

Identification of virulence determinants of the human pathogenic fungi *Aspergillus fumigatus* and *Candida albicans* by proteomics.

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Abstract

Both fungi *Candida albicans* and *Aspergillus fumigatus* can cause a number of life-threatening systemic infections in humans. The commensal yeast *C. albicans* is one of the main causes of nosocomial fungal infectious diseases, whereas the filamentous fungus *A. fumigatus* has become one of the most prevalent airborne fungal pathogens. Early diagnosis of these fungal infections is challenging, only a limited number of antifungals for treatment are available, and the molecular details of pathogenicity are hardly understood. The completion of both the *A. fumigatus* and *C. albicans* genome sequence provides the opportunity to improve diagnosis, to define new drug targets, to understand the functions of many uncharacterised proteins, and to study protein regulation on a global scale. With the application of proteomic tools, particularly two-dimensional gel electrophoresis and LC/MS-based methods, a comprehensive overview about the proteins of *A. fumigatus* and *C. albicans* present or induced during environmental changes and stress conditions has been obtained in the past 5 years. However, for the discovery of further putative

virulence determinants, more sensitive and targeted proteomic methods have to be applied. Here, we review the recent proteome data generated for *A. fumigatus* and *C. albicans* that are related to factors required for pathogenicity.

Beteiligte Forschungseinheiten

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