IECD 2022

The 2nd International Electronic Conference on Diversity

ANIMALS, PLANTS AND MICROBES

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diversity MDPI

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Abstract: DNA metabarcoding is becoming an important tool for surveying biodiversity thanks to its broad taxonomic coverage and the possibility of increased sample processing speed. Especially the complex world of zooplankton paired with the spatial and temporal variability of the study area, the Venice Lagoon, require high identification and sampling effort, which would particularly benefit from the rapidness and cost-effectiveness of DNA metabarcoding.

First, the reliability of DNA metabarcoding, based on a COI marker (Leray et al. 2013), was evaluated by comparing it to the classical morphological analysis. On one side, the molecular analysis resulted in higher taxa richness (224 vs. 88 taxa), discriminating better especially the meroplanktonic component, underlining the capability of metabarcoding to detect the 'hidden diversity' of zooplankton assemblages. On the other side, both methods revealed similar spatio-temporal patterns, and the sequence abundances were significantly correlated with individual counts for various taxonomic groups.

Following this preliminary validation, it was then applied at a higher spatial and temporal frequency, to exploit the advantages of this fast and reliable method in increasing the monitoring effort.

Finally, as first study, DNA metabarcoding was applied to investigate on the diet of the highly invasive zooplanktivorous ctenophore *Mnemiopsis leidyi*, with the benefit of identifying also (partially) digested prey. The comparison of the gut content with the *in-situ* mesozooplankton community indicated that *Mnemiopsis* feeds on a variety of prey, mostly coinciding with the *in-situ* zooplankton assemblage. However, some groups, like decapod larvae and the slow-swimming larvae of gastropods and bivalves seem to be favored.

Keywords: zooplankton; metabarcoding; COI

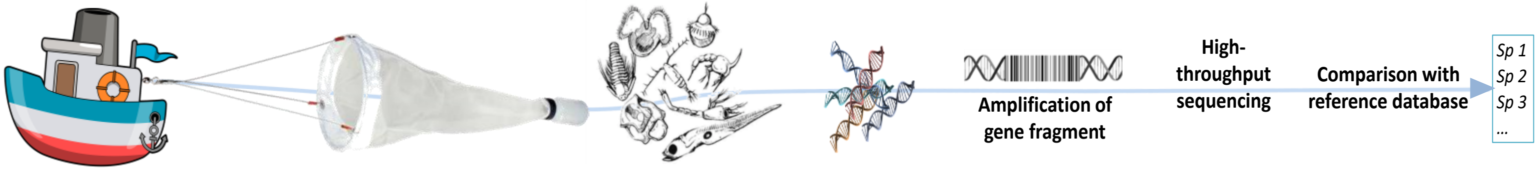
Introduction

As morphological assessments of zooplankton assemblages are labour intensive, there is an increasing **need of faster, more cost-effective and more objective methods** to characterize the spatio-temporal variability

LTER Marine Strategy Framework Directive (MSFD)

DNA metabarcoding is becoming a promising **tool for surveying marine biodiversity** thanks to the advantage of increased sample processing speed and the broad taxonomic coverage

DNA metabarcoding
Molecular method for species identification in a complex sample, based on sequencing a short standardized DNA fragment (barcode) that is unique to each species and can therefore be used for species discrimination.



