

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. Most zooplankton monitoring studies focus mainly on variability in biodiversity, densities and biomass. Advances in practical, cost-effective molecular approaches can help overcome the issues with morphology-based biomonitoring. While molecular studies are growing in popularity, a fundamental challenge remains the transport of biological material to a laboratory for DNA/RNA extractions and sequencing. The MinION™, a portable nanopore-based DNA/RNA sequencing platform (Oxford Nanopore Technologies), offers big potential advantages in the context of biodiversity research, i.e. portability and low costs of instrument and reagents. It weighs less than 100 g, is therefore easily transportable and is powered to sequence RNA using the USB port on a standard laptop, hence making it suitable for mobile research setups and real time monitoring campaigns onsite. In a first step, we wanted to understand how the gene expression in zooplankton fluctuates over the course of a short time period. Therefore, we monitored the gene expression of the dominant zooplankter, the calanoid copepod *Temora longicornis*, over a short time span (one day), making use of the infrastructure of the research vessel Simon Stevin. We compared gene expression results with in situ determined biotic and abiotic patterns. Moreover, due to the recent development of the VolTRAX, a small device designed to perform library preparation automatically, for the first time we were able to prepare a biological sample for analysis in situ and hands-free, making in-field, molecular monitoring of marine life possible.

Keywords: Zooplankton; Gene expression; Copepod; Nanopore sequencing; Minlon; Monitoring