

COMPARISON OF EXTRACTION METHODS FOR THE PROTEOMIC ANALYSIS OF SURFACE PROTEINS OF *SPOROTHRIX SCHENCKII*

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Sporothrix schenckii is the etiological agent of sporotrichosis, a human deep mycosis. This fungus exhibits dimorphism with a parasitic yeast-like phase and a mycelial phase. The aim of this work was to compare the efficiency of two chemical methods of extraction for proteomic analysis of surface proteins of *S. schenckii*. Also, we studied the proteins expressed on yeast cells depending on the morphological transition. First, we compared two methods of extraction using intact cells: (i) 2-mercaptoethanol at 37°C/30 min; (ii) DTT at 4°C/2h. The general profile of proteins extracted by the two methods was similar but the 2-DE gels of DTT extracts showed a better resolution. Also, more proteins were identified *per gel* by MS/MS. Surprisingly, we were able to identify proteins of the glycolytic pathway using this mild extraction, a result never shown in the literature. These proteins were already described on the surface of other pathogenic fungi but by other experimental approaches. Furthermore, significant differences on 2-DE images were observed when the initial agar slant started from a yeast phase or a mycelial phase. The cells obtained under the later condition gave 2-DE gels with a higher number of protein spots and also, the proteins were better focused. Supported by: CNPq and Faperj