

## Metabarcoding of marine zooplankton communities in the North Sea using nanopore sequencing

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Zooplankton are crucial organisms both in terms of biodiversity and their unique position in aquatic food webs. As such, it is crucial that we improve our insights into how anthropogenic and natural factors may affect these pelagic organisms. Although easily collected in large numbers, the subsequent processing and identification of specimens has usually been a barrier to large-scale biodiversity assessments. DNA barcoding, the use of standardized short gene regions to discriminate species, has been increasingly used by non-taxonomists to identify species. Here, we measured the diversity and community composition of zooplankton in the Belgian part of the North Sea over the course of one year. We identified zooplankton using both a traditional approach, based on morphological characteristics, and by metabarcoding of a 650 bp fragment of the 18S rRNA gene using the MinION™, a portable nanopore-based DNA sequencing platform. We established a method for characterizing zooplankton communities in marine samples using nanopore sequencing. We were able to identify several taxa at the species level, across a broad taxonomic scale and we thus could obtain several diversity metrics, allowing comparisons of diversity and community composition.

Keywords: Nanopore sequencing; Minlon; Metabarcoding; Biomonitoring; Zooplankton; Copepods; *Temora longicornis*