



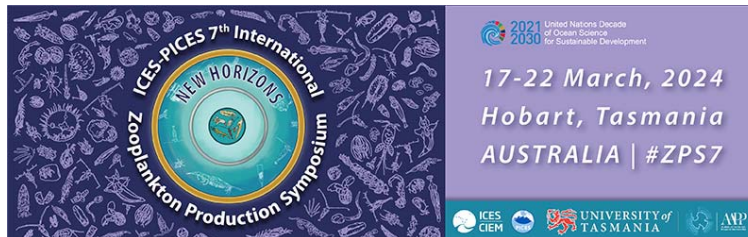
SCOR WG157

MetaZooGene



Annual Meeting - March 20, 2024

Institute for Marine and Antarctic Studies (IMAS)
University of Tasmania, Hobart, Tasmania



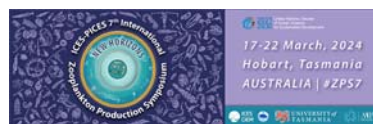
SCOR WG157

MetaZooGene

SCOR WG157 Annual Meeting Agenda



- | | |
|----------------|---|
| 5:30 pm | Doors open @ IMAS |
| 6:00 pm | Dinner buffet available |
| 7:00 pm | Introductions & MetaZooGene Overview |
| 7:20 pm | Presentation updates from WG157 members |
| 8:30 pm | Looking ahead: WG157 activities & goals for 2024 |
| 9:00 pm | Adjourn |





SCOR WG157

MetaZooGene

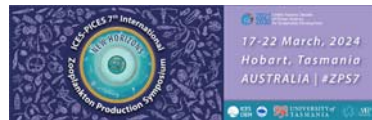
Annual Meeting Agenda



Institute for Marine and Antarctic Studies, University of Tasmania
 March 20, 2024, Hobart, Tasmania (AUS)

Presentation updates from WG157 members:

- | | |
|--|----------------------------|
| ▪ Katja Peijnenburg | • Leonie Suter |
| ▪ Ksenia Kosobokova / Dimitry Kulagin | • Mary Mar N. Payne |
| ▪ Agata Weydmann-Zwolicka | • Pennie Lindeque |
| ▪ Aino Hosia | • Silke Laakmann |
| ▪ Tone Falkenhaus / Elizaveta Ershova | • Todd O'Brien |
| ▪ Jenny Huggett | • Ann Bucklin |
| ▪ Junya Hirai | |



Katja Peijnenburg



Poster S18-P8

Making reads count

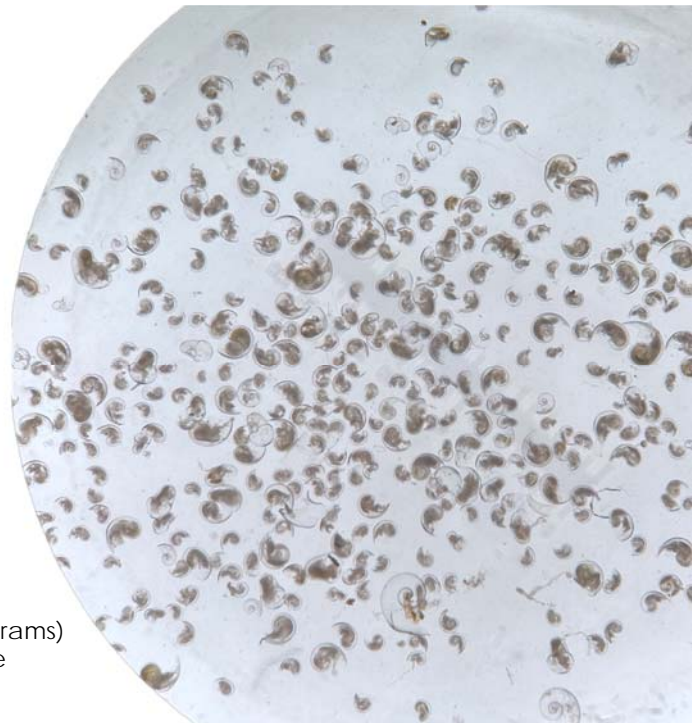
Metabarcoding of calcifying plankton

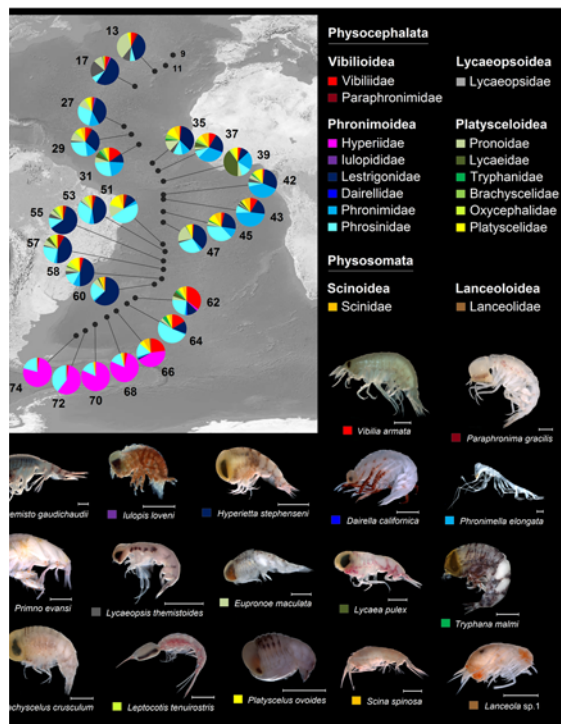
MSc students:

Robin van Dijk

Daniëlle van der Burg

- Reference libraries (pteropods, heteropods, forams)
- group-specific primers to estimate abundance





Katja Peijnenburg

Genetic diversity of hyperiid amphipods along a meridional transect in the Atlantic Ocean

Tump, Vonk, Beentjes, BurrIDGE, Goetze, Peijnenburg

- 273 specimens, 63 species
- 26 species with no prior reports in public databases
- no prior barcodes for hyperiids in from the South Atlantic
- phylogeographic patterns

BurrIDGE et al. 2017. Diversity and distribution of hyperiid amphipods along a latitudinal transect in the Atlantic Ocean. *Prog. Oceanogr.*

Ksenia Kosobokova & Dmitry Kulagin

P.P. Shirshov Institute of Oceanology RAS, Moscow

I. Biodiversity, distribution and population connectivity

Target groups:

1) Euphausiids

- > 2000 specimens of 48 species sorted for sequencing, including *Euphausia hanseni*, *Thysanoessa vicina*, *Thysanopoda astylata*, *T. egregia* and *T. microphthalmia* which have not been barcoded yet;
- new species of *Hansarsia* (former *Nematoscelis*) described based on morphology and genetics (COI, H3, ITS-1).

