

A comparative transcriptomic analysis provides insights into the cold-adaptation mechanisms of a psychrophilic yeast, *Glaciozyma antarctica* PI12

ABSTRACT

Glaciozyma antarctica PI12, a psychrophilic yeast from Antarctica, grows well at low temperatures. However, it is not clear how it responds and adapts to cold and freeze stresses. Hence, this project was set out to determine the cold-adaptation strategies and mechanisms of *G. antarctica* PI12 using a transcriptomic analysis approach. *G. antarctica* PI12 cells, grown in rich medium at 12 °C, were exposed to freeze stress at 0 and – 12 °C for 6 h and 24 h. Their transcriptomes were sequenced and analyzed. A hundred and sixty-eight genes were differentially expressed. The yeast gene expression patterns were found to be dependent on the severity of the cold with more genes being differentially expressed at – 12 °C than at 0 °C. *Glaciozyma antarctica* PI12 was found to share some common adaptation strategies with other yeasts, *Saccharomyces cerevisiae* and *Mrakia* spp., but at the same time, found to have some of its own unique strategies and mechanisms. Among the unique mechanisms was the production of antifreeze protein to prevent ice-crystallization inside and outside the cell. In addition, several molecular chaperones, detoxifiers of reactive oxygen species (ROS), and transcription and translation genes were constitutively expressed in *G. antarctica* PI12 to enable the cells to endure the fluctuating freezing temperatures. Interestingly, *G. antarctica* PI12 used nitrite as an alternative terminal acceptor of electrons when the oxygen level was low to minimize disruption of energy production in the cell. These mechanisms coupled with several other common mechanisms ensured that *G. antarctica* PI12 adapted well to the cold temperatures.