Abstract

Introduction: Paracoccidioidomycosis is an endemic systemic mycosis caused by Paracoccidioides brasiliensis, a thermally dimorphic fungus that in tissues and cultures at 37 °C grows as a yeast while at lower temperatures (less than 24 °C) it becomes a mold; however the genes that rule these processes and their expression are poorly understood. Objective: This research focused on the kinetic expression of certain genes in P. brasiliensis throughout the dimorphic process, one that involves the transition from the mycelium to yeast forms and the germination from the yeast to mycelium form. Materials and methods: A real-time quantitative polymerase chain reaction (RT-qPCR) was optimized to measure the expression of ten genes connected with diverse cellular functions including cell synthesis and wall structure, oxidative stress response, heat shock response, metabolism, proteins’ processing, solute transport across the cell membrane and signal transduction pathways at different time points during the mycelia to yeast transition, as well as in the yeast to mycelia germination processes. Results: Genes involved in cell synthesis and wall structure, metabolism and signal transduction were differentially expressed and highly up-regulated during the yeast to mycelia germination process; on the other hand, genes involved in heat shock response, cell synthesis and wall structure were highly up-regulated during the mycelia to yeast transition process. The remaining genes were differentially regulated during both processes. Conclusion: In this work the up-regulation of certain genes involved in the morphological changes occurring in P. brasiliensis yeast and mycelia forms were confirmed, indicating that these biological processes play an important role during the host-pathogen interactions, as well as in the fungus adaptation to environmental conditions.

Keywords

Paracoccidioides, paracoccidioidomycosis, yeasts, mycelium, germination, gene expression.