2) Pelagic shrimps (Decapoda)

- Genetic (COI and ITS-1) and morphological variation of mesopelagic shrimp *Styellispis debilis* in the Atlantic and South-West Indian Oceans

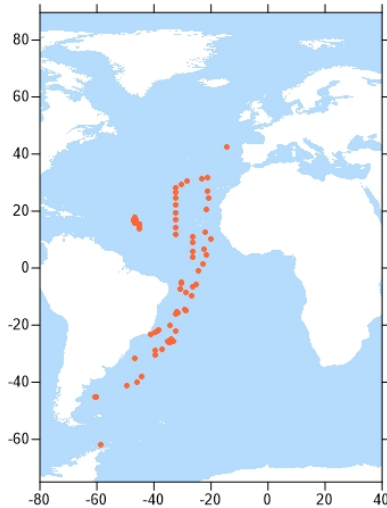
II. Phylogeny and cryptic diversity of pelagic shrimps (Hymenodoridae)

- Multigene analysis (COI, 16S, 18S, H3, NaK and enolase)
- cryptic species in *Hymenodora glacialis* and *H. gracilis*



Ksenia Kosobokova & Dmitry Kulagin
P.P. Shirshov Institute of Oceanology RAS, Moscow

Biodiversity and distribution of pelagic organisms in the Atlantic Ocean



Material

Target region: Atlantic Ocean.

- Nine research cruises (2012-2023).
- 100 stations (42°N-62°S).
- Depth-stratified vertical net tows and oblique trawls.
- Sampling at depths from surface to 600-3500 m.

Recent Publications



Ksenia Kosobokova & Dmitry Kulagin - Shirshov Institute of Oceanology RAS

 RESEARCH PAPER
<https://doi.org/10.1071/IS23034>

Invertebrate Systematics

An integrative taxonomic approach to the Atlantic *Hansarsia* (formerly *Nematoscelis*) yields new krill taxa (Crustacea: Euphausiidae)

D. N. Kulagin¹, U. V. Simakova¹, A. A. Lunina¹ and A. L. Vereshchaka¹

Article

Exploring Genetic and Morphological Integrity across Ocean Basins: A Case Study of the Mesopelagic Shrimp *Systellaspis debilis* (Decapoda: Oplophoridae)

Anna Shapkina¹, Dmitry Kulagin¹, Vadim Khalitov^{2,3}, Anastasiia Lunina¹ and Alexander Vereshchaka^{1,4}

Zoological Journal of the Linnean Society, 2023, XX, 1–58. With 16 figures.

Discovery of a new species and host record of *Holophryxus* Richardson, 1905 (Isopoda: Dajidae) from the central Arctic: a model of enhanced descriptive standards for epicaridean isopods

RONY HUYS¹, ALEXANDRA S. SAVCHENKO² and KSENIA N. KOSOBOKOVA¹



HIDEA – Hidden diversity of plankton in the European Arctic

Agata Weydmann-Zwolicka e-mail: agataw@ug.edu.pl



University
of Gdańsk

- The aim of the project: to assess the impact of increased transport of Atlantic water into the Arctic (Atlantification) on the biodiversity of Arctic plankton: from bacterioplankton, through protists, to zooplankton.
 - Sampling during summers 2019-2023
 - The collection of hydrological data, and four plankton size fractions (pico-, nano-, micro-, and mesoplankton).

Phytoplankton and zooplankton analysed based on morphology and metabarcoding



HIDEA – Hidden diversity of plankton in the European Arctic

Agata Weydmann-Zwolicka e-mail: agataw@ug.edu.pl



University
of Gdańsk

biology MDPI

Article

Contrasting Marine Microbial Communities of the Fram Strait with the First Confirmed Record of Cyanobacteria *Prochlorococcus marinus* in the Arctic Region

Monika Mioduchowska ^{1,2,*}, Joanna Pawłowska ³, Karol Mazanowski ² and Agata Weydmann-Zwolicka ^{2,*}

Marine Biodiversity
Comparison of DNA metabarcoding and microscopy in analysing planktonic protists from the European Arctic
--Manuscript Draft--

Manuscript Number: MARB-D-23-00139R3

Full Title: Comparison of DNA metabarcoding and microscopy in analysing planktonic protists from the European Arctic

Article Type: TC: Pelagic Biodiversity

water MDPI




Article

Challenges of Comparing Marine Microbiome Community Composition Data Provided by Different Commercial Laboratories and Classification Databases

Monika Mioduchowska ^{1,2,*}, Anna Iglíkowska ¹, Jan P. Jastrzębski ^{3,4}, Anna-Karina Kaczorowska ⁵, Ewa Kotłarska ⁶, Artur Trzebny ⁷ and Agata Weydmann-Zwolicka ²


S04:
Tracking the Atlantification of the Arctic with integrated:
taxonomy and metabarcoding
Thursday, 2:00 PM

Aino Hosia: Cnidaria & Ctenophora Team at UiB

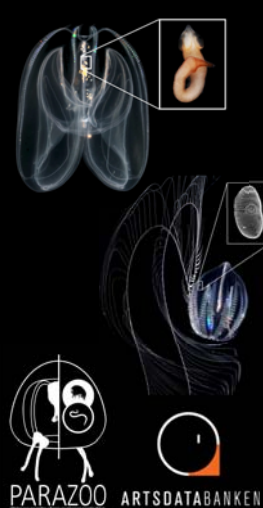




Aino Hosia
Luis Martell
Joan Soto-Angel


Aino Hosia: Cnidaria & Ctenophora Team at UiB



POLE2POLE
Bipolarity in Hydrozoa





ParaZoo
Parasites of jellyfish and arrow worms




NoAH
Norwegian Arctic Hydrozoa

Planktonics
Citizen Science eDNA pilot

HYDROINS
Anthoathecate hydrozoans in Swedish Waters
PhD project
Doris Björling (GU)

Siphonophore diversity



PhD project
Preveen Raj



2. Establishment of Zooplankton Inter-Calibration Experiment (Zoo-ICE)

Effective engagement with stakeholders to overcome logistical and policy challenges, and to provide a roadmap towards application of DNA-based methods in marine environmental management.

Jenny Huggett

Zooplankton Metabarcoding Initiatives in South Africa

Dept. Environment, Forestry and Fisheries: Jenny Huggett
SAAMBR (ORI): Johan Groeneveld and Ashree Gowder



1. Participation in the MetaZooGene Intercalibration Experiment (MZG-ICE)

Participating in the metabarcoding analysis of a set of reference samples across 10 groups to assess the impact and significance of different protocols worldwide to develop best practices for DNA metabarcoding of marine zooplankton diversity.

3. Contributing towards building South African online barcoding reference libraries

Foundational Biodiversity Information Programme (FBIP) for copepods, euphausiids, chaetognaths, amphipods, and decapods.

4. Designing mini-barcode markers to target specific zooplankton in South African waters for HTS

Lobster, prawn, crab, shrimp, fish, copepods, chaetognaths, euphausiids, and hydrozoa.

