b> <ul style="list-style-type: none"> <li>Recommended Reading</li> <li>New Publications</li> </ul> </li> <li>★ <b>Meetings and Workshops</b> <ul style="list-style-type: none"> <li>- 2020 @ OSM (San Diego)</li> <li>- 2019 @ ICES-ASC (Sweden)</li> <li>- MZG Symposium 2019</li> </ul> </li> </ul>	<p>Marine zooplankton biodiversity remains a significant unknown throughout the global ocean. Molecular approaches, including DNA barcoding (use of short DNA sequences for species recognition and discrimination) and metabarcoding (large-scale taxonomic identification of complex samples via analysis of one or few orthologous DNA barcode regions), are expected to significantly revise global estimates of zooplankton diversity.</p> <p>The MetaZooGene SCOR Working Group will develop a global vision for the continuing development of integrative molecular – morphological taxonomic analysis of marine zooplankton biodiversity through international communication, cooperation, and collaboration. Terms of Reference include: 1) create an open-access web portal for DNA barcodes for marine zooplankton; 2) design an optimal DNA barcoding pipeline for marine zooplankton; and 3) develop best practices for DNA metabarcoding of marine zooplankton biodiversity.</p> <p>Deliverables include a project website, web portal, and database; dissemination of best practices for DNA barcoding and metabarcoding of marine zooplankton; and publications and review papers in open access peer-reviewed journals. Workshops to build capacity for the MetaZooGene mission will be designed for early career scientists and those from developing countries, and will be held in association with international conferences.</p>



[www.metazoogene.org](http://www.metazoogene.org)

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## Scientific Committee on Oceanic Research



### International non-governmental organization

#### Vision and mission of SCOR:

- advance ocean research
- stimulate international cooperation
- strengthen infrastructure
- develop capacity worldwide

#### SCOR Working Groups should:

- advance a science topic
- document state of the science
- identify research priorities
- solve a scientific or technical issue
- budget (\$45,000) and time (3-4 years)

[www.scor-int.org](http://www.scor-int.org) and @SCOR\_Int

#### UPCOMING SCOR MEETING

19-23 October 2020  
Virtual meeting

[Past Annual Meetings](#)

#### WHO WE ARE

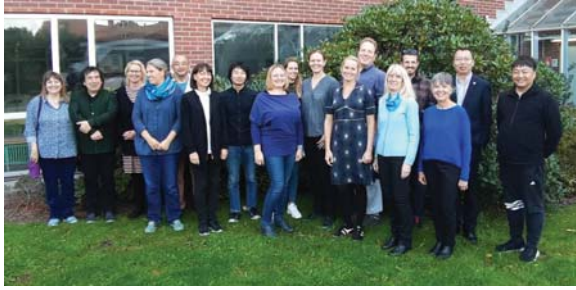
[History](#)  
[About](#)  
[Executive Committee](#)  
[National Committees](#)  
[Partner Organizations](#)  
[Affiliated Projects](#)

#### WHAT WE DO

[Working Groups](#)  
[Research Projects](#)  
[Infrastructural Projects](#)  
[Capacity Development](#)  
[Achievements](#)

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# MetaZooGene



2019 – Gothenburg Global Biodiversity Centre (Sweden)



2020 – Ocean Sciences Meeting, San Diego (USA)

## Chair and Co-Vice-Chairs

- Ann Bucklin (Chair), Univ. Connecticut (USA)
- Katja Peijnenburg (Vice-Chair), Univ. Amsterdam (NL)
- Ksenia Kosobokova (Vice-Chair), Russian Acad. Sciences (RU)

## SCOR WG157 Full Members:

- Leocadio Blanco-Bercial, Bermuda Inst. Ocean Sciences (BM)
- Tone Falkenhaus, Inst. Marine Research (NO)
- Junya Hirai, Univ. Tokyo (JP)
- Jenny Huggett, Dept. Environmental Affairs (SA)
- Chaolun Li, Chinese Acad. Sciences (CN)
- Ryuji Machida, Academia Sinica (TW)
- Todd O'Brien, NOAA Fisheries (USA)

## SCOR WG157 Associate Members:

- Keun-Hyung Choi, Chungnam National Univ. (KR)
- Astrid Cornils, Alfred Wegener Inst. (DE)
- Bruce Deagle, Australian Antarctic Div. (AU)
- Ruben Escribano, Univ. Concepción (CL)
- Erica Goetze, Univ. Hawaii at Manoa (USA)
- Aino Hosia, Univ. Museum of Bergen (NO)
- Silke Laakmann, Univ. Oldenburg (DE)
- Pennie Lindeque, Plymouth Marine Lab (UK)
- Maria Grazia Mazzochi, Stazione Zool. Anton Dohrn (IT)
- Mary Mar Noblezada, Univ. Philippines (PH)
- Naiara Rodriguez-Ezpeleta, AZTI (ES)
- Agata Weydmann, Univ. Gdańsk (PL)

Total of 22 members from 18 countries

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# MetaZooGene



## Primary focus:

~8,000 species of holozooplankton (15 phyla, 32 classes)  
of animals that drift with ocean currents

## Primary goal:

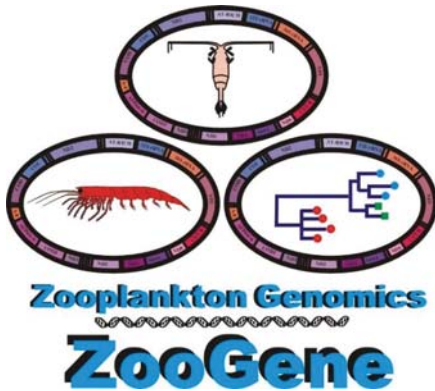
Integrative molecular – morphological taxonomic  
analysis of marine zooplankton biodiversity throughout  
global ocean

## Terms of Reference

- 1) Create an open-access web portal for DNA barcodes for marine zooplankton
- 2) Design an optimal DNA barcoding pipeline for marine zooplankton
- 3) Develop best practices for DNA metabarcoding of marine zooplankton biodiversity

# Welcome to ZooGene

## A DNA Sequence Database for Calanoid Copepods and Euphausiids



Ann Bucklin (University of New Hampshire)  
 Bruce W. Frost (University of Washington)  
 Peter H. Wiebe (Woods Hole Oceanographic Institution)  
 Michael J. Fogarty (Northeast Fisheries Science Center)

13 expert taxonomic consultants from 7 countries  
 Funded by US NSF – NOPP (2000 – 2004)

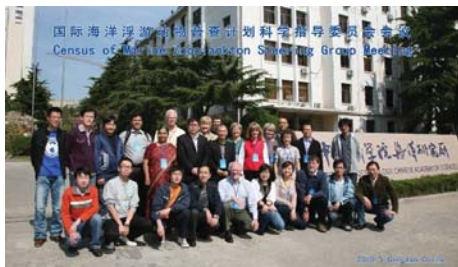
- DNA barcode sequences for mitochondrial COI
- Specimens identified by morphological taxonomic experts
- DNA sequences submitted to NCBI GenBank
- Accurate species' identification, including cryptic species

[www.zoogene.org](http://www.zoogene.org)



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## Census of Marine Zooplankton



CMarZ Steering Group, Qingdao (2010)

### Project Lead Scientists

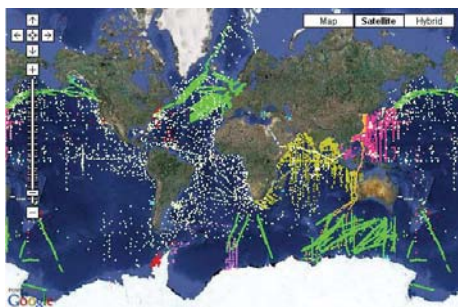
Ann Bucklin, Univ. Connecticut, USA  
 Shuhei Nishida, Ocean Research Inst., Japan  
 Sigrid Schnack-Schiel, Alfred Wegener Inst., Germany  
 Peter Wiebe, Woods Hole Oceanographic Inst., USA

