What´s The Catch?

Identification of juvenile and damaged hydrozoans using DNA barcoding

Authors
KIRSTI THELIN, JOAN J. SOTO-ANGEL, LUIS MARTELL

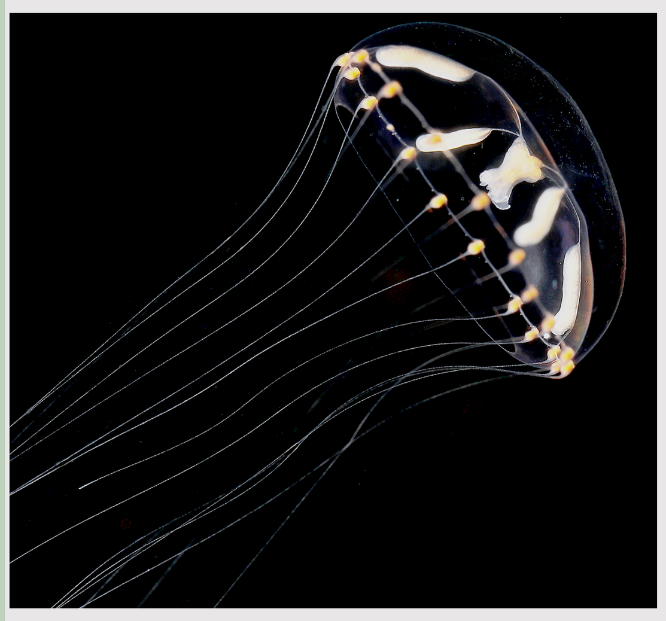
Photos
JOAN J. SOTO-ANGEL, KIRSTI THELIN

Affiliations
Institution for Biology, UiB, University Museum, Department of Natural History

Challenging Identification

Identifying marine organisms, particularly hydromedusae and hydroids within the Hydrozoa class, presents significant challenges due to their delicate nature and the propensity for damage during collection.

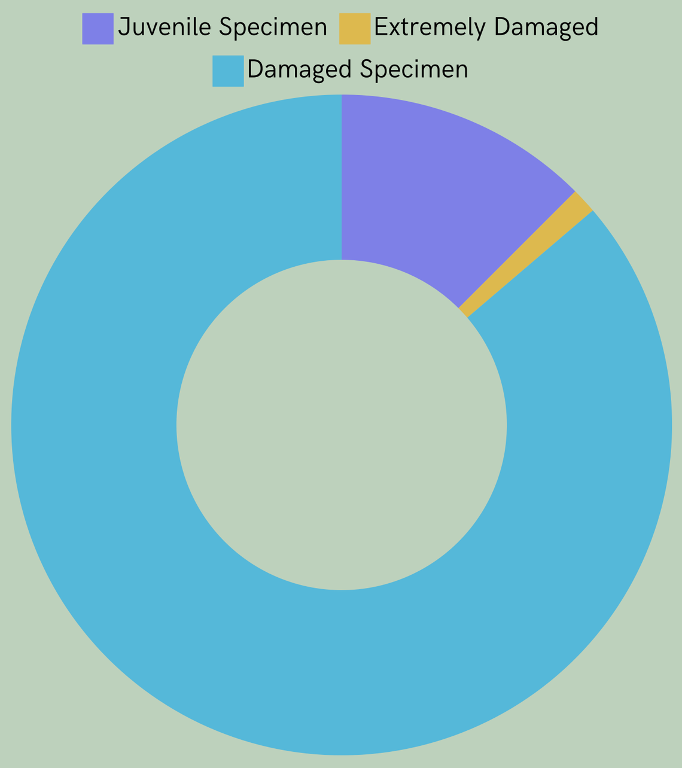
Traditionally, species identification relies on morphological characteristics, which can be distorted or lost due to the physical fragility of these organisms and the preservation methods typically employed. With DNA barcoding there is therefore no need to rely on morphology.



