

Spatio-temporal dynamics in the gene expression of the copepod *Temora longicornis* in response to environmental stressors

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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. Since responses to environmental stress are initially genome-driven, a genetic understanding on the physiological responses to stress can help predict potential responses to a changing environment in the future. In this project, we focus on the potential effects of various environmental stressors (changes in temperature, salinity and concentration of PCBs and PAHs as a proxy for chemical pollution) on the gene expression of the calanoid copepod species, *Temora longicornis*, the dominant zooplankton species of the southern part of the North Sea. Therefore, this study investigated transcriptome-level profiles of adult *T. longicornis* that were collected at four stations in the Belgian part of the North Sea (BPNS) at different time points in a four year sampling campaign. Zooplankton samples were collected with the research vessel (RV) Simon Stevin on 35 (bi)monthly sampling campaigns in 2018 till 2021. From the obtained data, we aimed to identify the most active metabolic pathways and we tried to place these results into a broader context of physiological activities. Next, we constructed gene-co-expression networks, identified hub genes and we tried to obtain a mathematical relationship between these networks/hub genes and (1) the measured environmental variables and (2) phenotypic characteristics of interest (i.e. densities and biomass), defined by a generalized additive model. As such, we aim to identify molecular endpoints that can be consistently anchored to phenotypic changes under multi-stress conditions and at the same account for potential biological variability.

Keywords: Zooplankton; Copepods; Monitoring; Environmental stressors; Transcriptomics; NGS