### CMarZ Steering Group Members

23 scientists from 14 countries

### Funded by

Census of Marine Life; Sloan Foundation (2005-2010)



CMarZ Cruise Tracks (2005-2010)

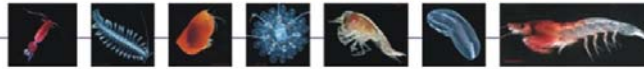
- Zooplankton species diversity and genetic variability of global ocean
- DNA “gold standard” barcoding, with taxonomic ID and photo
- Integrated morphological-molecular analysis
- Sampling throughout all ocean basins; surface to deep sea

[www.cmarz.org](http://www.cmarz.org)

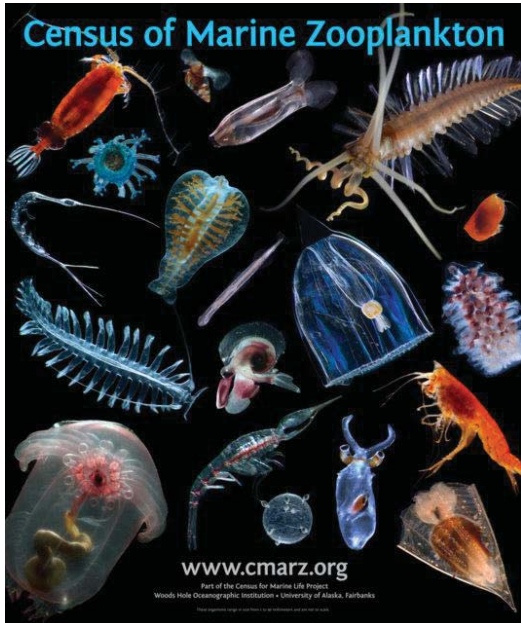
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# Census of Marine Zooplankton



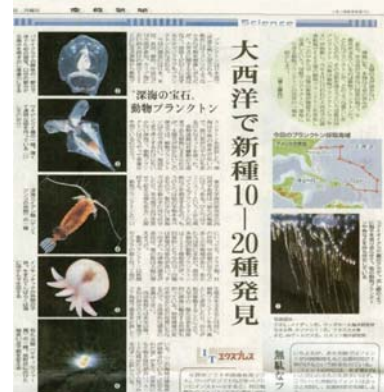
## CMarZ Zooplankton are "Media Stars"



Photos: R.R. Hopcroft (UAF), C.A. Clarke-Hopcroft (UAF), L.P. Madin (WHOI)



Los Angeles Times, August 2009



Sankei, May 2006



Nature, December 2009

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### CMarZ Zooplankton Photo Gallery

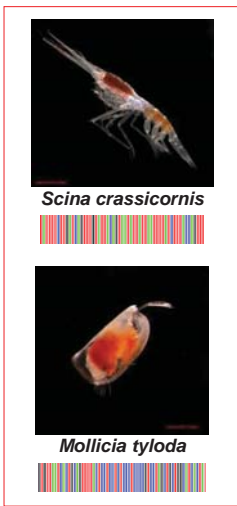
 <i>Tadpole nauplius</i> T4001979	 <i>Copepod nauplius</i> T4001973	 <i>Pteropod nauplius</i> T4001886	 <i>Limacina nauplius</i> T4001885	 <i>Eucypris nauplius</i> T4001884
 <i>Eucypris nauplius</i> T4001884	 <i>Crustacean nauplius</i> T4001883	 <i>Copepod nauplius</i> T4001882	 <i>Copepod nauplius</i> T4001881	 <i>Acartia nauplius</i> T4001880
 <i>Acartia nauplius</i> T4001880	 <i>Lucicutia nauplius</i> T4001870	 <i>Eurytemora nauplius</i> T4001869	 <i>Pteropod nauplius</i> T4001859	 <i>Limacina nauplius</i> T4001859
 <i>Diaptomus nauplius</i> T4001197	 <i>Goniatid nauplius</i> T4001145	 <i>Eubranchia nauplius</i> T4001114	 <i>Euphausia nauplius</i> T4001060	 <i>Pteropod nauplius</i> T4001013

- High-quality images of living zooplankton from the Census of Marine Zooplankton (CMarZ)
- ICES WGIMT (2008-present), NOAA COPEPOD and Copepedia websites
- Maintained by Todd O'Brien (NOAA)

International Council for the Exploration of the Sea (ICES)  
[www.ices.dk/community/groups/Pages/WGIMT.aspx](http://www.ices.dk/community/groups/Pages/WGIMT.aspx)  
[www.wgimt.net](http://www.wgimt.net)

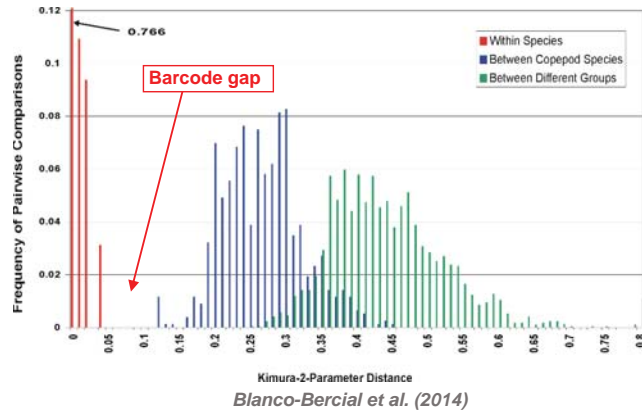
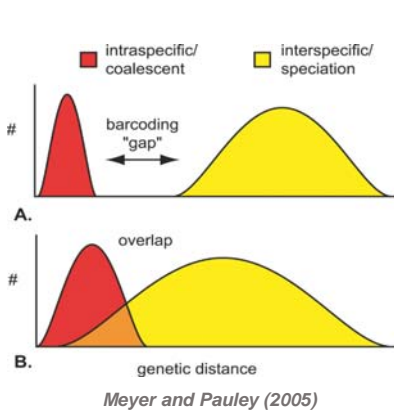


[www.st.nmfs.noaa.gov/copepod](http://www.st.nmfs.noaa.gov/copepod)



# DNA Barcoding of Marine Zooplankton

- DNA barcode: sequence for species identification and discrimination
- Mitochondrial cytochrome oxidase I (COI) most frequent barcode gene region for animals
- “Gold standard” barcodes with species ID and photo
- Polymerase Chain Reaction (PCR) uses “universal” primers
- Most invertebrate zooplankton groups show a definitive “barcode gap” that allows accurate species identification.

