THE EXPRESSION PATTERN OF CYTOCHOME C OXIDASE COMPLEX GENES DURING THE DIMORPHIC TRANSITION OF PARACOCCIDIOIDES BRASILIENSIS

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The thermo dimorphic fungus *Paracoccidioides brasiliensis* is a human pathogen, aetiological agent of paracoccidioidomycosis (PCM). The transition from mycelium to yeast is required for human infection and pathogenicity. Previous studies suggest that in this process there are marked changes in mitochondrial physiology including uncoupling of oxidative phosphorylation. In this work we examined, by real time RT-PCR, the expression pattern of some cytochrome c oxidase related genes during dimorphic transition of *P. brasiliensis* from mycelium to yeast and vice versa. Total RNA was extracted from *P. brasiliensis* cells, at six time points during the dimorphic transition induced by temperature shifting from 25°C (mycelium form) to 37°C degrees (yeast form) and reverse. After normalization of the real time RT-PCR results against the control gene *PbeIF3* we found that, altogether, cytochrome genes (*PbCOX2*, *PbCOX4*, *PbCOX5A*, *PbCOX6*, *PbCOX9*, *PbCOX12*, *PbCOX16*, *PbCOX17* and *PbCOX19*) are over expressed when transition goes from mycelium to yeast. When going from yeast to mycelium all genes were partially repressed except *PbCOX5A*, *PbCOX17* and *PbCOX19*. Our results are in disagreement with a down regulation of cellular respiration previously described in the literature. Alternatively, they suggest that if cytochrome c oxidase subunits are down regulated the regulation is part transcriptionally.

Key words: Paracoccidioides brasiliensis, Cytochome c oxidase, Real-time RT-PCR

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