



New inter-correlated genes targeted by diatom-derived polyunsaturated aldehydes in the sea urchin *Paracentrotus lividus*



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ABSTRACT

The marine environment is continually subjected to the action of stressors (including natural toxins), which represent a constant danger for benthic communities. In the present work using network analysis we identified ten genes on the basis of associated functions (*FOXA*, *FoxG*, *GFI-1*, *nodal*, *JNK*, *OneCut/Hnf6*, *TAK1*, *tcf4*, *TCF7*, *VEGF*) in the sea urchin *Paracentrotus lividus*, having key roles in different processes, such as embryonic development and asymmetry, cell fate specification, cell differentiation and morphogenesis, and skeletogenesis. These genes are correlated with three HUB genes, *Foxo*, *Jun* and *HIF1A*. Real Time qPCR revealed that during sea urchin embryonic development the expression levels of these genes were modulated by three diatom-derived polyunsaturated aldehydes (PUAs), decadienal, heptadienal and octadienal. Our findings show how changes in gene expression levels may be used as an early indicator of stressful conditions in the marine environment. The identification of key genes and the molecular pathways in which they are involved represents a fundamental tool in understanding how marine organisms try to afford protection against toxicants, to avoid deleterious consequences and irreversible damages. The genes identified in this work as targets for PUAs can be considered as possible biomarkers to detect exposure to different environmental pollutants.

1. Introduction

Marine organisms are continuously exposed to many environmental stimuli, some of which may induce stress. To afford protection from internal and environmental toxicants, organisms activate different stress response mechanisms, depending on the type of stress and its severity (Kültz et al., 2003; Milisav et al., 2012, 2015). Stress responses include induction of cell repair mechanisms, improved removal of damaged macromolecules by induced autophagy, and increased stress protection through upregulation of endogenous antioxidant defences (Filomeni et al., 2015). During embryogenesis a series of progressive morphological changes occur, which are encoded in the genome and are a direct consequence of differential gene expression controlled by dynamic networks of regulatory genes (Rafiq et al., 2014). Several studies have demonstrated that organisms respond to external stressors also by synchronized changes in the expression levels of multiple genes (Zhang and Andersen, 2007; de Nadal et al., 2011). In fact, at the

molecular level, stress responses require the up- and/or down-regulation of specific genes and the pathways in which they are involved (Richter et al., 2010; Runcie et al., 2012). Through the development of "omics" approaches it is now possible to study how environmental stress can influence gene-gene interactions and gene-environment interactions, thereby allowing for a greater understanding of how species may be able to adapt to environmental stress in the future (Masel et al., 2006; Loraine, 2009; Orlando et al., 2009; Sreenivasulu et al., 2010; Runcie et al., 2012).

Echinoderms represent an evolutionary link between invertebrates and vertebrates and play a key role in the maintenance of marine ecosystem integrity. Among the echinoderms, the sea urchin represents a useful model organism for different types of scientific studies, because it produces large numbers of synchronous and transparent embryos suitable for microscopic observations (Strathmann, 1987), and has a high fecundity (Sodergren et al., 2006). The sea urchin is a well-established marine model organisms in eco-toxicological studies,

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