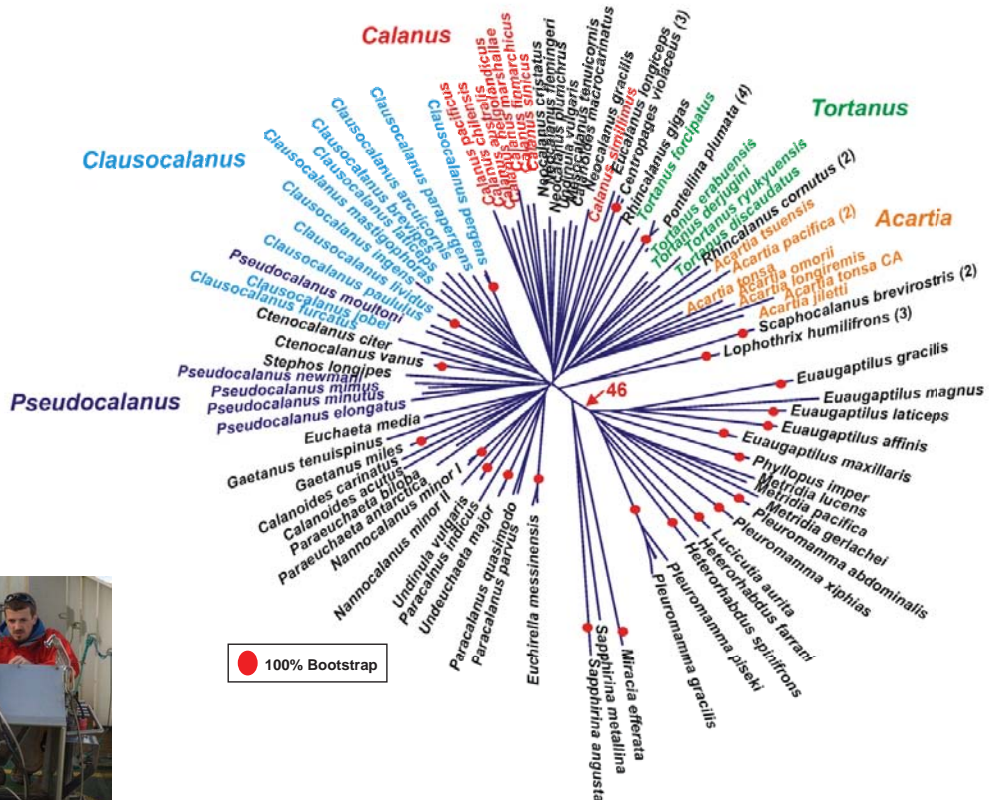


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# DNA Barcoding of Marine Copepods

Leocadio Blanco-Bercial\* et al. (2014) PLOS-Currents

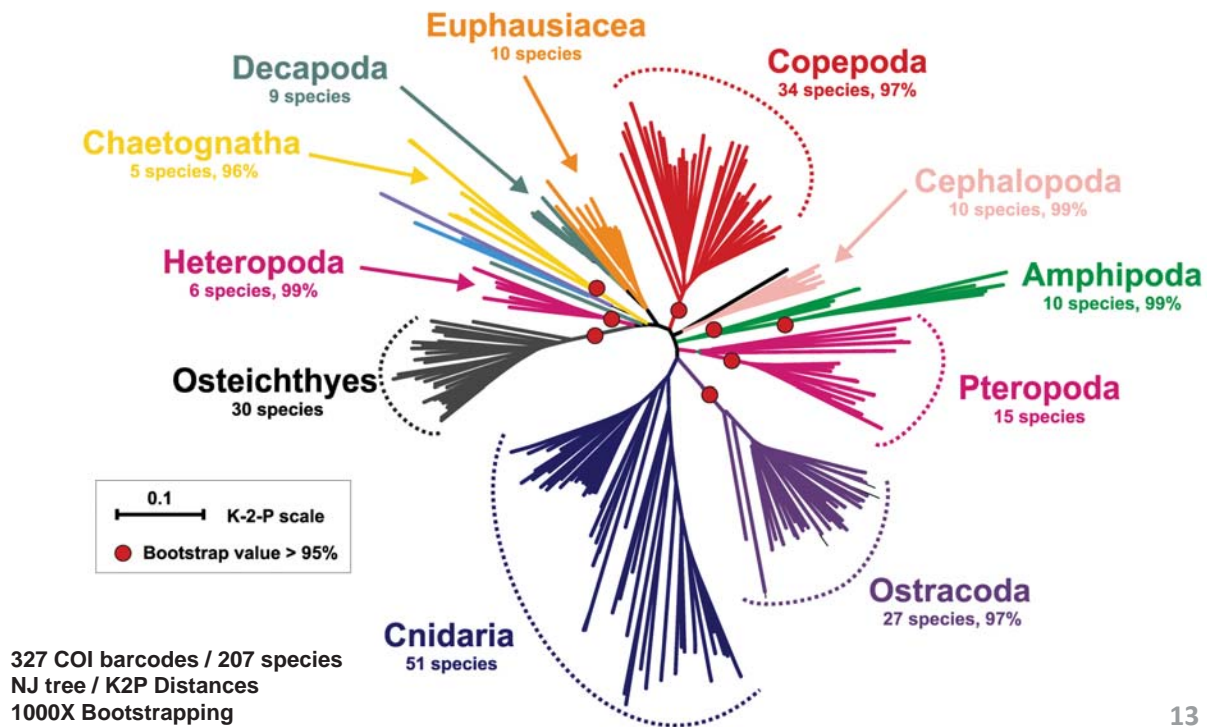


Barcodes for 1,391 specimens of 195 species

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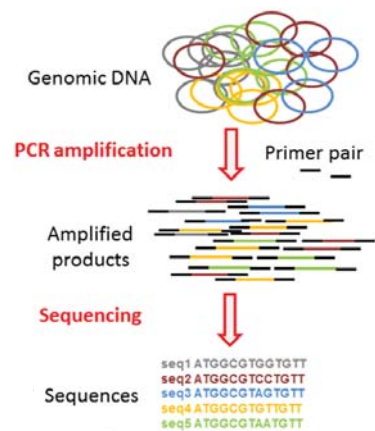
# A Rosetta Stone for Zooplankton Biodiversity COI barcodes for zooplankton of the Sargasso Sea

Bucklin\* et al. (2010) Deep-Sea Research  
Bucklin\* et al. (2011) Annual Review of Marine Sciences



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## Metabarcoding of Marine Zooplankton

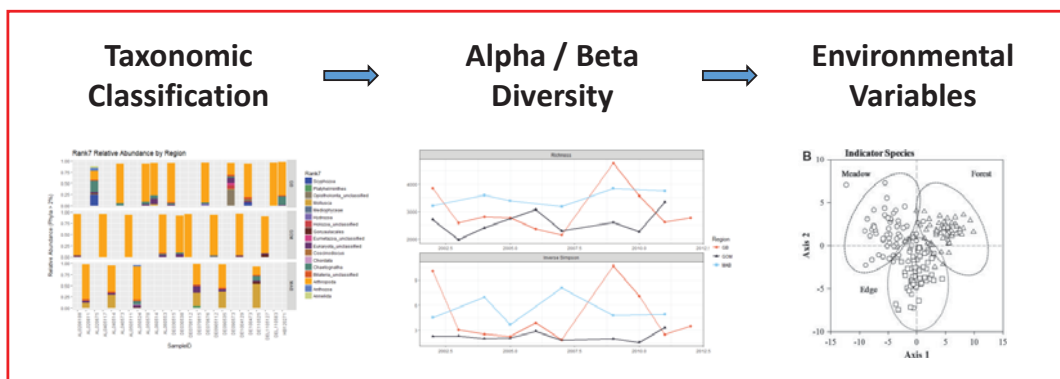
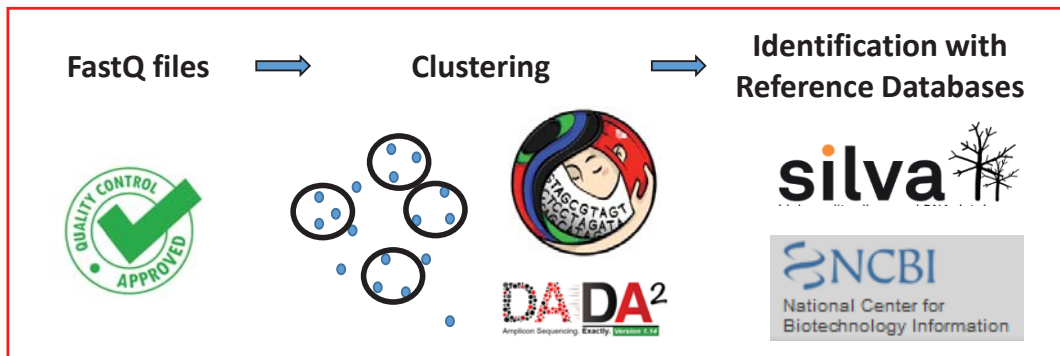


