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Abstract

Applications of DNA Metabarcoding on Marine Zooplankton †

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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 LTER site Venice Lagoon, require high identification and sampling effort, which would particularly benefit from the rapidness and cost-effectiveness of DNA metabarcoding. In this study, first, the reliability of DNA metabarcoding, based on a COI marker proposed by 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. Moreover, DNA metabarcoding was able to detect numerous non-indigenous species (NIS), highlighting its power as an early-detection system. 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, testing the advantages of this fast and reliable method in increasing the monitoring effort. This large dataset revealed the presence of monthly patterns in the zooplankton community, confirming the importance of high temporal frequency assessments to detect community changes over the year and enabling a more precise description of the zooplankton biodiversity in the Venice Lagoon. Finally, DNA metabarcoding was applied to investigate on the diet of the highly invasive zooplanktivorous ctenophore *Mnemiopsis leidyi.* Up until now, to study the diet of *M. leidyi*, the gut content was mainly analysed by morphological identification, while this is the first study investigating the feeding preference of this species utilizing DNA metabarcoding, 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

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