PROTEOMIC STUDY OF Aspergillus fumigatus DURING MORPHOLOGICAL TRANSITION BY 2D FLUORESCENCE DIFFERENCE GEL ANALYSIS TECHNOLOGY (2-D DIGE)

<u>Lopes-Bezerra, L.M</u>¹, Cardoso, J¹, Araújo, S.G¹, Gutiérrez, L², Matínez-Gomariz, M², Gil C²

¹ LMCProt, Instituto de Biologia Roberto Alcantara Gomes, UERJ; ² Unidad de Proteómica, Facultad de Farmácia, Universidad Complutense de Madrid. Invasive aspergillosis, typically caused by Aspergillus fumigatus, is the most common filamentous fungal infection following hematopoietic stem cell transplantation. Other high risk groups include solid-organ transplant recipients, cystic fibrosis patients and patients receiving chronic corticosteroid therapy. We have recently described that A. fumigatus hyphae, but not the conidia, can induce a prothrombotic phenotype on endothelial cells (ECs). Also, we observed that the injury of ECs correlates with the morphological transition of A. fumigatus. In the present work we have studied, by the DIGE technology, the expression of proteins on A. fumigatus germlings and hyphae. The whole cells were treated with 2mercaptoethanol (2-ME) after the morphological transition from conidia to hyphae. The germlings were obtained after 12 hours and the hyphae after 48 hours of growth in Sabouraud broth, respectively. The 2-ME extracts were further purified by precipitation with the 2-D clean up kit. Each extract was labeled with either Cy3 or Cy5 and fractionated by 2-D electrophoresis. The 2-D gels were analyzed by the DeCyder software and a total of 50 proteins were found to be differentially expressed during hyphae formation. Some are enzymes involved in cell wall remodeling that were identified by MALDI-TOF/TOF. Supported by CNPq and Faperj.