- Extraction of genomic DNA from environmental samples
- High-throughput DNA sequencing (Illumina MiSeq)
- PCR of short gene regions (e.g., 18S rRNA hypervariable regions)
- Bioinformatic pipelines (Mothur, DADA2) for sequence QC and analysis
- Statistical analysis of biodiversity (Mothur, R, MatLab)

Figure: Corell and Rodríguez-Ezpeleta\* (2014)

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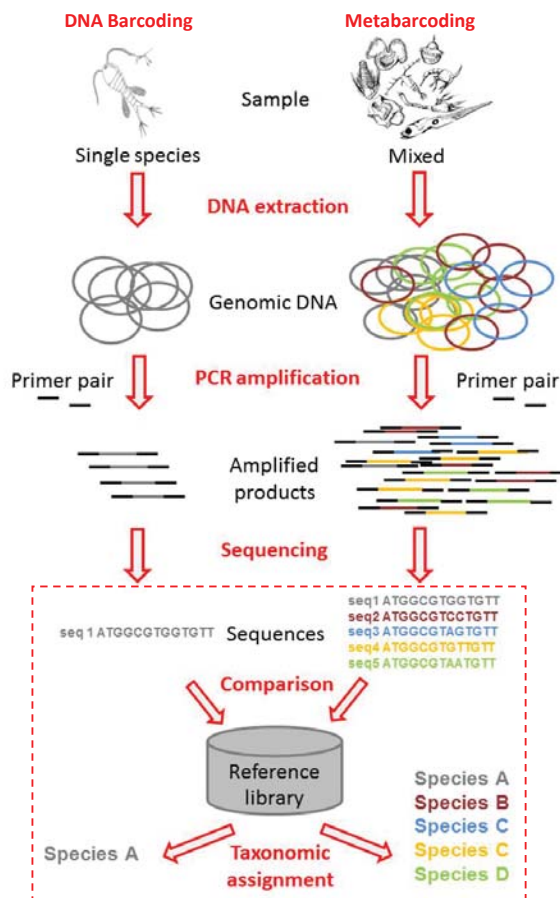
# Bioinformatics and Statistical Analysis of Metabarcoding Data



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## Reference DNA Sequence Database

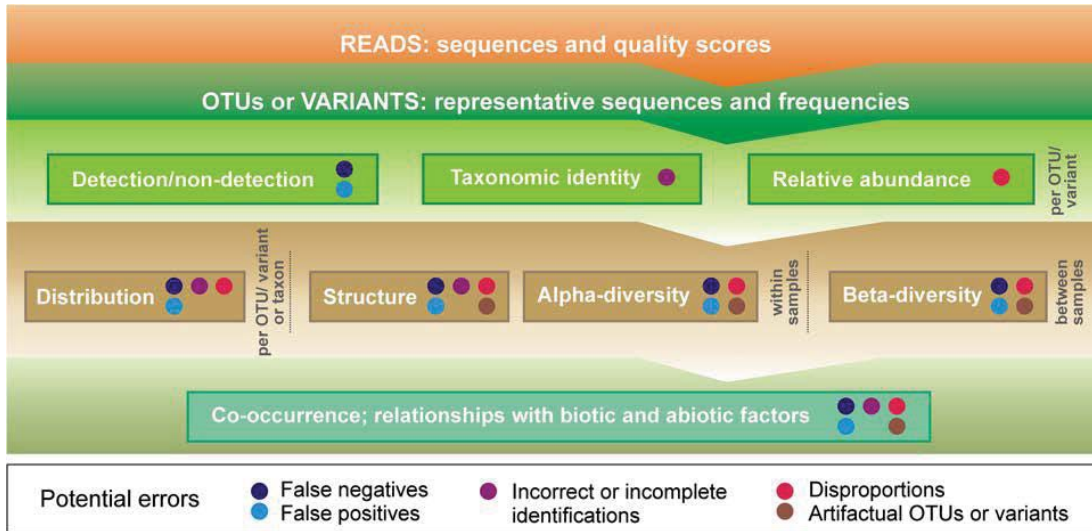
- Identification of sequences requires matching (alignment) to sequences from identified specimens
- Reference databases need to be taxonomically and geographically complete
- Critically needed for DNA barcoding and metabarcoding of marine zooplankton



Correll and Rodríguez-Ezpeleta\* (2014)

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- Information flow and potential error impacts in metabarcoding studies.
- Sequences clustered into Operational Taxonomic Units (OTUs) or Amplicon Sequence Variants (ASVs), with representative sequence.
  - Luciana Santoferrara (2019) Plankton metabarcoding: Optimization and error management. J. Plankton Res. Horizons doi:10.1093/plankt/fbz041

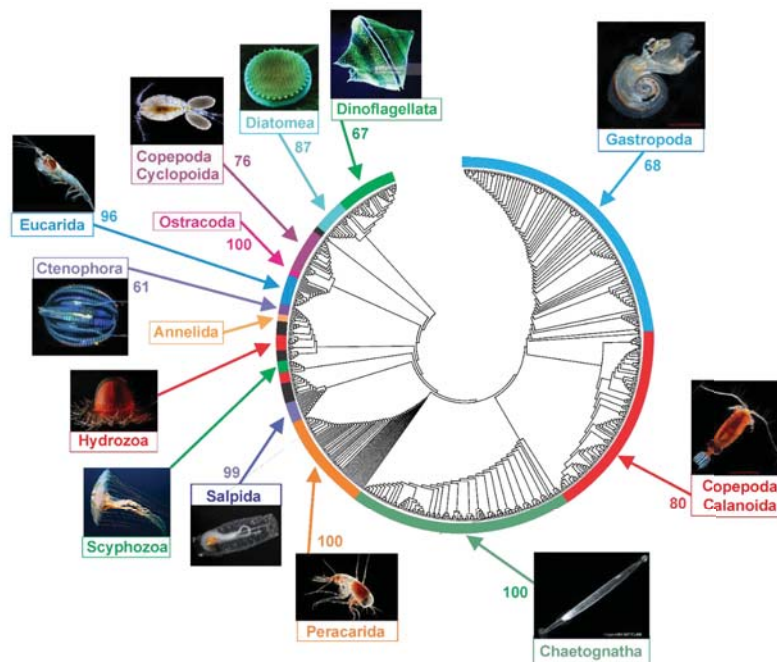
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## MetaZooGene



Metabarcoding of Zooplankton Diversity  
18S rRNA V9 resolves taxonomic groups - not species



Neighbor Joining tree for OTUs of V9 18S rRNA (Gulf of Maine; May 2005)  
Figure from: Bucklin et al. (2019) ICES Journal of Marine Science

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# MetaZooGene



## MZGdb: Web Portal and Atlas for DNA Barcodes of Marine Zooplankton Todd O'Brien\*, NOAA Fisheries (USA)

Taxonomic Group	Entire World B00	North Atlantic B02	South Atlantic B03	North Pacific B07	South Pacific B06	Indian Ocean B05	Arctic Ocean B01	Southern Ocean B04	Baltic Sea B21	Medit Sea B22
All_Taxa_Groups  T4000000  The data files in this row contain ALL of the groups listed individually in the rows below.										
	SEQs: 151163 uIDs: 10498 Species: 9182	SEQs: 81536 uIDs: 4310 Species: 3338	SEQs: 47626 uIDs: 2186 Species: 1484	SEQs: 87139 uIDs: 4353 Species: 3371	SEQs: 52733 uIDs: 3207 Species: 2345	SEQs: 56510 uIDs: 3178 Species: 2358	SEQs: 33880 uIDs: 1505 Species: 1012	SEQs: 31858 uIDs: 1395 Species: 842	SEQs: 19893 uIDs: 337 Species: 210	SEQs: 34777 uIDs: 1658 Species: 1140
	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV	MZGdb .CSV
	.PSV	.PSV	.PSV	.PSV	.PSV	.PSV	.PSV	.PSV	.PSV	.PSV
	.fasta	.fasta	.fasta	.fasta	.fasta	.fasta	.fasta	.fasta	.fasta	.fasta
.mothur	.mothur	.mothur	.mothur	.mothur	.mothur	.mothur	.mothur	.mothur	.mothur	

