

Gene expression patterns of *Glaciozyma antarctica* PI12 in response to cold, and freeze stress

ABSTRACT

Psychrophilic yeast, *Glaciozyma antarctica* PI12 was isolated from the sea ice in the Southern Ocean. Several recent studies have revealed some of the strategies employed by *G. antarctica* PI12 to grow and survive at low temperatures, but those information are still limited. Hence this project was carried out to sequence the whole transcriptome to generate additional information on the cold-adaptation strategies of *G. antarctica* PI12. The yeast grown optimally in *Saccharomyces cerevisiae* minimal medium at 12 °C was subsequently exposed to cold-shock at 0 °C and freeze-shock at –12 °C for 6 h and 24 h. RNA from those cells were extracted, sequenced, and analyzed. Interestingly, the results showed that *G. antarctica* PI12 remained metabolically active at –12 °C. Two hundred and five genes were differentially expressed in the cells. Among them, 107 genes were upregulated while 98 genes were downregulated. In the first 6 h after the cells were exposed to cold- and freeze-shocks, CCR4-NOT (carbon catabolite repressed 4 - negative on TATA-less) core subunit *cdc36*, DNA repair protein *Rad8*, Elongation factor 1- γ , 26s proteasome subunit 45, and Homocitrate synthase genes were commonly upregulated to perform several immediate and important tasks to ensure the cells survived. Apart from that, there were also genes upregulated and downregulated uniquely at 6 h and 24 h to facilitate the cells to adjust to the new temperatures. After overcoming the stress of the cold- and freeze-shocks for 24 h, the cells acclimatized to those temperatures and became metabolically active again, and the cell cycles related genes were up-regulated.