Proteome analysis for pathogenicity and new diagnostic markers for *Aspergillus fumigatus*.

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Abstract

With the completion of the Aspergillus fumigatus genome it is now possible to study protein regulation on a global scale. One of the most suitable protein separation techniques is based on 2D-gel electrophoresis, which allows the separation of proteins based on their charge and size in a gel matrix. In addition, gel-free proteomics techniques based on liquid-chromatography coupled with mass spectrometry have gained importance. With the application of proteomic tools a comprehensive overview about the proteins of A. fumigatus present or induced during environmental changes and stress conditions can be obtained. For A. fumigatus, several proteomic studies have already been published including the response of the fungus to oxidative stress that induced the up-regulation of many proteins including catalases and thioredoxin peroxidase. Since many of the identified proteins/genes were apparently regulated by a putative Saccharomyces cerevisiae Yap1 homolog, the corresponding gene of A. fumigatus was identified, designated Afyap1 and further characterized. In addition, some of the gene products expressed under stress conditions are also known fungal antigens, such as the thioredoxin peroxidase AspF3. Thus, besides pathogenicity studies, proteomics also delivers the tools to screen for new

antigens which could improve the diagnosis of diseases caused by A. fumigatus.

Involved units

Molecular and Applied Microbiology Axel Brakhage Read more

Leibniz-HKI-Authors



Axel A. Brakhage

Details



Olaf Kniemeyer

Details



Franziska Lessing

Details

Identifier

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