- Over 150,000 DNA sequences (~9,000 species) for COI barcode region
- Data from NCBI GenBank and BOLD (duplicates removed); unpublished MZG participant data.
- Users can download data by selecting taxonomic group and ocean region - *“only euphausiid species found in North Atlantic”*
- Still in development as of July 2020

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# MetaZooGene

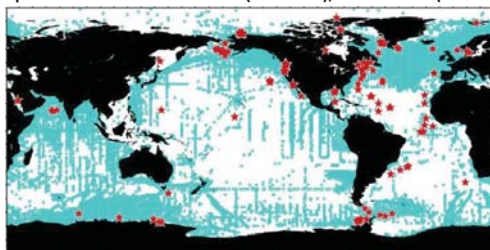


## MZGdb: DNA Barcodes for Euphausiid (Krill) Species

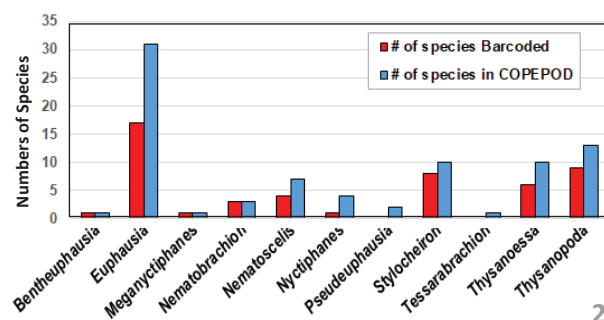
- Region-specific lists of species and
- Distribution maps based on NMFS COPEPOD database
- Summary of barcoding status by species, genus, and region.
- Guides prioritization of future barcoding efforts

Entire World B00	North Atlantic B02	South Atlantic B03	North Pacific B07	South Pacific B06	Indian Ocean B05	Arctic Ocean B01	Southern Ocean B04
SEQs: 1843 uIDs: 68	SEQs: 1752 uIDs: 55	SEQs: 608 uIDs: 37	SEQs: 1189 uIDs: 47	SEQs: 663 uIDs: 51	SEQs: 646 uIDs: 48	SEQs: 1071 uIDs: 17	SEQs: 604 uIDs: 19

Euphausiid records in COPEPOD (blue dots); COI barcode (red stars)



MetaZooGene plot of Euphausiacea



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# MetaZooGene

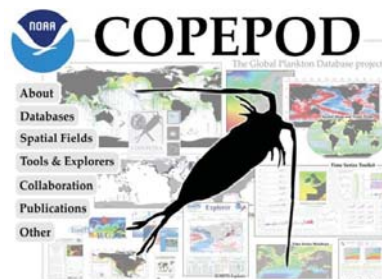


## MZGdb: Web Portal and Atlas for DNA Barcodes of Marine Zooplankton

Todd O'Brien\*, NOAA Fisheries (USA)

### MZGdb will:

- **Contribute to improved data quality**
- **Add additional search and access functionality**
  - barcode records, species distributions
  - species lists from COPEPOD/OBIS data
- **Flag conflicting information:**
  - questionable species identifications
- **Ensure open access to all data, metadata**
  - PCR primers and protocols



### MZGdb will not:

- **Change original records or identifications**
- **Serve as permanent database or archive for DNA sequence data**
- **Replace NCBI GenBank or BOLD**

COPEPOD: Coastal and Oceanic Plankton Ecology, Production, and Observation Database

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# MetaZooGene

## Best Practices for DNA Metabarcoding of Marine Zooplankton Biodiversity (WG157 ToR 3)

- **All protocol steps can be modified / designed for question or experiment**
- **Standardization is not appropriate or needed**
- **Intercalibration experiment planned to examine impacts of molecular protocols and bioinformatics pipelines**
- **Distribution of “standard samples” to participating MZG members**
- **Comparison of results at each step**

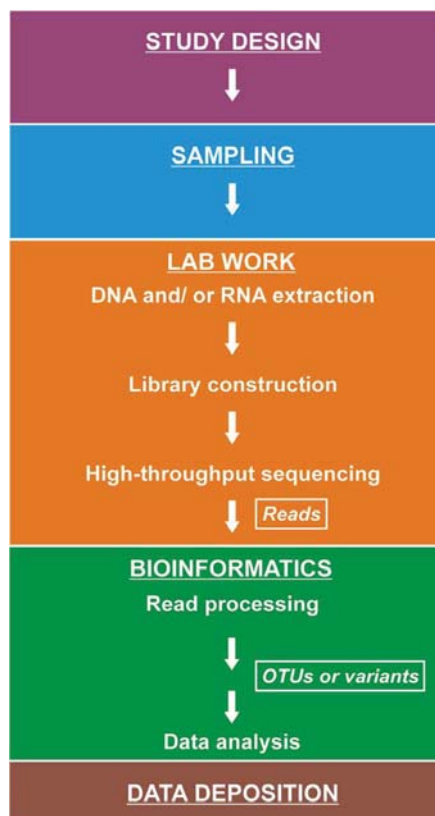


Figure: Santoferrara (2019) J. Plankton Research Doi:10.1093/plankt/fbz041



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## Research Goals and Applications

- **Accurate and reliable biodiversity estimates of marine zooplankton in global ocean**
  - all regions, all depth zones, all taxonomic groups
- **Species-level biodiversity analysis; detect rare and cryptic species**
- **Comparison of molecular methods and traditional morphological taxonomic methods**
- **Quantification (abundance or biomass) of groups or species from metabarcoding data**
- **Integration with ocean ecosystem assessment and fisheries monitoring surveys**

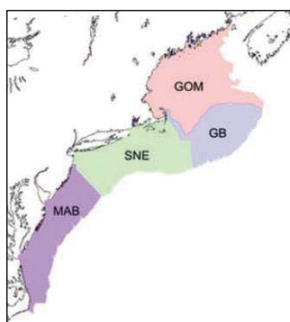
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## Metabarcoding of Marine Zooplankton Ecosystem Monitoring of NW Atlantic

**Ann Bucklin\***

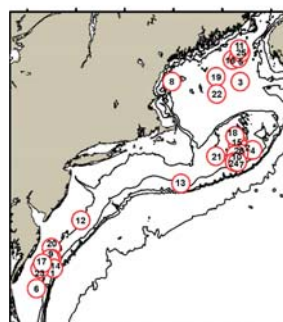
**University of Connecticut (USA)**



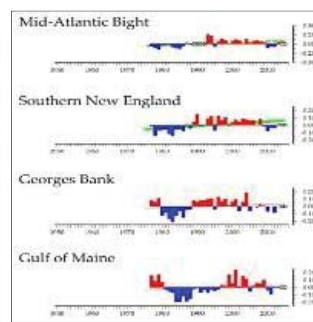
NW Atlantic Continental Shelf Regions



Bongo net samples



Station locations 2002-2012



Zooplankton displ. vol. O'Brien\* et al. (2013)

- **Time-series sampling: NOAA NMFS Ecosystem Monitoring (EcoMon) Surveys**
- **Taxonomic data from EcoMon: zooplankton species counts, biomass**
- **Spring cruises 2002-2012; 3 regions; total 26 samples**

Bucklin, Ann\*, H.D. Yeh, J.M. Questel, D.E. Richardson, B. Reese, N.J. Copley, P.H. Wiebe (2019) Time-series metabarcoding analysis of zooplankton diversity of the NW Atlantic continental shelf. *ICES J. Marine Sci.* doi:10.1093/icesjms/fsz021