Amplification of gene fragment

High-throughput sequencing

Comparison with reference database

Sp 1
Sp 2
Sp 3
…

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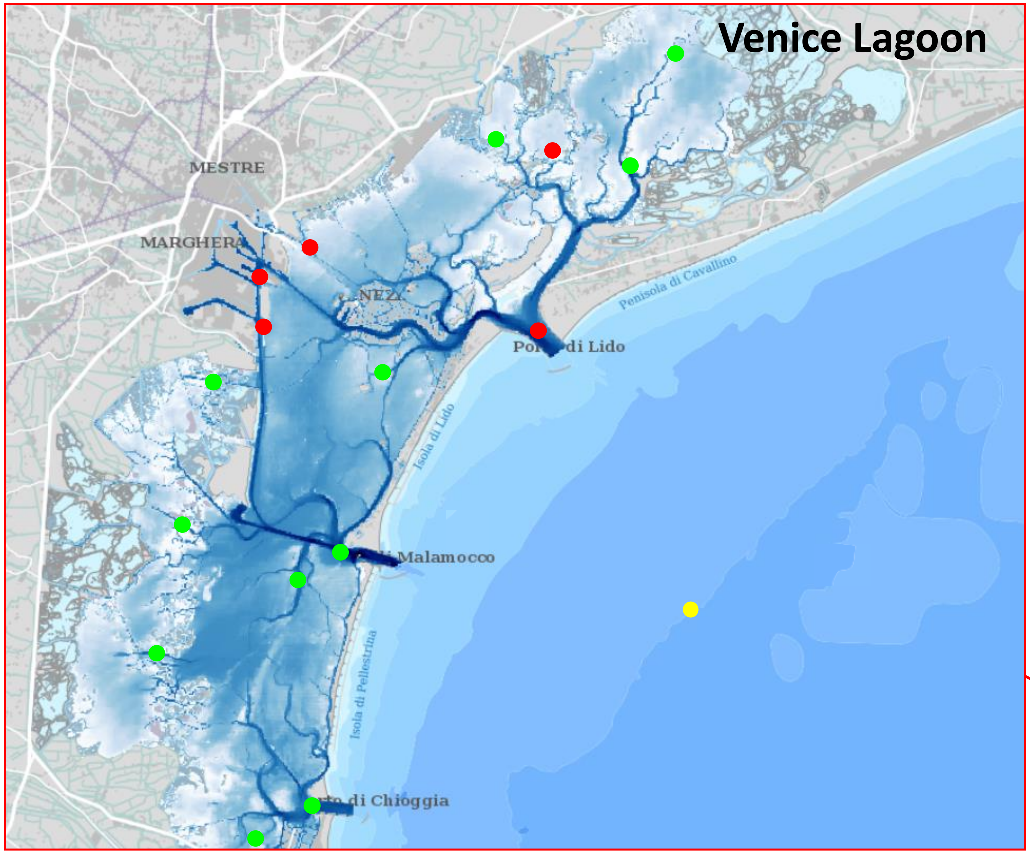
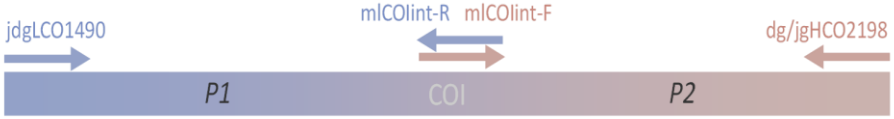
Introduction



- **Study A. Metabarcoding vs. morphological identification**:
  - 6 stations (red and yellow) seasonal sampling (2016-17) →24 samples
- **Study B. Application on higher frequency sampling:**
  - 16 stations (red and green), monthly sampling (2018-19) → 192 samples
- **Study C. Diet analysis of *Mnemiopsis leidyi:***
  - 16 stations (red and green), monthly sampling (2018-19) → 44 samples



