

STRUCTURAL ANALYSIS OF PB27 ANTIGENIC PROTEIN FROM *Paracoccidioides brasiliensis*

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The fungus *Paracoccidioides brasiliensis* causes paracoccidioidomycosis (PCM), a systemic infection disease that affects thousands of people in Latin America. Several antigenic proteins from *P. brasiliensis* have been identified and characterized, including the immunodominant antigen GP43. These antigens are being used in several studies aiming the development a suitable immune diagnostic assay and vaccine against PCM. Recombinant Pb27 antigenic protein (Pb27r), purified by affinity chromatography, has been described to be highly recognized by PCM patient antibodies. Crystallization trials performed so far failed to produce crystals amenable for x-ray diffraction studies. Nevertheless, in this work we have analyzed the structural properties of Pb27r by circular dichroism (CD). The tertiary structure of this protein shows to be highly stable as temperature increases. Thermal denaturation experiment conducted with a Jasco-815 circular dichroism spectropolarimeter indicates a melting temperature (T_m) of about 69.7 °C. Besides, CD data collected in the range of 195 to 260 nm and analyzed with CDNN2.1 program show that the secondary structure of PB27r is composed of 31%α-helix, 10,7%antiparallel β-sheet, 9,0%parallel β-sheet, 17,3%β-Turn and 32,4%random coil. The amino acid sequence of Pb27r was blasted against the PDB database to search for homologous proteins. Despite all hits displayed low amino acid similarity, molecular modeling was performed using the program Modeller 4.0 and a dihydrodipicolinate reductase as template (PDBID:1YL7). According to this model, Pb27r shows a copper amine oxidase-like domain suggesting this proteins is a new Frataxin Family member, regardless a large part of the protein were not modeled.