

A transcriptomic approach to unravel fatty acid pathways of harpacticoid copepods in a changing environment

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Global climate change is threatening coastal marine ecosystems by causing changes in oceanographic conditions such as temperature and pH. These shifts affect the physiological performance and productivity of organisms in marine food webs and thus the overall functioning of the ecosystem. A better understanding of the physiological response and adaptive capacity of coastal marine organisms is critical to assess their fate in a rapidly changing ocean.

Harpacticoid copepods are a dominant component of estuarine benthic meiofauna, efficient grazers on diatoms, and a major food source for juvenile fish. They are known to contain high levels of polyunsaturated fatty acids (PUFAs), which are essential dietary constituents for fish and humans as they can't produce these fatty acids themselves. Harpacticoid copepods on the other hand are able to bioconvert PUFAs that originate from primary producers, a process known as 'trophic upgrading'. This capacity for PUFA bioconversion might be an essential strategy for harpacticoid copepods to respond quickly to environmental changes. However, the underlying molecular mechanism and its activation are still unknown for these organisms. Therefore, we aim to uncover the genetic pathways of PUFA bioconversion and to which extent warming and acidification will affect this process.

Within our project, we are generating transcriptomic data from the estuarine harpacticoid copepod *Platychelipus littoralis* subjected to different diet, temperature and pH treatments. RNA sequencing and novel bioinformatic tools are used for *de novo* transcriptome assembly, and subsequent annotation and differential expression analysis of PUFA metabolism-related genes.

Keywords: transcriptomics; global change; harpacticoid copepods; fatty acid metabolism