Jenny Huggett: Zooplankton Metabarcoding Initiatives in South Africa

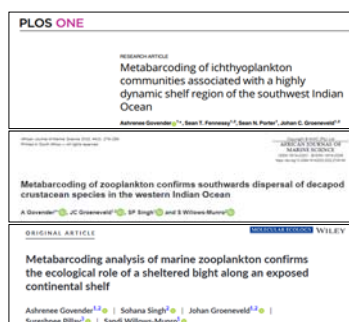
5. Zooplankton metabarcoding method development in South Africa



8. Sampling methodology testing

Testing the effects of different sampling gear (ring-, manta- and WP2 net), day and night sampling, and tow duration (5-, 10- and 15-minute tows) on the metagenetic composition of marine zooplankton samples collected in coastal waters of eastern South Africa for the planning of long-term monitoring programs in the region.

6. Zooplankton metabarcoding in ecological research in the Western Indian Ocean



9. Long-term monitoring sites within the Indian Ocean



7. Metabarcoding of zooplankton to derive indicators of pelagic ecosystem status



10. eDNA method testing:

Testing and validating eDNA protocols within a close aquarium system for future marine monitoring studies.

11. Comparing ZooScan & Metabarcoding

Comparing how well the two methods complement each other in characterizing zooplankton communities.



2024 MetaZooGene (SCOR WG 157) meeting

Junya Hirai (Atmosphere and Ocean Research Institute, The University of Tokyo)



Ongoing projects associated with the MetaZooGene

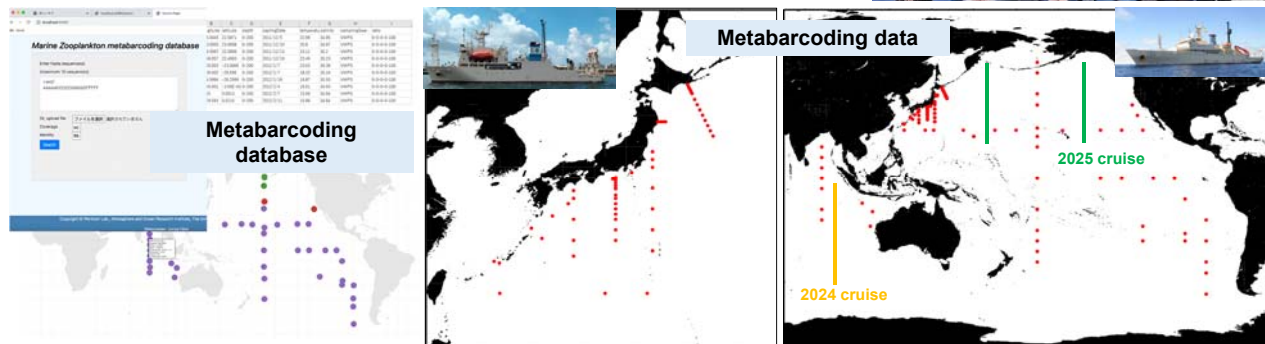
- Large-scale zooplankton metabarcoding (Indian & Pacific Oceans)
- Zooplankton monitoring by metabarcoding (around Japan)
- ➔ Marine zooplankton metabarcoding database
- Genome skimming project of key zooplankton species around Japan



Atmosphere and Ocean Research Institute
The University of Tokyo



Research cruise Eastern Indian (2024), North Pacific (2025)



Junya Hirai - 7th Zooplankton Production Symposium presentations

(W1) Junya Hirai. **Reference sequence data for marine zooplankton in the era of high-throughput sequencing**

(W1) Mary Mar N. Payne, Junya Hirai, Jean Rose Maquirang, Yasmin H. Primavera-Tirol, Wilfredo L. Campos. **Evaluation of zooplankton biodiversity in two critical coastal ecosystems in the Province of Aklan, Philippines using DNA metabarcoding: estuary versus coral reef.**

(S4) Kanako Amei, Junya Hirai, Erica Goetze, Yuichiro Nishibe. **Global species diversity of pelagic polychaetes in the family Tomopteridae as revealed by molecular approaches**

(S4) Misato Nakae, Junya Hirai, Naoki Iguchi, Yosuke Igeta, Kay Sakuma, Yuichiro Nishibe. **DNA metabarcoding reveals the community structure of copepod nauplii in the Japan Sea**

(S4) Junya Hirai, Seiji Katakura, Hiromi Kasai, Satoshi Nagai. **Copepod-virus interactions revealed by molecular and morphological approaches**

(S4) Nakako Tamamushi, Junya Hirai, Fanyu Zhou, Takuya Ohnishi, Atsushi Tsuda. **Metabarcoding analysis for comparing epipelagic/mesopelagic zooplankton communities in the Pacific and eastern Indian Oceans**

(S4) Stephanie A. Matthews, Katarina Kaminsky, Alexis E. Cazares, Jennifer M. Questel, Leocadio Blanco-Bercial, Junya Hirai, and Mark D. Ohman. **Zooplankton across the North Pacific Basin: Testing the effects of physical dispersal vs. environmental homogeneity**

(S4) Ann Bucklin, Leocadio Blanco-Bercial, Ruben Escribano, Tone Falkenhaus, Junya Hirai, Jenny Huggett, Pedro Martinez, Katja Peijnenburg, Leonie Suter, Agata Weydmann-Zwolicka, and Colleagues. **Metabarcoding Zooplankton Diversity: MetaZooGene Intercalibration Experiment (MZG-ICE)**

(S9) Kume G, Minagawa A, Jinno S, Hirai J, Shiozaki K, Ichinomiya M, Komorita T, Habano A, Kodama M, Kobari T. **The diet of *Anguilliformes leptocephali* in the Kuroshio Current and adjacent waters.**

(S9) Toru Kobari Taniguchi A, Kume G, Kodama M, Ichinomiya M, Komorita T, Hirai J. **Trophic sources and pathways toward fish larvae under spring phytoplankton bloom in the neighboring waters of the Kuroshio.**

(S15) Fanyu Zhou, Junya Hirai, Koji Hamasaki, Sachiko Horii, Takuya Sato, Atsushi Tsuda. **The wide distribution of *Euphausia* species in the low-latitude ecosystem supported by the flexible omnivory: two cases in the low-latitude Indian and Pacific Oceans**

(S18) Kazutaka Takahashi, Junya Hirai, Takuhei Shiozaki, Fuminori Hashihama. **Enhanced nitrogen regeneration by planktonic copepods in the oligotrophic subtropical ocean under active N₂ fixation.**

