

Transcriptomic analysis of *Gracilaria changii* (Rhodophyta) in response to hyper- and hypo-osmotic stresses

Abstract

Osmotic stress is one of the most significant natural abiotic stresses that occur in the intertidal zones. Seaweeds may physiologically acclimate to changing osmolarity by altering their transcriptome. Here, we investigated the transcriptomic changes of *Gracilaria changii* (B. M. Xia et I. A. Abbott) I. A. Abbott, J. Zhang et B. M. Xia in response to hyper- and hypoosmotic stresses using a cDNA microarray approach. Microarray analysis revealed that 199 and 200 genes from 3,300 genes examined were up-and down-regulated by >2-fold in seaweed samples treated at 50 parts per thousand (ppt) artificial sea-water (ASW) compared with those at 30 ppt ASW, respectively. The number of genes that were up-and down-regulated by >2-fold in seaweed samples treated at 10 ppt ASW compared with those at 30 ppt ASW were 154 and 187, respectively. A majority of these genes were only differentially expressed under hyper- or hypoosmotic conditions, whereas 67 transcripts were affected by both stresses. The findings of this study have shed light on the expression profiles of many transcripts during the acclimation of *G. changii* to hyperosmotic and hypoosmotic conditions. This information may assist in the prioritization of genes to be examined in future studies.

Keyword: cDNA microarray; *Gracilaria changii*; osmotic stresses; real-time PCR; seaweed