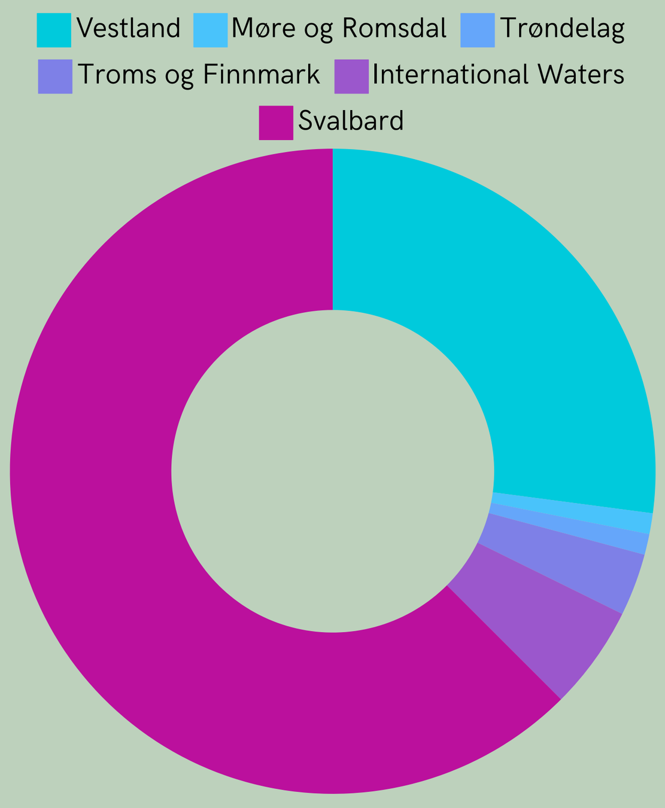
Alive, undamage adult jellyfish of Clytia gracilis.

Damage specimen of Clytia sp, unidentifiable through morphology.

State of Specimens



Provenance of the samples



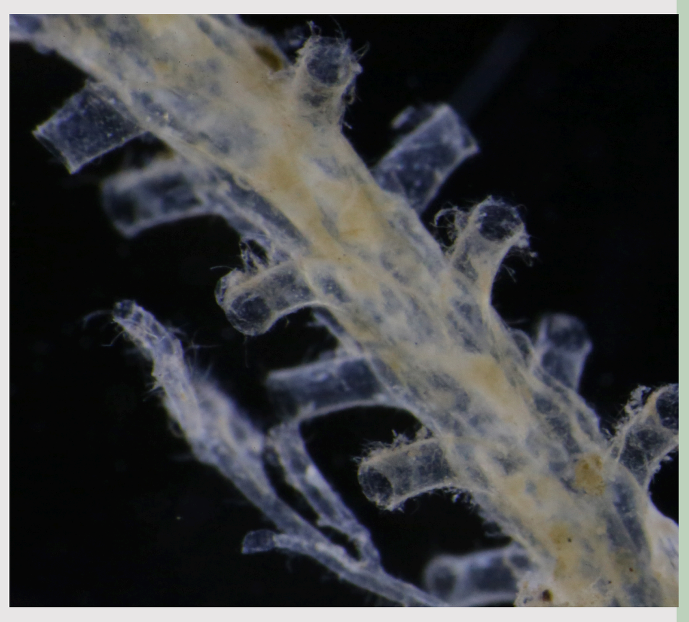
Objective

To accurately identify damaged and juvenile hydromedusae and hydroids in Norwegian waters using DNA barcoding with 2 mitochondrial markers (COI and 16S)

Target taxa

To test the efficiency of DNA barcoding in a wide range of hydrozoan taxa and life stages, both pelagic hydromedusae (34 specimens) and benthic polyps (62 specimens) belonging to different potential species were included in this study.

Grammaria abietina, live polyps and undamaged.



Damaged Grammaria abietina, dead polyps.

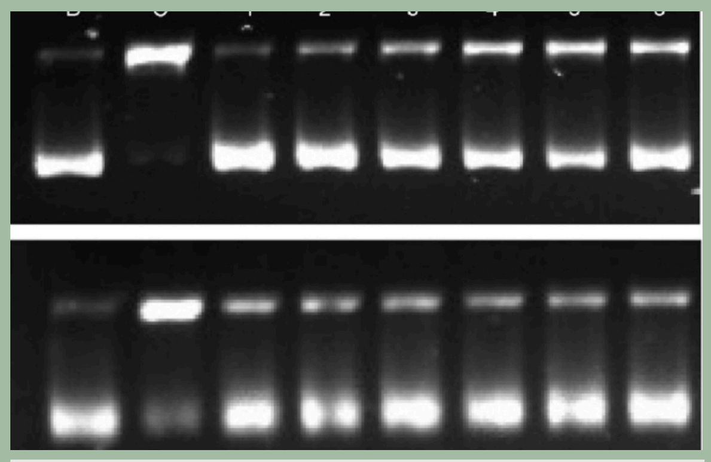
Methodology

1. Sampling, sorting and fixation

Museum samples:
Samples collected from previous trips from various locations and year. Pre-fixated in ethanol.

