



Key genes as stress indicators in the ubiquitous diatom *Skeletonema marinoi*

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RESEARCH ARTICLE

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Key genes as stress indicators in the ubiquitous diatom *Skeletonema marinoi*

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Abstract

Background: The dense phytoplankton blooms that characterize productive regions and seasons in the oceans are dominated, from high to low latitudes and from coast line to open ocean, by comparatively few, often cosmopolitan species of diatoms. These key dominant species may undergo dramatic changes due to global climate change.

Results: In order to identify molecular stress-indicators for the ubiquitous diatom species *Skeletonema marinoi*, we tested stress-related genes in different environmental conditions (i.e. nutrient starvation/depletion, CO₂-enrichment and combined effects of these stressors) using RT-qPCR. The data show that these stressors impact algal growth rate, inducing early aging and profound changes in expression levels of the genes of interest.

Conclusions: Most analyzed genes (e.g. antioxidant-related and aldehyde dehydrogenases) were strongly down-regulated which may indicate a strategy to avoid unnecessary over-investment in their respective proteins. By contrast, key genes were activated (e.g. HSPs, GOX) which may allow the diatom species to better cope with adverse conditions. We propose the use of this panel of genes as early bio-indicators of environmental stress factors in a changing ocean.

Keywords: Diatoms, Stress-related genes, Molecular indicators, Nutrient starvation, Ocean acidification

Background

Diatoms are eukaryotic unicellular plants that constitute one of the major components of marine phytoplankton [1] comprising up to 40% of annual productivity at sea [2] and representing up to 25% of global carbon-fixation [3]. Natural (e.g. cold/heat and nutrient limitation) and/or anthropogenic (e.g. ocean acidification and pollutants) factors may alter the physiology and survival of diatoms, thereby influencing current levels of ocean primary productivity [4,5]. Here we use Reverse Transcription-quantitative PCR (RT-qPCR) to identify key genes as indicators of defense processes activated in response to various stressful conditions in the ubiquitous diatom *Skeletonema marinoi*, a species which forms massive blooms in many of the world's coastal oceans [6-8]. Previous studies on *S. marinoi* have focused on its genetic structure [8], secondary metabolite production [9], physiological response to nutrient limitation [10] and interactions with zooplankton species [6,7,11,12]. This is the first

study focusing on stress-related genes as health-status indicators in this diatom species.

The stress conditions tested were senescence, silicic acid limitation/starvation, CO₂-enrichment and the combination of these conditions. Si-concentrations vary extensively in the world's oceans, depending on the regions and depths analyzed [13] and it is generally assumed that biogenic silicate content of some diatoms decreases under ocean acidification conditions [14]. Since diatoms incorporate inorganic silicon into the cell as silica [15] and use it to construct their outer cell wall, the availability and distribution of silicic acid can strongly modify diatom growth and population dynamics [16]. Hence we hypothesized that the combination of ocean acidification and variations in silicic acid availability would potentially negatively impact diatom growth and modify stress gene expression levels [14,16-18].

Current levels of atmospheric CO₂ are predicted to be more than double by 2100 (Intergovernmental Panel on Climate Change IPCC 2007). Studies have reported contrasting results on the effects of ocean acidification in different phytoplankton species. Some studies speculate

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