

## Metatranscriptome of a marine pelagic crustacean community using nanopore sequencing

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Due to their rapid responses to environmental variation, planktonic organisms are used as bio-indicators of ecosystem changes. With the need for better understanding the impact of a changing environment on zooplankton communities, zooplankton monitoring programs have been carried out in the marine environment globally since the early 20th century. Most zooplankton monitoring studies focus mainly on variability in biodiversity and biomass. However, this approach is hindered by challenges in the identification, which is time-consuming, complicated and requires biological expertise. Advances in practical, cost-effective molecular approaches, such as (meta)barcoding, helped overcome the issues with morphology-based biomonitoring. Yet, a more comprehensive molecular data set would be able to identify and assess the impact of the main drivers of changes in the marine ecosystem, rather than only determining species richness. Studying the functional activities of a community has been facilitated by metatranscriptomics, the study of community gene transcription. Metatranscriptomics is generally employed to assess both the functional and the taxonomic components of a community. Here, we sequenced the metatranscriptome of a pelagic crustacean community in the BPNS, using the MinION™, a portable nanopore-based DNA/RNA sequencing platform (Oxford Nanopore Technologies). We establish a method for capturing the metatranscriptome of zooplankton communities in marine samples.

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