TITLE: PHOSPHOPROTEOMIC ANALYSIS OF MEMBERS OF THE *PARACOCCIDIOIDES* GENUS

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ABSTRACT

The genus *Paracoccidioides* comprises thermally dimorphic fungi, which cause paracoccidioidomycosis, the most prevalent systemic mycosis in Latin America. This genus is composed by the species *Paracoccidioides lutzii* and *Paracoccidoides brasiliensis*, with four different phylogenetic lineages (S1, PS2, PS3, PS4). After the cell machinery synthesizes proteins, important modifications, including phosphorylation, occur to specify various cellular and molecular aspects of those molecules, such as function, compartmentalization, structure and stability. Given the importance of phosphorylated proteins in organisms, proteomics techniques, have been used for the identification and characterization of proteins that present phosphorylation. This work aims to identify and functionally classify phosphorylated proteins in two members of the genus *Paracoccidioides*: *Paracoccidioides brasiliensis* and *Paracoccidioides lutzii*, characterizing differences and similarities between them. Firstly, we realized *in silico* analysis of kinases of the isolates *Pb* 03, *Pb* 18 and *P. lutzzi*. Also, proteome analysis was performed utilizing iTRAQ, and phosphoproteome was performed utilizing titanium dioxide, for phosphoenrichment. *In silico* analysis showed that *Pb* 03 have 242 kinases (96 tyrosines, 43 serines and 40 threonines), *Pb* 18 have 236 kinases (98 tyrosines, 32 serines, 29 threonines and *P. lutzii* have 237 kinases (93 tyrosines, 35 serines and 31 threonines), indicating differential phosphorylation among isolates. Some proteins are putative kinases, but were unclassified. Posteriorly it was realized a proteomic analysis of the three isolates by mass spectrometry in the equipment Orbitrap LC-MS (ThermoFisher Scientific). It were identified 387 proteins after TiO2 enrichment assays and 171 phosphoproteins were obtained. The next steps is the analyses and identification of phosphoproteins of each isolate.

Keywords: fungus, phosphorylation, proteomics, post-translational modification.

Development Agency: CAPES; CNPq, INCT-IPH, FAPEG.