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Comparison of Metabarcoding and Microscopy for Estuarine Plankton Monitoring: Quantitative Character and Non-Indigenous Species Detectability.

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During the last decades, plankton has been used as an indicator of ecosystem change because of its rapid response to variation. Monitoring programs has usually relied on microscopy, which is time-consuming and requires wide expertise. The advent of metabarcoding, where a short DNA region is sequenced for the whole community sample, provided an alternative to overcome those issues. This approach generates large amounts of information about biodiversity and allows the identification of species at any life stage in complex ecosystem assemblages. Although the sensitivity of metabarcoding has already been described, its applicability for monitoring biological invasions has only been suggested: in the present work we demonstrated the suitability of metabarcoding for early detection of Non-Indigenous Species (NIS) at extremely low abundances. We also found significant correlations when comparing metabarcoding and microscopy-based relative abundances, suggesting at least a semi-quantitative nature for this approach. Furthermore, we discovered that metabarcoding is capable of replicating the temporal and spatial patterns of an estuary's plankton community better for zooplankton than for phytoplankton. This reduced performance for the lowest size fractions is mainly related with database incompleteness, highlighting that DNA-barcoding is necessary and complementary to metabarcoding. Overall, we believe that the extreme sensitivity and relatively low time/cost of metabarcoding turns this technique into a promising alternative for the early detection of NIS or plankton biodiversity shifts.

Keywords: Metabarcoding, 18SrDNA, Microscopy, Biodiversity, Plankton, Non-Indigenous Species, Estuaries.

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