# Molecules versus Morphology Ecosystem Monitoring in NW Atlantic

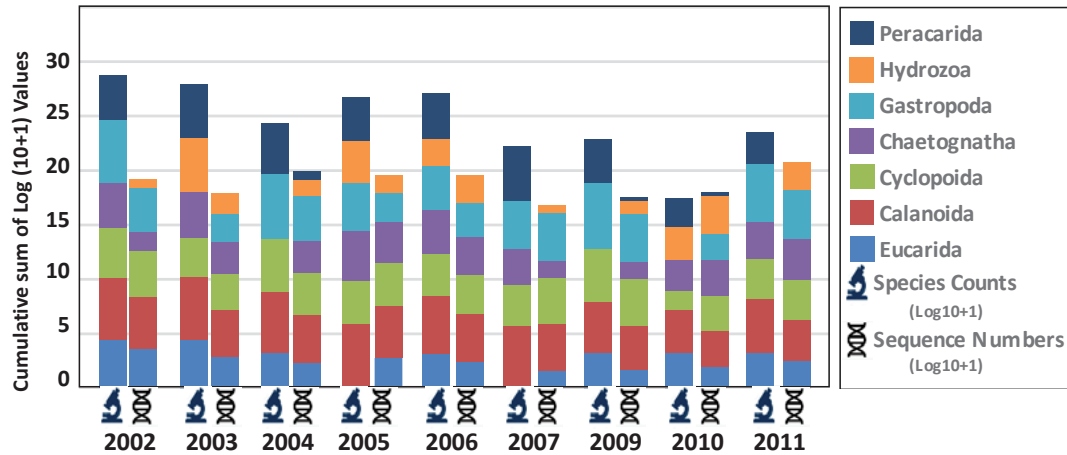


Ann Bucklin\*

University of Connecticut (USA)

- V9 sequence numbers and morphological species counts by group
- Taxonomic data from NOAA Fisheries EcoMon Surveys

## Middle Atlantic Bight (MAB)



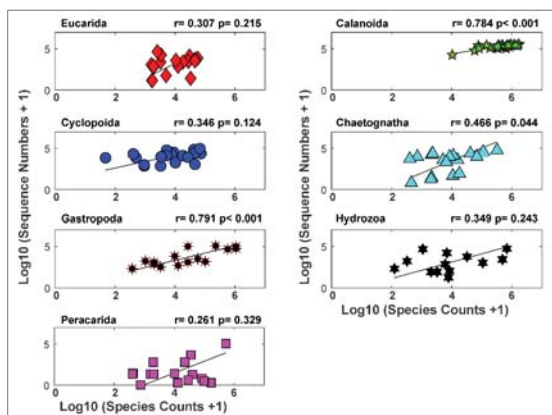
# Molecules versus Morphology Ecosystem Monitoring in NW Atlantic



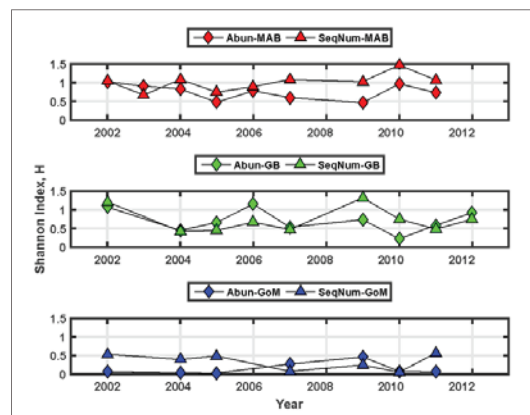
Ann Bucklin\*

University of Connecticut (USA)

## Regression Analysis: SeqNums vs Counts



## Shannon Index of Diversity



- Significant regression of sequence numbers and species abundances for several groups ( $p < 0.05$ ; paired t-test of the means)
- Diversity indices (Shannon, Simpson) for V9 sequence numbers and species counts highly correlated ( $r = 0.624$ ;  $p < 0.001$ ). All data Log 10 transformed +1



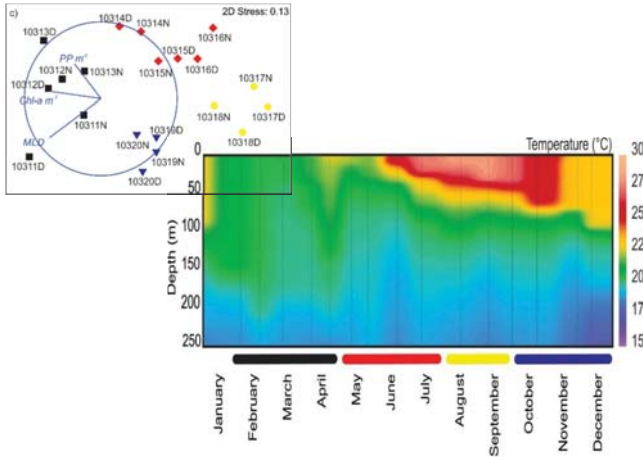


# Seasonality of Zooplankton Communities Bermuda Atlantic Time-series Station (BATS)



**Leocadio Blanco-Bercial\***

**Bermuda Institute of Ocean Sciences (Bermuda)**



- V9 metabarcoding of samples from BATS
- Clear seasonality, with 4 distinct communities throughout year
- Community composition correlated to measured vertical flux (export)

Graphical ordination of the monthly samples based on community composition (MDS) and match to seasonal cycle

Blanco-Bercial, L. (2020) Metabarcoding analyses and seasonality of the zooplankton community at BATS. *Frontiers Marine Sci.* doi: 10.3389/fmars.2020.00173

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# Metabarcoding of Continuous Plankton Recorder DNA

**Bruce Deagle\***

**Australian Antarctic Division (Tasmania)**

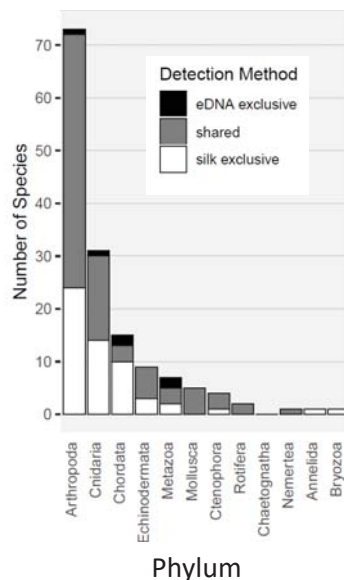


**Southern Ocean Transects**

Environmental DNA  
(2 L per sample)

VS.

CPR zooplankton  
metabarcoding  
(1500 L per sample)



- Compared COI metabarcoding of CPR zooplankton sample and eDNA in water sample.
- More taxa from metabarcoding CPR samples
- eDNA from 2L water sample found most (2/3) metazoans; picoplanktonic algae very abundant
- DNA metabarcoding methods need to be refined for ship-based surveys.

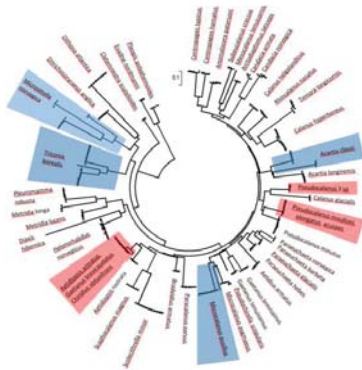
Leonie Suter, Andrea Polanowski, Laurence Clarke, John Kitchener, Bruce Deagle (In revision) Capturing open ocean biodiversity: comparing environmental DNA metabarcoding to the continuous plankton recorder. *Molecular Ecology*

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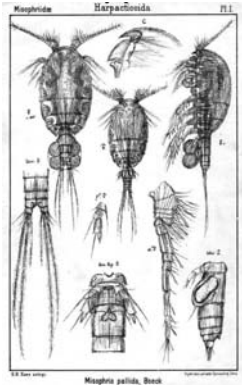


# Inventory of Copepods in Norwegian Waters

Tone Falkenhaus\*  
Institute of Marine Research (Norway)



Neighbor-joining tree of marine copepods. Species groups with suspected cryptic taxa are highlighted in blue, while red highlights indicate identification errors.