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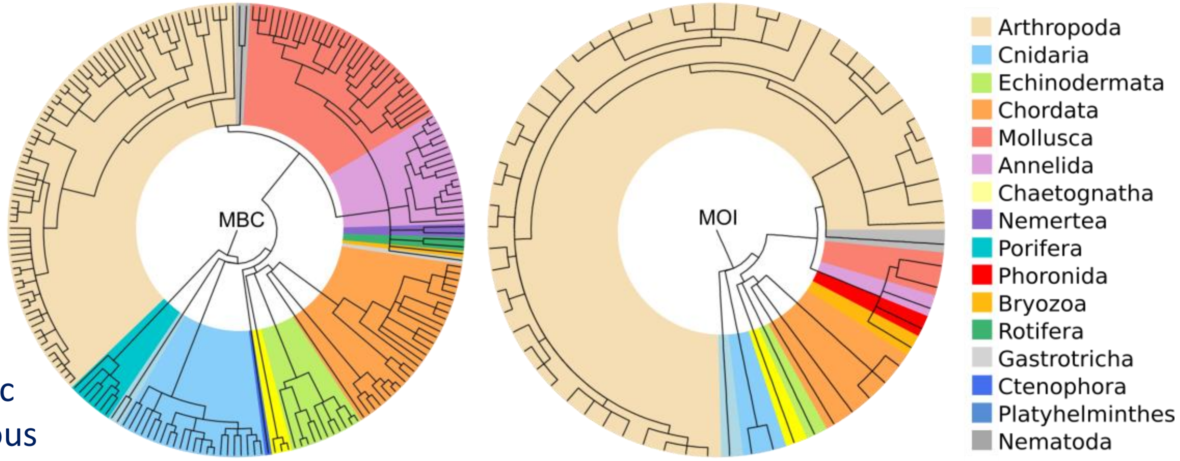
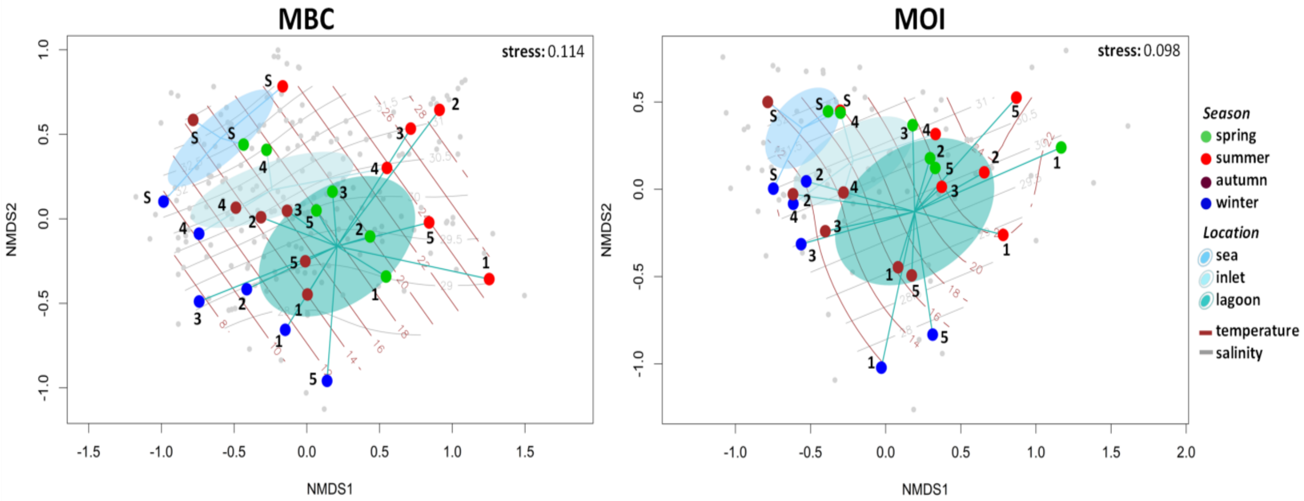
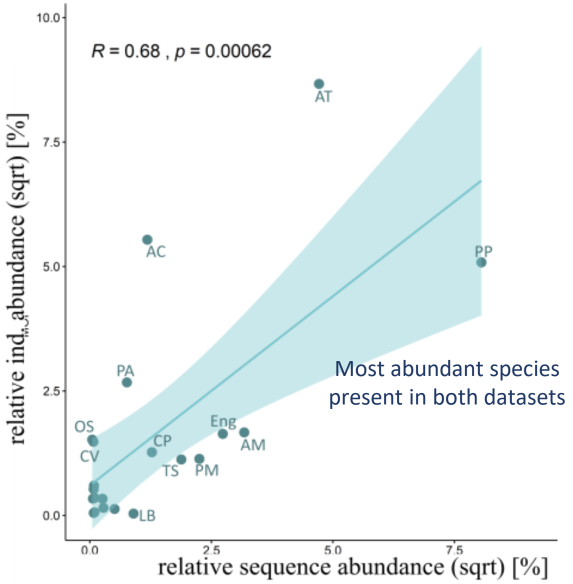
STUDY A