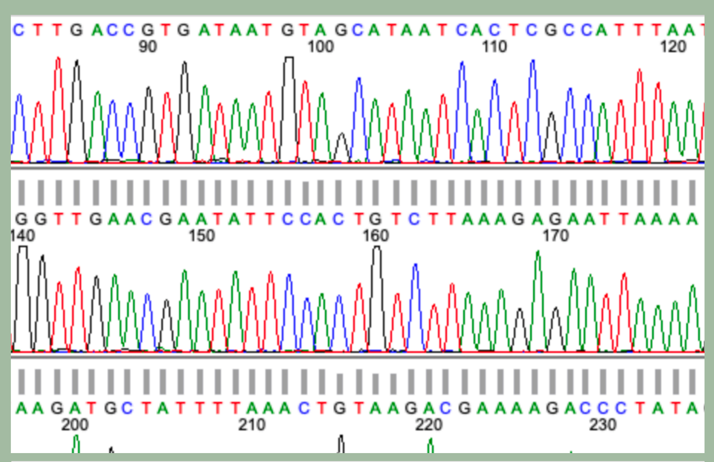
Freshly Collected Specimens:
We gathered new samples using a plankton net from stations in Korsfjorden and Fanafjorden, Norway.

2. DNA extraction and amplification



QuickExtract method.
Protocol for DNA extraction for samples.
PCR Amplification:
Utilizing two mitochondrial markers, COI and 16S were used.
Gel Electrophoresis:
To verify the success of the PCR amplification, and quality assessment

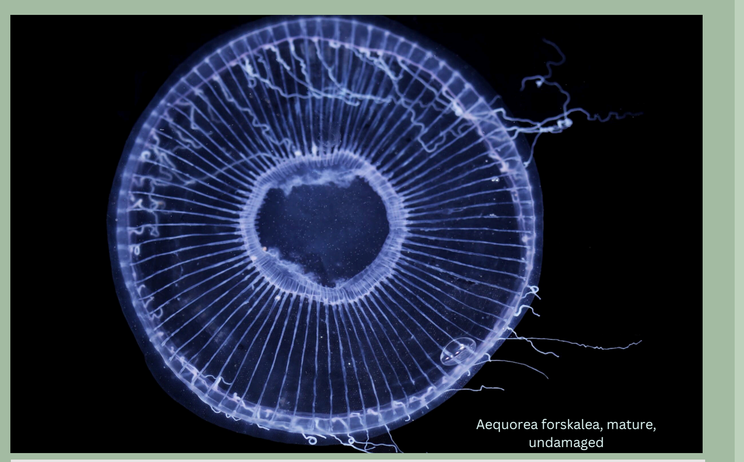
3. Sanger sequencing and Sequence edition



Sanger Sequencing:
EXOSAP was used to purify. Samples were sequenced at AZENTA in Germany for genetic data.