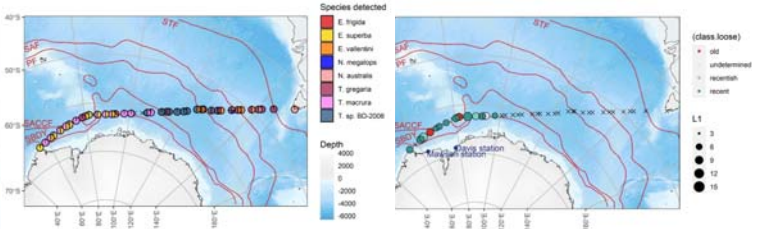
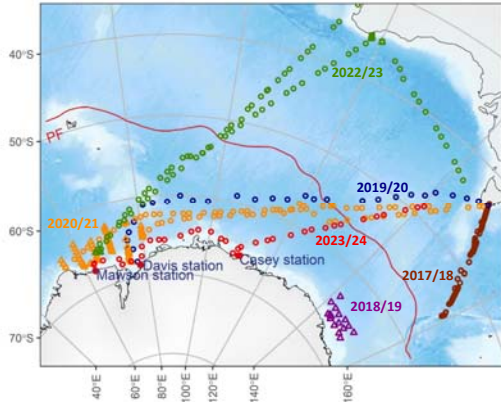


Metabarcoding markers:

- Leray COI marker
- Customised 16S markers:
 - Krill
 - Fish
 - Mammals

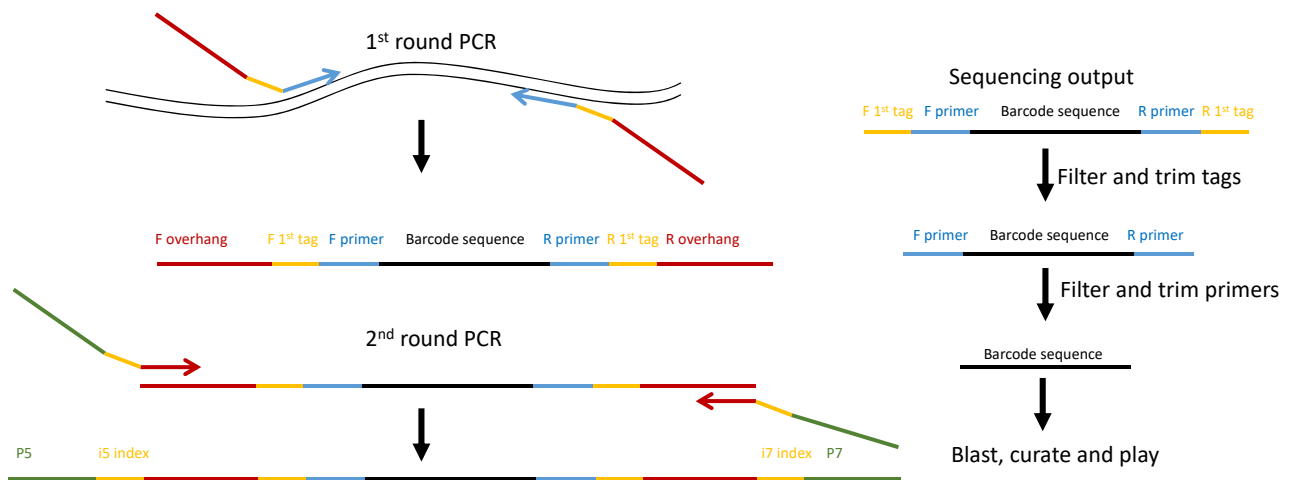
Species specific markers:

Euphausia superba, set of markers to determine presence, abundance and fragmentation



Currently working on:

Comparisons to continuous plankton recorder, visual, trawl, acoustic data...
 Effect of environmental variables
 Long-term trends



Mary Mar Noblezada Payne, PhD

SCOR Working Group 157 MetaZooGene

Associate Member, Philippines

College of Fisheries and Aquatic Sciences , Iloilo State
University of Fisheries Science and Technology, Barotac
Nuevo, Iloilo, Philippines, mmpnoblezada@gmail.com



Meeting and Scholarship

1. SCOR exceptional scholar 2022 hosted by Dr. Junya Hirai of the AORI, The University of Tokyo, Japan
2. 7th Zooplankton Production Symposium, Hobart, Tasmania, Australia




MATERIALS AND METHODS

ZOOPLANKTON SAMPLES COLLECTION

- Batan (night sampling) and Tangalan (rough sea condition) Bays, Aklan, Philippines
- 200 microns mesh plankton net
- 10 minutes horizontal tow

SCOR 2022 Exceptional Scholar
COLLABORATIVE SCIENTIFIC ACTIVITY REPORT


March 24 – 15 April 2023
Atmosphere and Ocean Research Institute
The University of Tokyo, Japan

Name of Guest: Mary Mar A. Payne, PhD
 Name of Host: Junya Hirai, PhD
 Name of Host Institution: Atmosphere and Ocean Research Institute, The University of Tokyo, Japan
 Name of Guest Institution: College of Fisheries and Aquatic Sciences, Iloilo State University of Fisheries Science and Technology, Barotac Nuevo, Iloilo, Philippines
 SCOR Working Group: SCOR WG 157 MetaZooGene

DNA METABARCODING

1 extraction, amplification and sequencing
AORI (Atmosphere and Ocean Research Institute) of the University of Tokyo, Japan
16S and CO1
➢ sequencing using illumina MiSeq NGS of AORI



Evaluation Of Zooplankton Biodiversity In Two Critical Coastal Ecosystems In The Province Of Aklan, Philippines Using DNA Metabarcoding: Estuary Versus Coral Reef

Mary Mar Noblezada Payne, Junya Hirai, Jean Rose Maquirang, Yasmin H. Primavera-Tirol, Wilfredo L. Campos

College of Fisheries and Aquatic Sciences
Iloilo State University of Fisheries Science and Technology
Barotac Nuevo, Iloilo, Philippines

2





Publication

Journal of the Marine Biological Association of the United Kingdom, 2013, 93(1), 138–146. © Marine Biological Association of the United Kingdom, 2013. doi:10.1017/S0025315212000001

Phylogeography of the planktonic shrimp *Lucifer hanseni* Nobili 1905 in the Indo-Malayan Archipelago

MARY MAR NOBLEZADA^{1,2,3}, HIROIMI MIYAMOTO⁴, WILFREDO L. CAMPOS⁵, FATIMAH MD. YUSOFF⁶ AND SHUHEI NISHIDA¹

¹Atmosphere and Ocean Research Institute, University of Tokyo, 1-1-8 Kashiwanoha, Kashiwa 277-8564, Japan; ²The Marine Science Institute, University of the Philippines Diliman, Velasquez St., 1101 Quezon City, Philippines; ³OceanBio Laboratory, Division of Biological Sciences, College of Arts and Sciences, The University of Philippines Visayas, 1014 Miagao, Iloilo, Philippines; ⁴Tohoku National Fisheries Research Institute, Fisheries Research Agency, 3-12-9 Shirohama, Shirohama 989-0001, Japan; ⁵Department of Aquaculture, Faculty of Agriculture, Institute of Bioscience, Universiti Putra Malaysia, 41000 UPM, Serdang, Selangor, Malaysia

