

Optimisation of a 2-D gel electrophoresis protocol for the human-pathogenic fungus *Aspergillus fumigatus*.

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Abstract

Aspergillus fumigatus is the most important airborne fungal pathogen causing life-threatening infections in immunosuppressed patients. One of the important questions concerning *A. fumigatus* is the identification of pathogenicity determinants. To obtain a comprehensive overview about the proteins produced at different physiological conditions that are related to the infectious process a proteomic approach has been applied. Here, 2-D gel electrophoresis for filamentous fungi was optimised concerning removal of interfering compounds, protein extraction and separation methods. A trichloroacetic acid-based precipitation method of proteins with their subsequent solubilisation by the use of a combination of CHAPS with a second sulfobetaine detergent gave the best results. The optimised protocol was evaluated by the analysis of the proteomes of *A. fumigatus* grown on two different carbon sources, i.e., glucose and ethanol. Carbon catabolite repression has not been studied in detail at the protein level in *A. fumigatus* yet. In addition, growth on ethanol leads to activation of the glyoxylate cycle which was shown to be essential for pathogenesis in bacteria and fungi. In *A. fumigatus*, differential patterns of enzymes of the

gluconeogenesis, glyoxylate cycle and ethanol degradation pathway during growth on glucose and ethanol were observed.

Involved units

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