- Goal: To build national knowledge and expertise in biosystematics and DNA barcoding in Norway
- Results: DNA-barcode library with 253 COI sequences for 64 species from Norwegian waters; linked metadata, images, and voucher specimens.
- Funding: Norwegian Taxonomy Initiative, Norwegian Biodiversity Information Centre (NBIC) and Norwegian Barcode of Life (NorBOL)

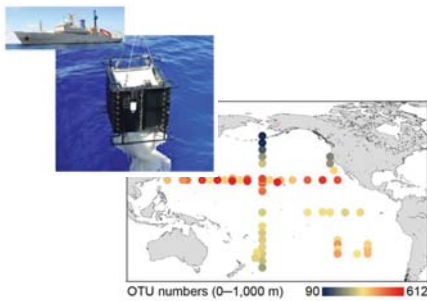


Tone Falkenhaus\*, A. Hobæk, E. Willassen, J. Kongsrud; COPCLAD: Inventory of marine Copepoda and Cladocera in Norway (2015-2017); and HYP COP: Copepods in Hyperbenthic Habitats (2020-2022)

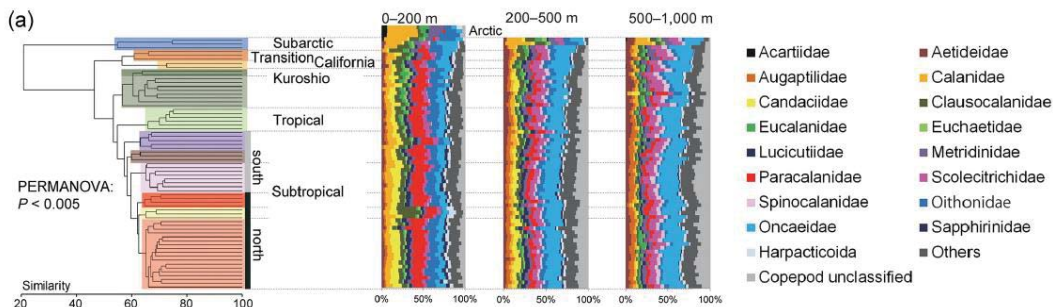


# Metabarcoding Copepod Diversity of the Pacific Ocean

Junya Hirai\*  
University of Tokyo (Japan)



- Metabarcoding using 28S rRNA revealed large-scale patterns of copepod diversity
- Epipelagic and mesopelagic diversity highly correlated to SST, indicating future impacts of global warming

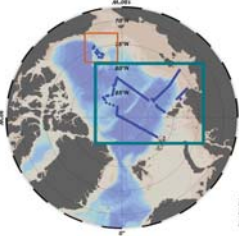


Junya Hirai\*, Aiko Tachibana, Atsushi Tsuda (2020) Large-scale metabarcoding analysis of epipelagic and mesopelagic copepods in the Pacific. PLoS ONE

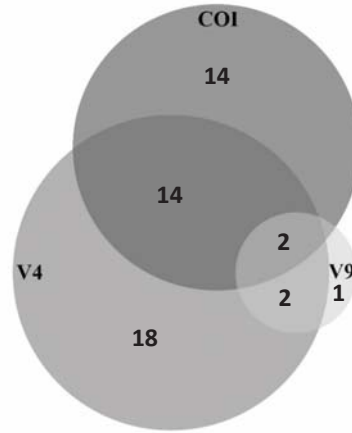


# Metabarcoding Arctic Copepods: Multi-gene Markers and Region-specific Database

Jennifer M. Questel, Russell R. Hopcroft, Hayley DeHart,  
Caitlin Smoot, Ksenia Kosobokova\*, Ann Bucklin\*

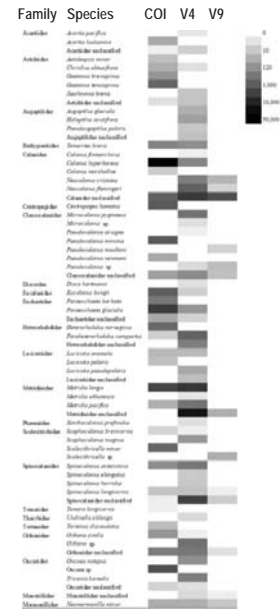


Arctic (blue box) and Chukchi Borderland (red box) sampling; taxonomy-at-sea



Above: Euler diagram of copepod species identified by COI, V4, V9

Right: Heatmap of copepod OTUs ( $\log_{10}$ ) for COI, V4, and V9



Questel, J.M. et al. (In Revision) Metabarcoding of zooplankton diversity within the Chukchi Borderlands, Arctic Ocean: Improved resolution from multi-gene markers and region-specific DNA databases. *Marine Biodiversity*



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## Zooplankton Diversity & Evolution Toward an Optimal DNA Barcode Pipeline

Katja Peijnenburg\* and Debbie Wall-Palmer  
Naturalis Biodiversity Center and  
University of Amsterdam (Netherlands)



The 'plankton team' 2020

### Chaetognaths and Amphipods

*With Annelies Pierrot-Bults, Ronald Vonk, Ferdinand Marlétaz, et al.*

- Taxonomic experts for accurate species identification
- New COI data: >240 COI barcodes for Atlantic Ocean
- Streamlined barcoding pipeline
- Extensive museum collections



Gastropods: Winged Snails

### Planktonic Gastropods (Pteropods & Heteropods)

*With Arie Janssen, Jaap de Boer, Le Qin Choo, Alice Burrige, et al.*

- Taxonomic experts for accurate species identification
- New COI data: >1,030 sequences
- Diversity, distribution and population structure
- Barcodes allow matching of juveniles and adults
- Latitudinal transects through North and South Atlantic

Marlétaz et al. (2019) A new spiralian phylogeny places the enigmatic arrow worms among gnathiferans. *Curr. Biol.*

Peijnenburg\* et al. (In review) The origin and diversification of pteropods predate past perturbations in the Earth's carbon cycle. *Proc. Natl. Acad. Sci.*

Wall-Palmer et al. (In review) Fossil-calibrated molecular phylogeny of atlantid heteropods (Gastropoda, Pterotracheoidea). *BMC Evol. Biol.*

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## Barcoding Pelagic Hydrozoa Aino Hosia\* and Luis Martell University Museum of Bergen (Norway)



Photos by projects HYPNO & NorHydro

- Barcoding hydrozoan fauna of Norway since 2015
- Morphological species ID, photos, DNA from ~80 pelagic spp. (~80% of Norwegian fauna)
- Species-level sequencing successful for COI (85%) and 16S rRNA (95%), to date
- Reference sequence database is valuable resource for taxonomy, metabarcoding, eDNA applications

Martell, L., A.H.S. Tandberg, A. Hosia (2018) The illusion of rarity and extreme endemism in an epibenthic jellyfish: facts and artefacts in the distribution of *Tesserogastria musculosus* (Hydrozoa, Ptychogastridae). *Helgol. Mar. Res.*

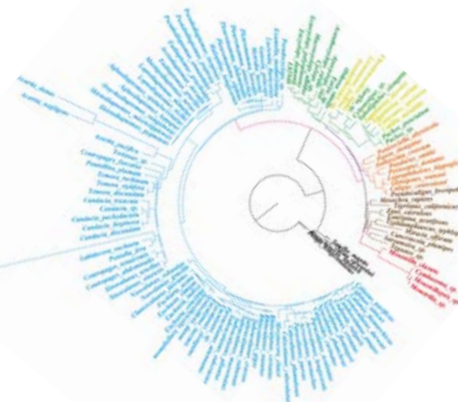
Schuchert, P., A. Hosia, L. Leclère (2017) Identification of the polyp stage of three leptomedusa species using DNA barcoding. *Rev. Suisse Zool.* DOI: 10.5281/zenodo.322675