Using partial sequences of two mitochondrial genes, cytochrome *c* oxidase subunit I (COI) and 16S ribosomal RNA (16S rRNA), and one nuclear gene, 18S ribosomal RNA (18S rRNA), we investigated population genetics of the holoplanktonic shrimp *Lucifer hanseni* Nobili, 1905 in the Indo-Malayan Archipelago (IMA) encompassing Andaman Sea, Malacca Strait, Gulf of Thailand, Borneo Island, Philippines (hereafter collectively referred to as the Thailand-Malaysia-Philippines area: TMP), Celebes Sea (CS), and the waters near islands in the Western Pacific (WP) including Palau, Papua New Guinea and Solomon Islands. The samples from the TMP showed the highest number of haplotypes. Significant phylogeographic structure was revealed. The total mean revealed two major alle and WP populations 1 compared with the all haplotype network. TM4 which is suggested as 8 time and corroborates

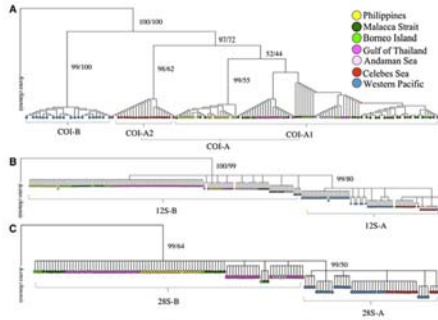


Fig. 4. Bayesian tree based on sequences of COI (A) 16S rRNA (B) and 18S rRNA (C) of *Lucifer hanseni*. Numerical values are Bayesian posterior probabilities (left) and maximum likelihood bootstrap values (right). For easy visualization, we have displayed the tree based on mitochondrial gene COI as a phylogenetic tree based on mitochondrial gene 16S rRNA and nuclear gene 18S rRNA as ultrametric trees.

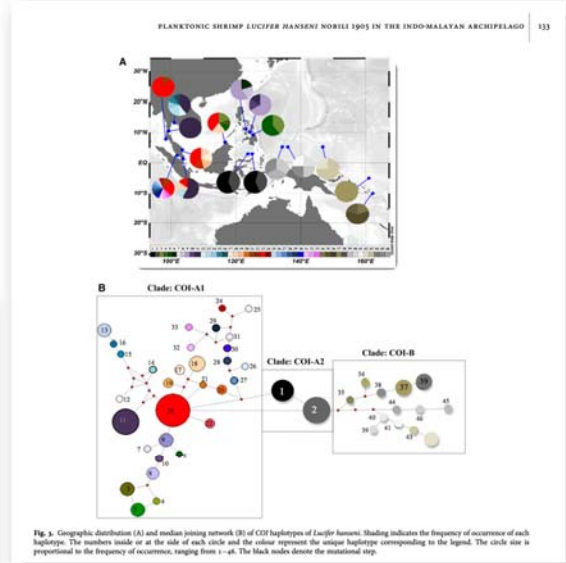
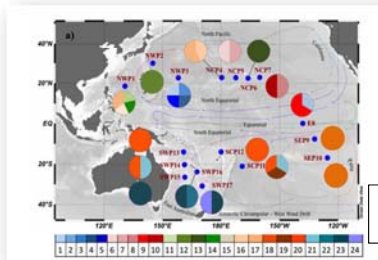


Fig. 5. Geographic distribution (A) and median joining network (B) of COI haplotypes of *Lucifer hanseni*. Shading indicates the frequency of occurrence of each haplotype. The numbers inside or at the side of each circle and the colour represent the unique haplotype corresponding to the legend. The circle size is proportional to the frequency of occurrence, ranging from 1–45. The black nodes denote the mutational step.

Publication in preparation

1. Molecular-genetic analysis of *Oithona attenuata* (Copepod, Cyclopoida) populations in the coastal waters of Southeast Asia
2. Molecular phylogeny of the Family Oithonidae
3. Phylogeography of the planktonic shrimp *Lucifer typus* in the Pacific Ocean



3

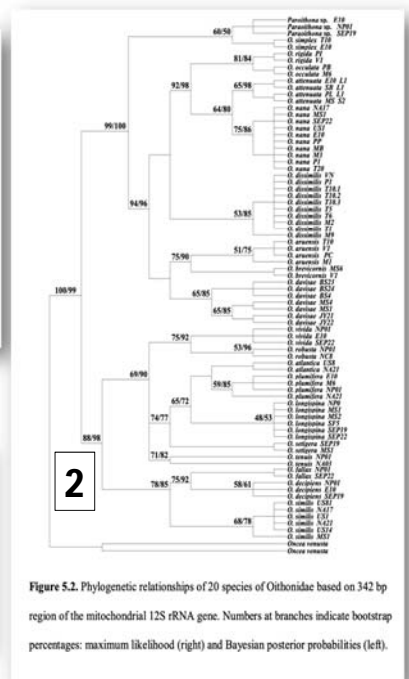
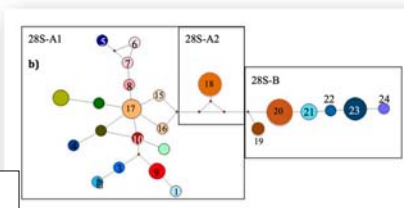
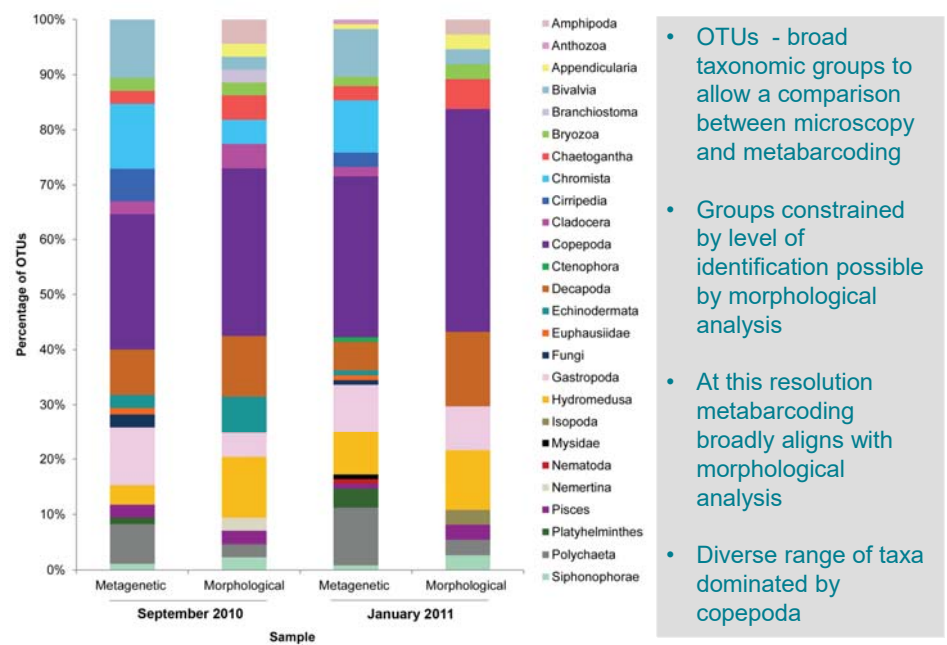


Figure 5.2. Phylogenetic relationships of 20 species of Oithonidae based on 342 bp region of the mitochondrial 12S rRNA gene. Numbers at branches indicate bootstrap percentages: maximum likelihood (right) and Bayesian posterior probabilities (left).

