Integrative analysis of the heat shock response in *Aspergillus fumigatus*.

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Abstract

Aspergillus fumigatus is a thermotolerant human-pathogenic mold and the most common cause of invasive aspergillosis (IA) in immunocompromised patients. Its predominance is based on several factors most of which are still unknown. The thermotolerance of *A. fumigatus* is one of the traits which have been assigned to pathogenicity. It allows the fungus to grow at temperatures up to and above that of a fevered human host. To elucidate the mechanisms of heat resistance, we analyzed the change of the *A. fumigatus* proteome during a temperature shift from 30 degrees C to 48 degrees C by 2D-fluorescence difference gel electrophoresis (DIGE). To improve 2D gel image analysis results, protein spot quantitation was optimized by missing value imputation and normalization. Differentially regulated proteins were compared to previously published transcriptome data of *A. fumigatus*. The study was augmented by bioinformatical analysis of transcription factor binding sites (TFBSs) in the promoter region of genes whose corresponding proteins were differentially regulated upon heat shock.

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Topics

Management of heterogeneous experimental data

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