PROTEOMIC ANALYSIS OF THE CELL WALL FROM GENETICALLY DISTINCT *PARACOCCIDIOIDES BRASILIENSIS* ISOLATES THAT DIFFER IN PATHOGENICITY.

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Paracoccidioides brasiliensis is the fungal species responsible for paracoccidioidomycosis (PCM), which is prevalent in endemic areas of Latin America. Recently, three distinct *P. brasiliensis* lineages S1, PS2 and PS3 have been recognized using a combined data set of polymorphism in five nuclear loci. Most of the samples fall into S1, while PS3 assembles Colombian isolates. PS2 corresponds to a cryptic phylogenetic species that assembles six isolates so far. The genetic variation in *P. brasiliensis* is largely reflected at the Pb*GP43* (encoding a major antigen) gene, especially in exon 2 and promoter region. PS2 isolates (e.g. Pb3) contain highly substituted Pb*GP43* sequences and provoked regressive, Th1-driven infection in B10.A mice, in contrast with isolates from S1 group (e.g. Pb18), which evoked a progressive, lethal and Th2-driven type of disease. In order to search for surface molecules that could explain the differences in fungal pathogenicity, we have performed a proteomic analysis of proteins covalently associated to the cell wall from Pb3 and Pb18. The fungal pathogenic yeast phase was cultivated in defined medium in the absence or in the presence of fetal calf serum and isolated cell walls were extracted with both NaOH and HF-pyridine. Extracted proteins were digested with trypsin and the generated peptides were analyzed by liquid chromatography followed by mass spectrometry (LC/MS-MS). Proteins were identified by comparison with fungal databases using Mascot and Phenyx softwares. A comprehensive analysis of the generated data will be presented and discussed.

Financed by FAPESP, CNPq and BBRC/Biology/UTEP (NIH #5G12RR008124)