Pennie Lindeque - Metabarcoding of Zooplankton in the WEC

Pennie Lindeque - Metabarcoding of Zooplankton in the WEC



- OTUs - broad taxonomic groups to allow a comparison between microscopy and metabarcoding
- Groups constrained by level of identification possible by morphological analysis
- At this resolution metabarcoding broadly aligns with morphological analysis
- Diverse range of taxa dominated by copepoda

Pennie Lindeque - Metabarcoding of Zooplankton in the WEC

- Metabarcoding of 18S amplicons is a powerful tool for elucidating the true diversity and species richness of zooplankton communities
- Reveals a previously hidden taxonomic richness
 - Copepoda
 - Meroplankton (Bivalvia, Gastropoda and Polychaeta)
- Reveals rare species and parasites.
- ❖ Critical need for reference libraries of accurately identified individuals
- Traditional monitoring of shelf sea zooplankton with vertical hauled plankton nets does not critically misrepresent zooplankton in the water column by under-sampling those close to the sea floor
- But epibenthic sled does provide more information.



Pennie Lindeque - Metabarcoding of Zooplankton in the WEC

PML WCO L4 molecular time-series

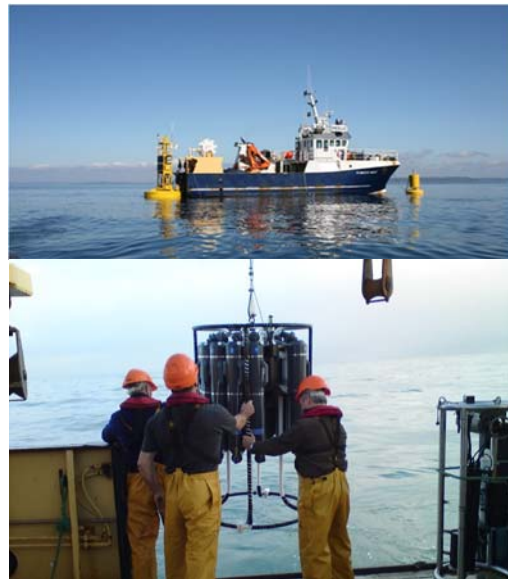
Water (sterivex)

- 2012 – present day ~ weekly sampling
- Surface water sterivex sample
- 2012 – 2023 18S V9 rRNA gene sequence data
- Processed with Qiime2 pipeline and DADA2; taxonomy assigned using NCBI database
- Animalia sequences (428 unique) manually checked and compared to morphological dataset

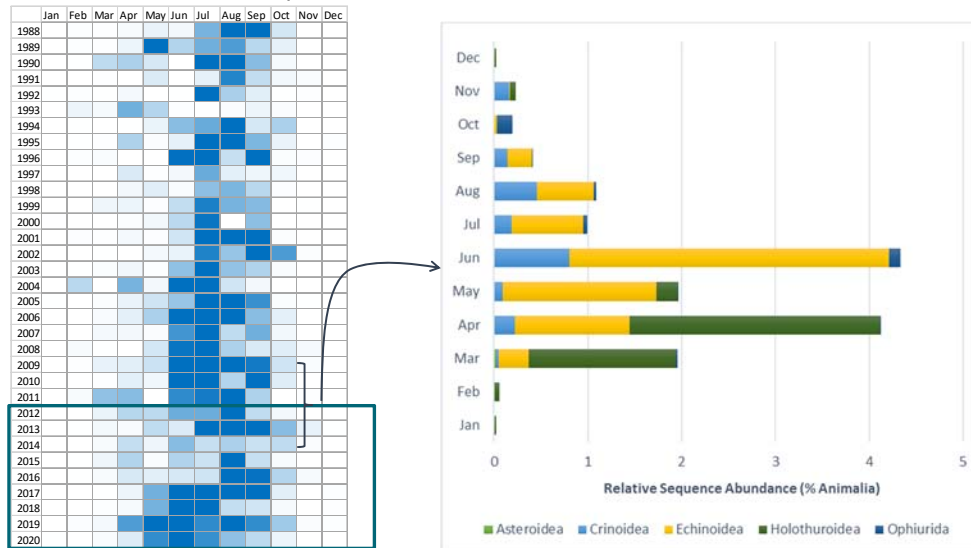
Sediment (bulk ~0.5 g)

- 2012 – present day ~ weekly sampling
- Surface sediment sample
- 2012 – 2023 18S V9 rRNA gene sequence data

Slides courtesy of Karen Tait and Helen Parry
ktait@pml.ac.uk



Echinoderm meroplankton



- Echinodermata meroplankton abundance increasing earlier in the year

Pennie Lindeque - Metabarcoding of Zooplankton in the WEC

Slides courtesy of Karen Tait and Helen Parry
ktait@pml.ac.uk



Silke Laakmann
Alica Ohnesorge



Capturing drifting species and molecules—Lessons learned from integrated approaches to assess marine metazoan diversity in highly dynamic waters

Alica Ohnesorge ✉ Uwe John, Sarah Taudien, Stefan Neuhaus, Lucie Kuczynski, Silke Laakmann ✉

First published: 11 October 2023 | <https://doi.org/10.1002/edn3.478>

AIM:

Do we have sufficient reference data & appropriate methods to identify marine fauna in the North Sea?

→ Yes: **354** species from eDNA & zooplankton metabarcoding with **>90%** known from the **North Sea**

! S04: Tomorrow 2:30 PM Talk by A. Ohnesorge: „Zooplankton is the perfect candidate for validating eDNA metabarcoding for analyzing North Sea marine fauna“ !

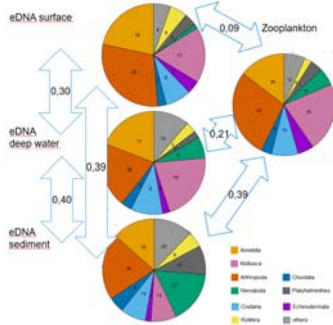


Silke Laakmann
Alica Ohnesorge



Roaming the seas – Assessing marine fauna biodiversity throughout salinity gradients with zooplankton and eDNA metabarcoding

Alica Ohnesorge, Uwe John, Lucie Kuczynski, Stefan Neuhaus, Kingsly Chuo Beng, Bernd Krock, Silke Laakmann
submitted to Environmental DNA (06.03.24)



“Our study confirms the value of metabarcoding to identify the North & Baltic Sea fauna & underscores the importance of combining multiple molecular approaches to identify & understand invertebrate biodiversity & its change in the marine realm.”

