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Identification *in silico* of gpi (glycosylphosphatidylinositol)-proteins in *Paracoccidioides brasiliensis* and *Paracoccidioides lutzii*

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Introduction. Species of the genus *Paracoccidioides* are thermal dimorphic fungi and the etiological agents of paracoccidioidomycosis (PCM), the most prevalent systemic mycosis in Latin America. Strains of *P. lutzii* are more resistant to antifungal treatments and usually found in the central-western Brazil, while strains of *P. brasiliensis* are frequent in the southeast and northern regions. In fungi, GPI-proteins (glycosylphosphatidylinositol-anchored proteins) are involved in cell wall integrity, as well as in pathogenic processes such as adhesion, degradation of host tissue and immune response interplay. The GPI-proteins frequently display a common structural organization such as an N-terminal signal peptide for translocation across the membrane of the endoplasmic reticulum and a C-terminal consensus sequence for GPI attachment. These features allow their identification using *in silico* approaches based on genome sequence. **Objectives.** In this study, we identified ORFs (open reading frames) predicted to encode GPI-proteins in the genomes of *P. brasiliensis* and *P. lutzii* by bioinformatics analysis. **Material and methods.** The *P. brasiliensis* and *P. lutzii* ORFs databases from Broad Institute (http://www.broadinstitute.org/) were analyzed by five different strategies for the identification of GPI-proteins and the orthologs identified in each species by reciprocal inspection. The ORFs were manually confirmed for the correct exon/intron prediction by comparison of the respective orthologs in *Paracoccidioides* and other fungal databases at NCBI (http://www.ncbi.nlm.nih.gov/). **Results and conclusions.**A number of 180 candidates for GPI-proteins were identified in *P. brasiliensis* and *P. lutzii* genomes by not less than two *in silico* approaches. Fifty of these ORFs can be grouped into six different functional classes of GPI-proteins (such as glycoside hydrolases, carbohydrate processing proteins and cell wall biogenesis) and 95 ORFs have homology to hypothetical proteins conserved in other organisms. Another 35 identified ORFs comprises a set of false positives because their orthologs are functionally characterized in other organisms and they do not perform cell surface functions. The results of this analysis show a small difference between *P. brasiliensis* and *P. lutzii* in the total number of predicted GPI-proteins and a high conservation of these ORFs in Eurotiomycete class members.

Keywords: *Paracoccidioides brasiliensis*, *Paracoccidioides lutzii*, GPI-proteins.

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