

ANALYSIS OF CANDIDA ALBICANS SURFACE PROTEINS IN EXPONENTIAL AND STATIONARY PHASES OF GROWTH

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Invasive candidiasis is a significant cause of morbidity and mortality in critical care units. The cell wall is the first point of contact between fungus and host arousing great interest in the search for new therapeutic targets, diagnostic and prognostic markers or vaccines. The analysis of cell wall proteins involves the use of laborious protocols. These facts, coupled with the interest in understanding the involvement of these proteins in the infectious process of this fungus, led us to characterize the exposed surface proteins of *C. albicans* in vivo yeasts by a rapid proteomic approach. This non-gel proteomic approach was based on a short period of trypsin treatment followed by peptide separation and identification using mass spectrometry. We conducted this study in two phases of growth, exponential and stationary, and performed three biological replicates of each phase. The viability of trypsin treated cells was assessed by flow cytometry. This analysis allowed the identification of a total of 28 proteins in the exponential phase and 50 in stationary phase. Of the proteins identified, only 16 were found in both phases studied. All proteins were classified into functional categories according to their involvement in biological processes, using Candida Genome Database (CGD). Proteins related with the organization of cell wall organization, metabolic processes, translation, protein folding, stress response and unknown function were identified. Taking into account the importance of *C. albicans* dimorphic transition in the pathogenic process, new experiments to identify surface proteins of both, hyphae and yeast obtained by different stimuli are currently being done.