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## Updated DNA Barcode Database in China

Chaolun Li\* and Minxiao Wang  
Institute of Oceanology, Chinese Academy of Sciences



Phylum	Class	Species	Barcode S	[ COI	ITS	18S
Arthropoda	Branchiopoda	3	38	38	0	0
	Hexanauplia (Copepoda)	182	1850	1409	302	139
	Malacostraca	88	260	227	5	28
Chaetognatha	Ostracoda	19	54	52	1	1
	Sagittoidea	21	774	718	43	13
Cnidaria	Hydrozoa	50	289	231	45	13
	Scyphozoa	6	125	125	0	0
Ctenophora	Nuda	1	2	2	0	0
	Tentaculata	2	5	3	1	1
Annelida	Polychaeta	2	17	15	1	1
Rotifera	Monogononta	1	1	1	0	0
Echinodermata	Echinoidea	2	15	3	11	1
	Eleutherozoa	2	6	4	1	1
Mollusca	Bivalvia	5	7	7	0	0
	Gastropoda	23	145	73	63	9
	Cephalopoda	4	4	4	0	0
Chordata	Appendicularia	3	9	3	1	5
	Cephalochordata	1	1	1	0	0
	Thalassacea	4	16	10	1	5
	Actinopteri	43	122	117	1	4
Sum		462	3740	3043	476	221

- 150 stations sampled since 2015 (orange shadow zones)
- > 345 species identified; 450 voucher specimens archived
- > 3700 sequences for COI, ITS, and 18S rRNA

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# Zooplankton Metabarcoding Initiatives in South Africa

Jenny Huggett\*

Dept. Environment, Forestry and Fisheries (South Africa)



# Zooplankton Metabarcoding Initiatives in South Africa

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Dept. Environment, Forestry and Fisheries (South Africa)



**CAPTOR: C**onnectivity **A**nd **d**is**P**ersal **b**e**T**ween **p**r**O**TECTED **a**REAs; Johan Groeneveld, Oceanographic Research Institute (ORI), Durban

- Zooplankton metabarcoding with local DNA barcode reference library; Singh et al. (submitted)
- MSc project (Adam Rawoot): Integrative morphological-molecular taxonomic study of marine copepods: DNA reference library for metabarcoding studies



The case for taxon-specific primers; Ashrenee Govender (PhD student)

- Mini-barcodes for decapods and fish larvae provide higher detection rates of targeted and rare species; improved estimates of biodiversity



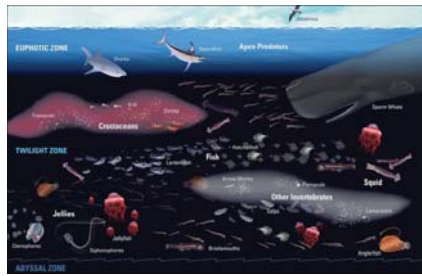
Singh et al. (Submitted) DNA metabarcoding of marine zooplankton in South Africa: how good is the reference library?

Govender et al. (In review) Marine zooplankton, mini-barcodes, and DNA metabarcoding: The case for taxon-specific primers. Ecological Applications



# Metabarcoding Diet Diversity of Mesopelagic Fishes

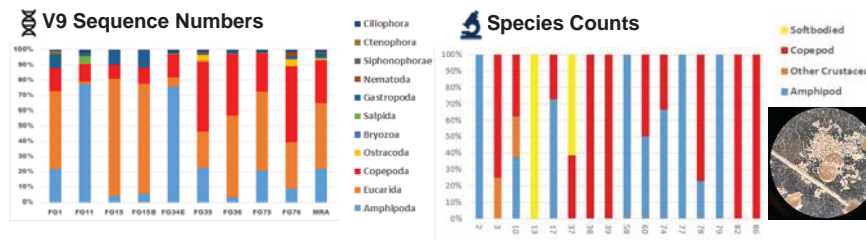
Ann Bucklin\* and Paola Batta-Lona  
University of Connecticut (USA)



<https://www.whoi.edu/oceanus>

- Novel look at mesopelagic trophic pathways; focus on fish and salps
- COI and V9 metabarcoding and morphological (microscopic) analysis of gut contents
- V9 can reveal importance of gelatinous organisms in mesopelagic food web and sources of productivity (phytoplankton vs detritus)

*Hygophum hygomi*  
Lanternfish



Bucklin, A.\*, P.G. Batta-Lona, M. Wojcicki, S.G. Glancy, A. Govindarajan, P.H. Wiebe, J.L. Llopiz (2020) Metabarcoding analysis of diet diversity of mesopelagic fishes and salps. Ocean Sciences Meeting

Photos: Paul Caiger (WHOI); Sarah Glancy (WHOI)



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## MetaZooGene Review Article



Silke Laakmann\*, University of Oldenburg (Germany)  
Leocadio Blanco-Bercial\*, Bermuda Institute of Ocean Sciences (Bermuda)  
Astrid Cornils\*, Alfred Wegener Institute (Germany)

*The crossover from microscopy to genes in marine diversity – from species to assemblages in marine pelagic copepods*

Philos. Trans. Roy. Soc. B. (Accepted) Doi:10.1098/rstb.2019.0446.

- Summary of progress from morphological to molecular identification of species and bulk samples
- Highlights power of integrative taxonomic approaches to identify and record marine biodiversity of pelagic copepods

## ***Patterns of Biodiversity of Marine Zooplankton Based on Molecular Analysis***

Open call for papers for special issue on revisiting biodiversity of marine zooplankton based on novel molecular approaches. Suggested topics, among others:

- biodiversity, biogeography, and trophic dynamics of marine zooplankton
- best practices for barcoding and metabarcoding analysis
- progress toward and use of DNA sequence reference databases
- discovery, detection, and functional importance of rare and cryptic species

Manuscript deadline: October 30, 2020

**Howard I. Browman, ICES JMS Editor-in-Chief**  
**Ann Bucklin, Katja Peijnenburg, Ksenia Kosobokova, Ryuji Machida**  
**Themed Set motivators**

[https://academic.oup.com/icesjms/pages/themed\\_sets](https://academic.oup.com/icesjms/pages/themed_sets)

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## Acknowledgements



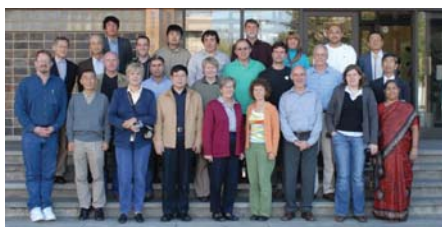
SCOR WG157 - Gothenburg, Sweden (2019)

**MetaZooGene SCOR WG157**  
**Scientific Committee for Oceanic Research (SCOR)**



ICES WGIMT - Boulogne-sur-Mer, France (2017)

**Working Group for Integrative Morphological and Molecular Taxonomy (WGIMT)**  
**International Council for the Exploration of the Sea (ICES)**



CMarZ Steering Group - Tokyo, Japan (2006)

**Census of Marine Zooplankton (CMarZ) Steering Group**  
**Census of Marine Life (CoML)**  
**Alfred P. Sloan Foundation**



Appreciation: University of Connecticut: Institute for Systems Genomics (ISG), Computational Biology Core (CBC), Center for Genomic Innovation (CGI)

Photo credits: R.R. Hopcroft, UAF; L.P. Madin, WHOI (USA)



<https://isg.uconn.edu/>

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