Results

- Higher estimation of taxonomic richness with MBC compared to MOI
- Numbers of sequences and abundance counts based on morphological taxonomic identifications show correlations for various taxonomic groups.
- similar spatio-temporal patterns







Most abundant species present in both datasets

Conclusions

- DNA metabarcoding is a promising and valuable tool for biodiversity assessment
- Cons: no information about population structure + dependency on reliable reference databases

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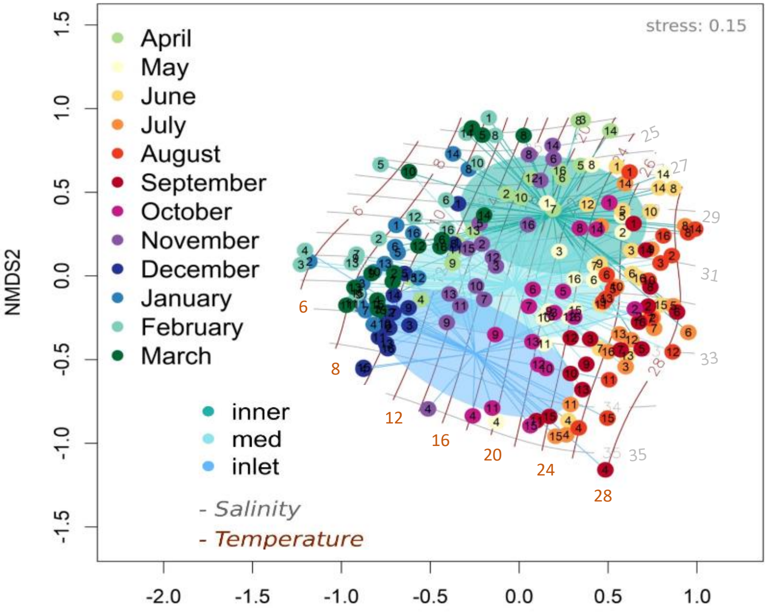
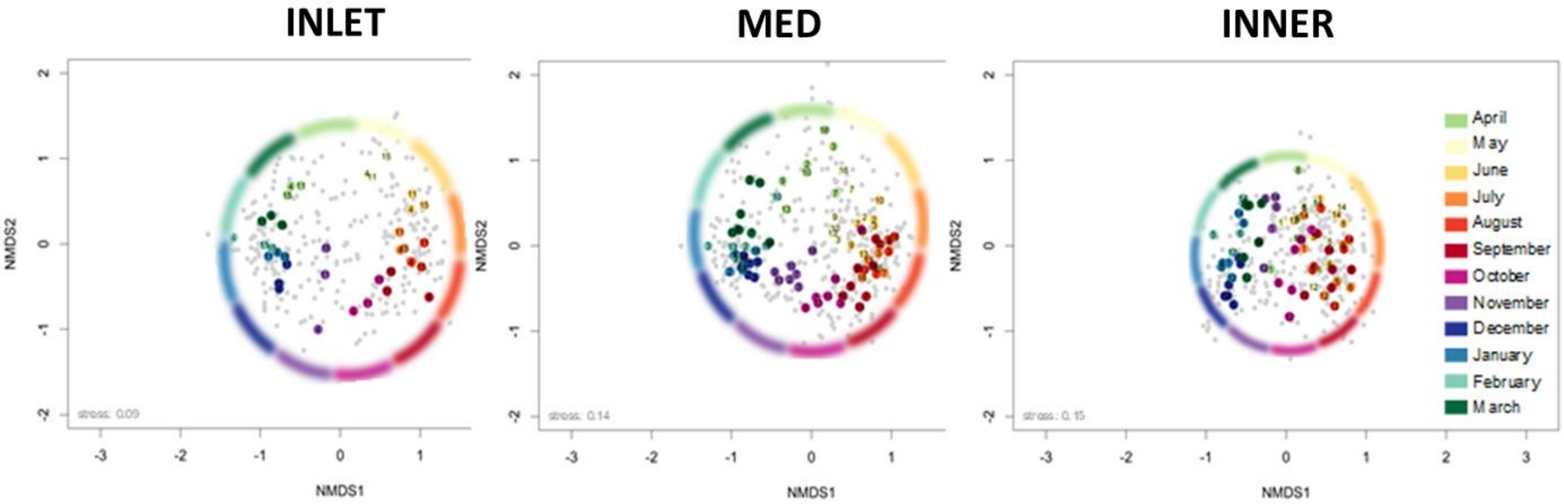
Schroeder et al. 2020

