

A characterization of the fatty acid metabolism genes of the harpacticoid copepod *Platychelipus littoralis*

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By 2100; global warming is predicted to significantly reduce the production of long-chain polyunsaturated fatty acids (LC-PUFA) by marine algae. These omega-3 and omega-6 fatty acids are considered essential dietary constituents for higher trophic levels. Harpacticoid copepods (Crustacea); primary consumers of those algae; might mitigate the adverse effects on the food web by an increased bioconversion of LC-PUFAs. In contrast to fish or humans; these crustaceans have the ability to efficiently synthesize and upgrade LC-PUFAs themselves; using a complex series of fatty acid desaturase and elongase enzymes. Several aspects on the origin; function and diversity of the genes involved in LC-PUFA biosynthesis by copepods remain insufficiently understood.

We generated a high quality *de novo* transcriptome of the harpacticoid copepod *Platychelipus littoralis*; exposed to changes in both dietary LC-PUFA availability and temperature (+3°C). Using this transcriptome; we detected multiple genes putatively encoding for LC-PUFA-bioconverting front-end fatty acid desaturases and elongases; and performed phylogenetic analyses to identify their relationship with sequences of other crustacean and non-crustacean taxa. None of the putative desaturase or elongase transcripts were found differentially expressed under the applied treatments. Therefore; we investigated whether these genes are differentially expressed under a combination of multiple climate drivers (dietary LC-PUFA availability; ocean warming and ocean acidification) using gene-specific quantitative PCR. Overall; we were able to increase our understanding about the molecular pathways of LC-PUFA biosynthesis in harpacticoid copepods and how they might respond in future environments.

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