

Effects of temperature on the transcriptome of the marine copepod *Temora longicornis*

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Over the past decades, the world's oceans and seas have been influenced by several human-induced impacts, including climate change. In the North Sea region, the average sea surface temperature of the water has already risen with 1-2 °C over the past twenty-five years and is likely to rise further. Understanding the impacts of this changing environmental condition in zooplankton communities is crucial, as changes in the zooplankton communities can affect entire marine ecosystems. Here, we focus on the potential effects of an increase in temperature on the calanoid copepod species, *Temora longicornis*, the dominant zooplankton species of the southern part of the North Sea. Since responses to environmental stress are genome-driven, a genetic study on the physiological responses to thermal stress can provide an increased mechanistic understanding and help predict potential responses to climate change in this copepod species. Therefore, we sequenced the whole transcriptome (using RNA-seq technology) of *T. longicornis*, after being exposed to thermal stress, with the aim to investigate gene expression differences as a response to temperature fluctuations. As such, this dataset will provide us with new insights on how exposure to increased seawater temperatures may affect the fitness of the most dominant zooplankton species of the southern part of the North Sea.

Keywords: transcriptomics; global change; zooplankton; copepods; temperature; North Sea