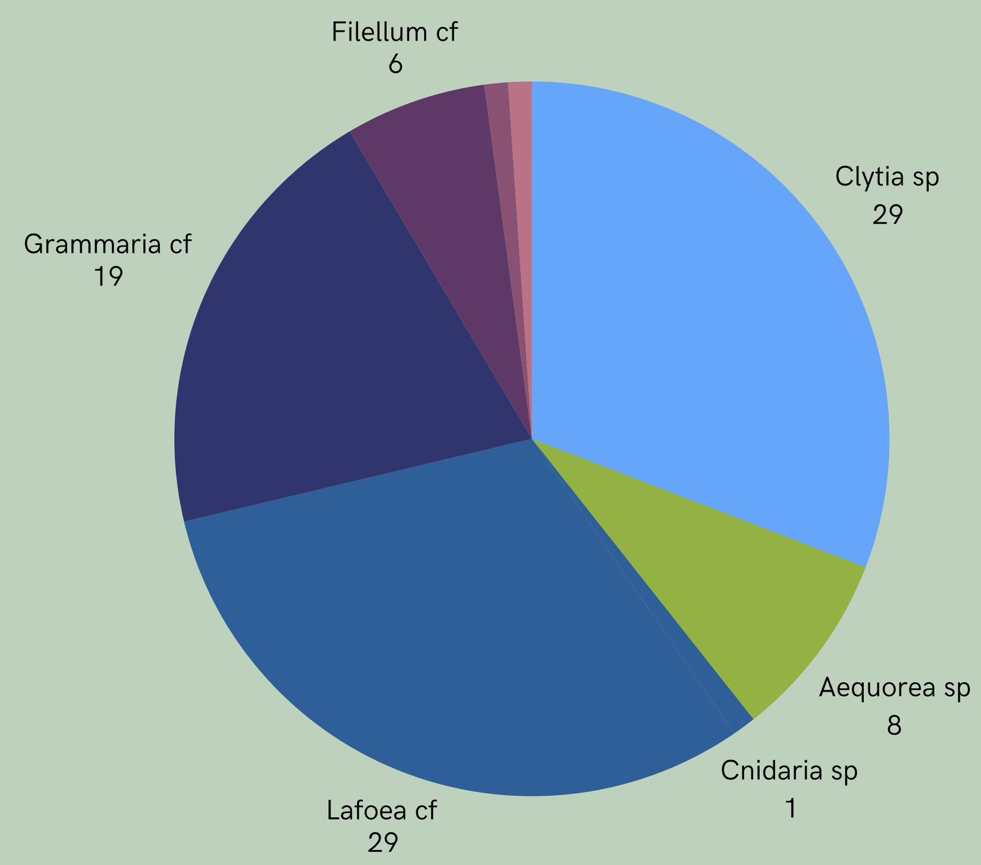
Contig Assembly:
Contigs were quality checked before assemblies built using Geneious software to visualize genetic markers.

4. Molecular identification



Sequence Comparison:
BLAST was used to search against NCBI's online databases and local reference databases from the Bergen University Museum to compare our sequences.
Taxonomic Assignment:
Based on sequence similarities, we assigned taxonomic classifications to our specimens.

Diversity array of taxa



Out of 96 specimens

78 samples Yielded molecular information for at least 1 genetic marker

10 high-quality Sequences of COI were obtained

48 high-quality sequences of 16S were obtained

A total of 2 taxa were identified, and the molecular information generated for each of them contributes to the improvement of the DNA reference databases for Hydrozoa in the region.

Conclusion

DNA barcoding with COI and 16S markers effectively identified damaged and juvenile hydromedusae and hydroids in Norwegian waters, enhancing traditional identification methods.

Contribution to research

This study confirms the utility of DNA barcoding for the successful identification of damaged and juvenile hydromedusae and hydroids in Norwegian waters.

The DNA sequences generated will significantly improve the regional reference databases for genera Clytia, Aequorea, Lafoea, Grammaria, and Filellum, allowing future researchers to implement monitoring methods based on either COI or 16S sequences.

What does It Mean?

While the success of DNA barcoding as an aid for identification of damaged and juvenile hydrozoans was confirmed, there were some specimens for which this method did not yield good results.

Age of samples:
Samples are from 2003-2023, specimens collected before 2007 had a lower success rate than fresher samples.

Primer specificity:
The primers used for sequencing were general primers that may not work well with specific taxa, such as Capitata sp.

References

1. Peter Schuchert, Aino Hosia, Lucas Leclère "Identification of the polyp stage of three leptomedusa species using DNA barcoding," Revue suisse de Zoologie, 124(1), 167-182, (1 January 2020)
2. Gong, S., Ding, Y., Wang, Y., Jiang, G., & Zhu, C. (2018). Advances in DNA Barcoding of Toxic Marine Organisms. International journal of molecular sciences, 19(10), 2931. https://doi.org/10.3390/ijms19102931

Special Thanks
I would like to add a special thanks to my advisors along with the Cnidaria+Ctenophora Research Group from the University Museum, the users at the Marine Biodiversity Lab at Uib, and Louise Lindblom. It is thanks to all of your help that made this project and poster possible!

Bio299_8_Forskingsrapport

SCAN ME