→ 279 species from eDNA & zooplankton metabarcoding with >87% known from the North & Baltic Sea

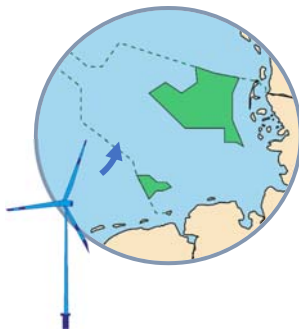


Silke Laakmann



Meroplankton, eDNA & key species (i.e. European flat oyster) metabarcoding to identify reef restoration success & Marine Protected Area network functions in the German Bight, North Sea

Kingsly Chuo Beng, Silke Laakmann, Anne F. Sell & others
Ongoing work



SPONSORED BY THE
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EXPLORING BIODIVERSITY REFUGIA: PATTERNS OF MEROPLANKTON BIODIVERSITY IN THE VICINITY OF RESTORED OYSTER REEFS

INTRODUCTION
Restoration activities are important components of reef ecosystem health, however, the diversity and distribution of species that occur near to restoration or protection projects of marine ecosystems remains unclear. Understanding the patterns of biodiversity in these systems is essential for assessing the success of restoration efforts.

OBJECTIVES
To explore patterns in the diversity and composition of meroplankton communities in the vicinity of restored oyster reefs, we conducted a metabarcoding study of meroplankton diversity in the vicinity of restored oyster reefs in the German Bight. We aimed to identify patterns in the diversity and composition of meroplankton communities in the vicinity of restored oyster reefs.

METHODS
We collected meroplankton samples from the vicinity of restored oyster reefs in the German Bight. We used metabarcoding to identify species in the vicinity of restored oyster reefs. We used a combination of metabarcoding and microscopy to identify species in the vicinity of restored oyster reefs.

RESULTS
We identified a total of 100 meroplankton species in the vicinity of restored oyster reefs. We found that the diversity and composition of meroplankton communities in the vicinity of restored oyster reefs were significantly higher than in the vicinity of non-restored oyster reefs.

DISCUSSION
Our results suggest that restored oyster reefs may serve as biodiversity refugia for meroplankton communities. We found that the diversity and composition of meroplankton communities in the vicinity of restored oyster reefs were significantly higher than in the vicinity of non-restored oyster reefs. This suggests that restored oyster reefs may serve as biodiversity refugia for meroplankton communities.

Tone Falkenhaus, Institute of Marine Research, Norway

Inventories of copepods in Norwegian waters

- using integrative morphological and molecular approaches

Projects:

- **COPCLAD 2015-2017:** Inventory of marine planktonic Copepoda and Cladocera (Crustacea) in Norway
- **HYPCOP 2020-2023:** Copepods in hyperbenthic habitats:

Aims and results:

- The projects have contributed to a validated DNA-barcode library of Norwegian copepod species, including COI barcodes with linked metadata, specimen pictures, and voucher specimens
- 7 species potentially new to science, including 1 new genus.
- 12 new species to Norway
- Development of a successful protocol for integrated morphological and molecular approach to identification of copepods

Publications

Eilertsen, M.H., Kongsrud, J.A., Tandberg, A.H.S., Alvestad, T., Budaeva, N., Martell, L., Ramalho, S.P., Falkenhaus, T. et al. Diversity, habitat endemism and trophic ecology of the fauna of Loki's Castle vent field on the Arctic Mid-Ocean Ridge. *Sci Rep* 14, 103 (2024).

<https://doi.org/10.1038/s41598-023-46434-z>

Book chapter: Rauch, C., Hobæk, A., Falkenhaus, T. 2022. Hopp i havet med hoppekreps (*Into the sea with copepods*). Pp 176-185 in Yearbook for the Bergen University museum 2022.



NORWEGIAN BIODIVERSITY
INFORMATION CENTRE



Development and application of phyto- and zooplankton metabarcoding as routine tools for ecosystem monitoring cruises

Elizaveta Ershova, Tone Falkenhaus, Jon-Ivar Westgaard, Sarah Lerch

Ongoing and planned activities:

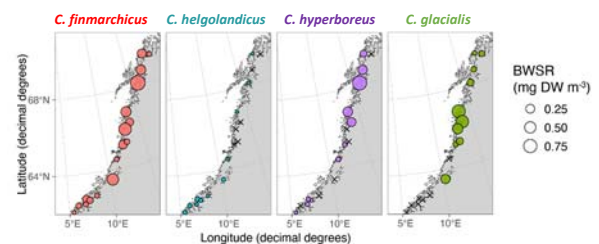
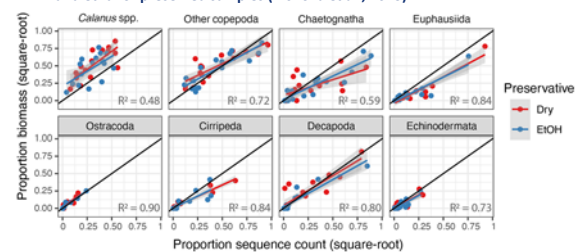
- Optimisation of DNA preservation and extraction protocols for maximum quality and time/cost efficiency
- Comparative analysis between data produced by different IMR labs and sequencers (Illumina MiSeq vs. Ion Torrent)
- Quantification of biases in metabarcoding protocols using a mock sample approach
- Establishment of a framework for quantitative interpretation of COI metabarcoding data
- High-resolution mapping of zooplankton species distribution in Norwegian waters using metabarcoding

Publications

Elizaveta A. Ershova, Owen S. Wangensteen, Tone Falkenhaus (2023) Mock samples resolve biases in diversity estimates and quantitative interpretation of zooplankton metabarcoding data. *Marine Biodiversity*. 53, 66. DOI: 10.1007/s12526-023-01372-x

Elizaveta A. Ershova, Terje Berge, Tone Falkenhaus (in preparation) Latitudinal gradients in zooplankton communities in Norwegian fjords resolved by an integrated morphological and molecular approach

Correlations between % biomass and % sequence reads in dehydrated and ethanol-preserved samples (Ershova et al., 2023)



Todd O'Brien : NOAA Fisheries / "COPEPOD"

- **I am a Minnesota oceanographer!** Computers/limnology -> estuarine ecology -> satellite biological oceanography -> zooplankton data management -> product and tools development ... (spatial fields, time series, molecular, maybe even image-based methods).
- I like to work with researchers and working groups by building data tools and compilations that can help them answer larger questions.
- My favorite people to work with are those that are willing to chat and ask questions, report issues or strange results, or suggest improvements.
- Some of the best MZGdb features/additions came from people asking "would it be possible to ..." or "could you add ..." (or "this is broken").



Todd O'Brien : NOAA Fisheries / "COPEPOD"

MZGdb will continue ...

