

Unraveling fatty acid bioconversion in harpacticoid copepods facing a changing environment

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As climate change is a global challenge that affects everyone, everywhere, reducing its impacts is a key action point of the UN Sustainable Development Goals (SDG 13: *take urgent action to combat climate change and its impacts*). Shifts in oceanographic conditions such as temperature and pCO₂ are affecting the physiological performance and productivity of organisms in coastal food webs and thereby threatening the overall functioning of the coastal ecosystem. A better understanding of the physiological response and adaptive capacity of coastal marine organisms is critical to assess their fate and to conserve coastal ecosystems in a rapidly changing ocean (SDG 14: *conserve and sustainably use the oceans, seas and marine resources*).

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 the latter can't produce these omega-3 and omega-6 fatty acids themselves. Harpacticoid copepods on the other hand are able to bioconvert PUFAs that originate from primary producers. This capacity might be an essential strategy for harpacticoid copepods to respond quickly to environmental changes, since climate change reduces the amount of PUFAs within primary producers, and thus, their availability for higher trophic levels.

Our research aims to uncover the genetic pathways of PUFA bioconversion in harpacticoid copepods and how these mechanisms respond following a combination of a reduced PUFA diet and realistic future warming. Our species of interest is *Platychelipus littoralis*, a harpacticoid copepod occurring abundantly in the Westerscheldt estuary. We generated RNA-Seq data and fatty acid profiles from *P. littoralis* subjected to different diet and temperature treatments. Even when fed a PUFA-deficient diet (i.e. the chlorophyte *Dunaliella tertiolecta*), *P. littoralis* always maintains sufficient PUFA levels compared with a control treatment. By means of a *de novo* transcriptome assembly and subsequent annotation and differential gene expression analysis, we are able to link the fatty acid profiles to potential PUFA bioconversion-related genes.

Keywords: Transcriptomics; Global change; Harpacticoid copepods; Fatty acid metabolism