STUDY B

Results

- ➢ the sample communities are moderately separated by locations (following the salinity gradient), as well as by season (following a temperature gradient)
- ➢ the differences between months were less evident, as partially masked by the spatial variability.
- ➢ NMDS plots divided by location (inlet, medium, and inner stations) were computed to better visualize the temporal variability, which in fact showed an almost perfect circular succession of the months regarding the community composition





Future analyses

- ➢ environmental driving factors on the zooplankton community
- ➢ species life cycles (spawning times etc.), modelling larval dispersion

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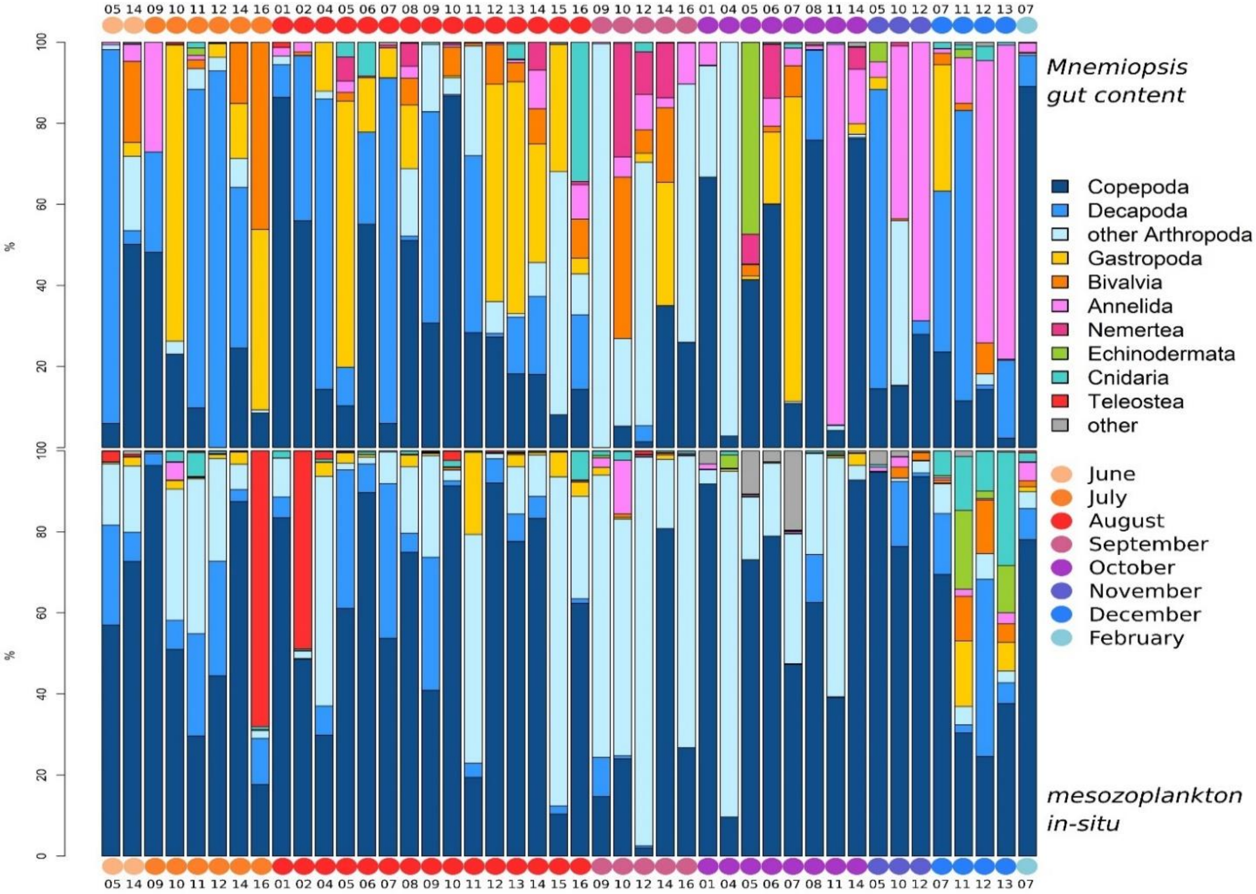
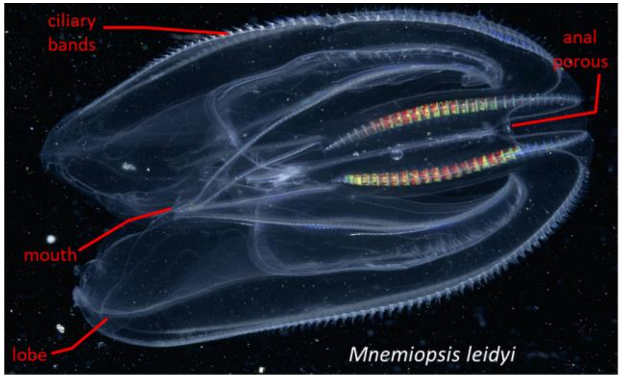
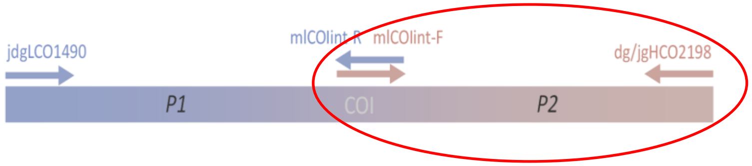
Results

STUDY C







Schroeder et al. 2021; Schroeder et al. (under revision)

Conclusions

- first study applying DNA metabarcoding on the diet assessment of *M. leidyi*
- *Mnemiopsis* is a generalist, but especially meroplanktonic taxa, such as bivalves, gastropods and decapods seem to be preferentially fed
- fish larvae or eggs were not abundant, neither in the gut contents nor *in-situ* (non-planktonic eggs? Different spawning times?)
- Possible impact on species of commercial interest in the Venice Lagoon, such as the clam *Ruditapes.*

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Links:

Schroeder, A., Stanković, D., Pallavicini, A., Gionechetti, F., Pansera, M., & Camatti, E. (2020). DNA metabarcoding and morphological analysis- Assessment of zooplankton biodiversity in transitional waters. *Marine Environmental Research*, *160*, 104946. https://www.sciencedirect.com/science/article/abs/pii/S0141113619308852?via%3Dihub

Schroeder, A., Pallavicini, A., Edomi, P., Pansera, M., & Camatti, E. (2021). Suitability of a dual COI marker for marine zooplankton DNA metabarcoding. *Marine Environmental Research*, *170*, 105444. https://www.sciencedirect.com/science/article/abs/pii/S0141113621002002?via%3Dihub

Schroeder, A., Camatti, E., Pansera, M., & Pallavicini, A. Applying DNA metabarcoding for the diet investigation of the invasive ctenophore *Mnemiopsis leidyi* in a transitional environment. Under review