- *It is one of my favorite projects, and one of the most popular.*
- **Ongoing Community:** Many of the MetaZooGene members are also in ICES WGIMT ... members or work with other WGIMT members. Many are also friends, and I am happy to stay in contact via email and at conferences.
- **Semi-Automation:** MZGdb is usually 5% Todd time and 95% computer time.
- **On the horizon:** LME's, and lists of under-barcoded species ranked by *frequency-of-reported-observation* (by ocean, taxonomic group and Mtype).



Todd O'Brien : NOAA Fisheries / "COPEPOD"

"What works for me ..."

A loose hybrid-informational database of primers and protocols that have been used by individuals and labs with casual details that may help guide others towards (or away from) certain methods / equipment / chemicals / protocols or other decisions.

- Broken down by target taxa group, method, and any other influencing factors (e.g. works great with stomach contents, or works quite well with [taxa group]).
- **This is NOT a "best practices" effort!** It should be a humble and honest discussion area, a place to share information on successes *and failures*.
- Explaining failed attempts or less-than-perfect results can be equally as valuable, especially if it keeps someone else from repeating it again.
- For best success, this page should also not be anonymous, and should instead encourage outreach and sharing of ideas and information.



Ann Bucklin & Paola Batta-Lona (UConn)
Metabarcoding Zooplankton (Cryptic) Diversity:
Time-series Ecosystem Monitoring & Assessment

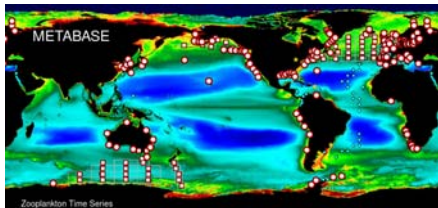
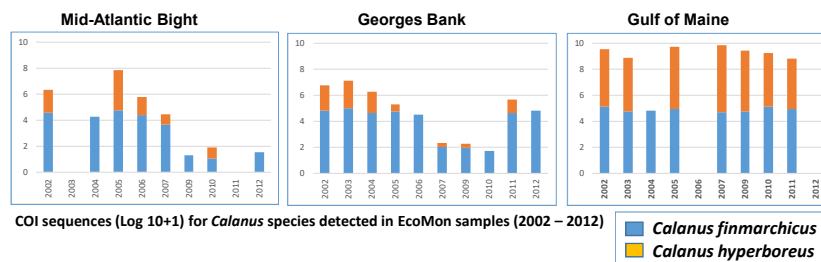
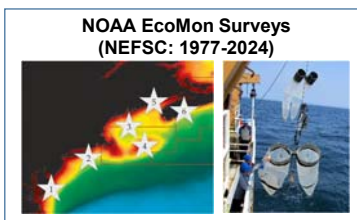


Image: O'Brien et al. (2013)

- DNA metabarcoding of 26 samples from EcoMon Surveys (May 2002-2012)
 - 181 species across 23 taxonomic groups detected
 - 67 species of 15 taxonomic groups > 50 COI sequences
 - 23 species >1,000 COI sequences
- Copepod *Calanus finmarchicus*
 - abundant in all NW Atlantic shelf regions
 - important prey species for fisheries
 - range shifts reflect climate change



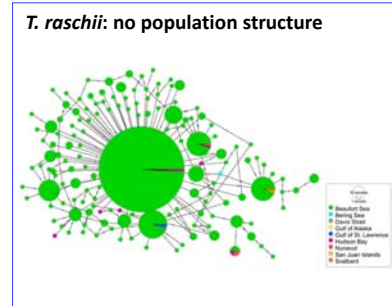
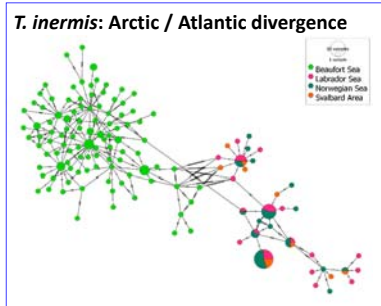
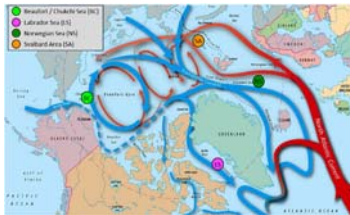


COI Barcoding of Euphausiids

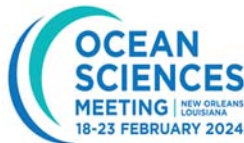
Ann Bucklin, Jenn Questel, Paola Batta-Lona, Peter Wiebe et al.



- Atlantic Boreal / Arctic species: *Thysanoessa inermis* & *T. raschii*
- COI diversity & structure; Minimum Spanning Networks (MSN)
- Hypotheses or speculations of different demographic histories



Bucklin, A., J.M. Questel, P.G. Batta-Lona, M. Reid, A. Frenzel, C. Gelfman, P.H. Wiebe, R.G. Campbell, C.J. Ashjian (2023) Marine Biodiversity <https://doi.org/10.1007/s12526-023-01371-y>



MetaZooGene Presentation
 Ocean Sciences Meeting OSM-2024
 New Orleans, LA (USA)
 February 22, 2024



Session OT41A - Expanding the Ocean Biomolecular Observing Network to New Locations, Technology, and Data Platforms II

Reference Sequences for DNA-based Analysis of Global Marine Diversity: MetaZooGene Atlas and Database



Ann Bucklin¹, Todd D. O'Brien², Leocadio Blanco-Bercial³, Jennifer M. Questel⁴, Paola G. Batta-Lona¹

¹Department of Marine Sciences, University of Connecticut, Groton, CT

²NOAA Fisheries, Office of Science & Technology, Silver Spring, MD

³Bermuda Institute of Ocean Sciences, Arizona State University, St Georges, Bermuda

⁴College of Fisheries & Ocean Sciences, University of Alaska Fairbanks, Fairbanks, AK





SCOR WG157

MetaZooGene

Annual Meeting



Institute for Marine and Antarctic Studies, University of Tasmania
 March 20, 2024, Hobart, Tasmania (AUS)

Presentation updates from WG157 members:

- **Katja Peijnenburg**
- **Ksenia Kosobokova / Dmitry Kulagin**
- **Agata Weydmann-Zwolicka**
- **Aino Hosia**
- **Tone Falkenhaus / Elizaveta Ershova**
- **Jenny Huggett**
- **Junya Hirai**
- **Leonie Suter**
- **Mary Mar N. Payne**
- **Pennie Lindeque**
- **Silke Laakmann**
- **Todd O'Brien**
- **Ann Bucklin**



SCOR WG157

MetaZooGene

SCOR WG157 Annual Meeting Agenda



- 5:30 pm** **Doors open @ IMAS**
- 6:00 pm** **Dinner buffet available**
- 7:00 pm** **Introductions & MetaZooGene Overview**
- 7:20 pm** **Presentation updates from WG157 members**
- 8:30 pm** **Looking ahead: WG157 activities & goals for 2024**
- 9:00 pm** **Adjourn**

