



Targeted-metabolomics of phytoplankton blooms
in the Gulf of Naples and effects of algal oxylipins
on the reproduction and gene expression of the
copepod *Temora stylifera*

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Abstract

Diatoms, dominant phytoplankton in the world's ocean, synthesize a large number of oxylipins, fatty-acid-derived bioactive metabolites that impair cell proliferation. Oxylipins were originally proposed as defensive molecules hindering the reproductive success of grazer copepods through a maternal effect. In the present thesis, a targeted-metabolomics approach was applied to quantify six non-volatile oxylipins and the fatty acids from surface phytoplankton collected in the Gulf of Naples (Italy) along the year 2017. Potential effects of biotic and abiotic factors on the population dynamics of *Temora stylifera* (a dominating copepod species in the sampling area) were analysed in terms of reproductive potential and molecular responses of wild copepods captured in the sampling year. A *de novo* transcriptomic approach allowed comparing the transcriptional profiling of adult females at high and low naupliar survival rates. Expression of 13 sequences selected after the RNA-Seq analysis was quantified through RT-qPCR in wild copepod females along 2017. In the laboratory, physiological and molecular responses of *T. stylifera* females were analysed after feeding on four diatom mono-algal diets isolated from the Gulf of Naples and characterized in terms of oxylipin synthesis potential and nutritional value. Overall, the results shed more light on plankton ecology and in particular on diatom-copepod interactions. A potential role of oxylipins as signalling molecules in natural diatom communities is proposed and discussed, opening new scenarios in diatom chemical ecology studies. No clear effects of NVOs on the reproductive potential and the molecular responses of wild *T. stylifera* females were detected. A delayed negative effect of *Chaetoceros* (one of the most abundant diatom genera in the Gulf of Naples) on naupliar survival rates was observed, partially explaining the maximum population density of *T. stylifera* occurring in autumn. Transcriptional profiling suggested a gene regulation possibly aimed at maximizing the reproductive success of the copepod. The genes *ATP-Dependent RNA Helicase (me31b)*, *Very Low-Density Lipoprotein Receptor (VLDLR)* and *cAMP-Responsive Element-Binding Protein (CREBL)* were significantly related to egg

production and could constitute sentinel sequences to estimate the reproductive potential of wild copepods in subsequent field surveys. Laboratory experiments suggested different physiological and molecular responses of *T. stylifera* females to the four diatoms, possibly indicating gene expression modulation in response to different chemical signatures of the diets.