

Thermal stress responses in Antarctic yeast, *Glaciozyma antarctica* PI12, characterized by real-time quantitative PCR

Abstract

Living organisms have some common and unique strategies to respond to thermal stress. However, the amount of data on thermal stress response of certain organism is still lacking, especially psychrophilic yeast from the extreme habitat. Therefore, it is not known whether psychrophilic yeast shares the common responses of other organisms when exposed to thermal stresses. In this work, the cold shock and heat shock responses in Antarctic psychrophilic yeast *Glaciozyma antarctica* PI12 which had an optimal growth temperature of 12 °C were determined. The expression levels of 14 thermal stress-related genes were measured using real-time quantitative PCR (qPCR) when the yeast cells were exposed to cold shock (0 °C), mild cold shock (5 °C), and heat shock (22 °C) conditions. The expression profiles of the 14 genes at these three temperatures varied indicating that these genes had their specific roles to ensure the survival of the yeast. Under cold shock condition, the *afp4* and *fad* genes were over-expressed possibly as a way for the *G. antarctica* PI12 to avoid ice crystallization in the cell and to maintain the membrane fluidity. Under the heat shock condition, *hsp70* was significantly up-regulated possibly to ensure the proteins fold properly. Among the six oxidative stress-related genes, *MnSOD* and *prx* were up-regulated under cold shock and heat shock, respectively, possibly to reduce the negative effects caused by oxidative stress. Interestingly, it was found that the trehalase gene, *nth1* that plays a role in degrading excess trehalose, was down-regulated under the heat shock condition possibly as an alternative way to accumulate trehalose in the cells to protecting them from being damaged.