

TITLE: PHOSPHOPROTEOMIC ANALYSIS OF *Paracoccidioides brasiliensis* during dimorphic transition.

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ABSTRACT:

Paracoccidioidomycosis (PCM) is an important systemic mycosis in Latin America, with a high incidence in Brazil, Argentina, Colombia and Venezuela. The disease is attributed to the thermodynamically dimorphic fungi *Paracoccidioides* spp. transmitted through the inhalation of conidia and or mycelia fragments. Once in the host, due to the increase of the body temperature occurs the transition from mycelium to yeast. This transition is vital in the pathogenesis of PCM allowing the survival of the fungus inside the host. Phosphoproteomic analysis is an important tool for studying protein phosphorylation events, allowing a better understanding of fungal biology, as during the morphological transition in *Paracoccidioides*, since signaling pathways that control the morphological transition are largely unknown. The present study aims to investigate changes in protein abundance and phosphorylation events during the dimorphic transition using iTRAQ-labeled peptides, allowing relative and absolute quantification through MS/MS analysis. In a previous analysis, 427 proteins were identified comprehending 168 in mycelium, 132 in transition from mycelium to yeast cells and 127 in yeast. The in silico analysis most of the identified kinases were distributed in cellular components that include soluble fraction, cell wall and vesicles. The biological processes were associated mainly with metabolism of glucose, and response to stress. A large diversity of protein kinases were annotated in molecular functions with ATPase activity, transferase, kinase and nucleotide binding proteins. It is noteworthy that the approach proposed for the present study allowed a more accurate view of the cellular differentiation process of *Pb18*.

Keywords: *Paracoccidioides*, phosphoproteome, iTRAQ, transition

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