

ANALYSE OF TRANSCRIPTIONAL RESPONSE IN THE RED MACROALGA
GRACILARIA TENUISTIPITATA UNDER STRESSES BY HEAVY METALS,
COPPER AND CADMIUM

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Gracilaria tenuistipitata is a red algae economically important for production of the agar, utilized by pharmaceutical, nutritional and biotechnological industries. Moreover, due to its tolerance to salinity, temperature and pH, this specie is widely studied as a model for many biochemical analyses. One of the problems that affects the development of this algae is the contamination by chemical agents such as heavy metals that induce severe stress reactions in organisms. Previous studies showed variations in concentration of the enzymes important for metabolism. Such variations were caused by stress induced by metals. Using DNA microarray techniques for *Gracilaria tenuistipitata*, it is possible to analyse differential expression of several enzymes when the algae is submitted to 50% of a sublethal concentration of Cu²⁺ and Cd²⁺ metals. It was used in the microarray construction a sequenced cDNA library, representing normal culture conditions. This library has in total 3631 ESTs, 2387 unique sequences and 53,4% redundancy. Probables genes as superoxide dismutase, glutathione peroxidase, ascorbate peroxidase and others, localized in the cDNA libray, increase their concentration in response to stresses as a defense mechanism. Finally, it is possible to investigate large-scale genes expression in different environmental stresses.