Proteome profiling and functional classification of intracellular proteins from conidia of the human-pathogenic mold *Aspergillus fumigatus*.

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Projects

Integration of transcriptome and proteome data from human-pathogenic fungi
Details

Abstract

Aspergillus fumigatus is a ubiquitously distributed filamentous fungus that has emerged as one of the most serious life-threatening pathogens in immunocompromised patients. The mechanisms for its pathogenicity are poorly understood. Here, we analyzed the proteome of dormant *A. fumigatus* conidia as the fungal entity having the initial contact with the host. Applying two-dimensional polyacrylamide gel electrophoresis (2-D PAGE), we established a 2-D reference map of conidial proteins. By MALDI-TOF mass spectrometry, we identified a total number of 449 different proteins. We show that 57 proteins of our map are over-represented in resting conidia compared to mycelium. Enzymes involved in reactive oxygen intermediates (ROI) detoxification, pigment biosynthesis, and conidial rodlet layer formation were highly abundant in *A. fumigatus* spores and most probably account for their enormous stress resistance. Interestingly, pyruvate decarboxylase and alcohol dehydrogenase were detectable in dormant conidia, suggesting that alcoholic fermentation plays a role during dormancy or early germination. Moreover, we show that enzymes for rapid reactivation of protein biosynthesis and metabolic processes are preserved in resting conidia, which therefore feature the potential to immediately respond to an environmental stimulus by germination. The generated data lay the foundations for further proteomic analyses and a better understanding of fungal pathogenesis.

Identifier

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