

Discovery of gene regulatory networks in *Aspergillus fumigatus*.

Guthke R, Kniemeyer O, Albrecht D, Brakhage AA, Moeller U (2007) Discovery of gene regulatory networks in *Aspergillus fumigatus*. *Lect Notes Bioinf* 4366,

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Abstract

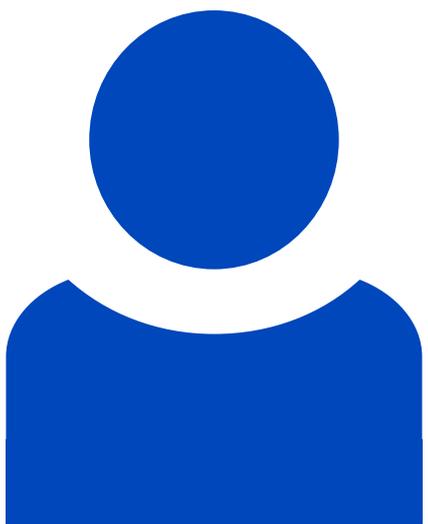
Aspergillus fumigatus is the most important airborne fungal pathogen causing life-threatening infections in immunosuppressed patients. During the infection process, *A. fumigatus* has to cope with a dramatic change of environmental conditions, such as temperature shifts. Recently, gene expression data monitoring the stress response to a temperature shift from 30 °C to 48 °C was published. In the present work, these data were analyzed by reverse engineering to discover gene regulatory mechanisms of temperature resistance of *A. fumigatus*. Time series data, i.e. expression profiles of 1926 differentially expressed genes, were clustered by fuzzy c-means. The number of clusters was optimized using a set of optimization criteria. From each cluster a representative gene was selected by text mining in the gene descriptions and evaluating gene ontology terms. The expression profiles of these genes were simulated by a differential equation system, whose structure and parameters were optimized minimizing both the number of non-vanishing parameters and the mean square error of model fit to the microarray data.

Beteiligte Forschungseinheiten

[Molekulare und Angewandte Mikrobiologie Axel Brakhage](#) [Mehr erfahren](#)

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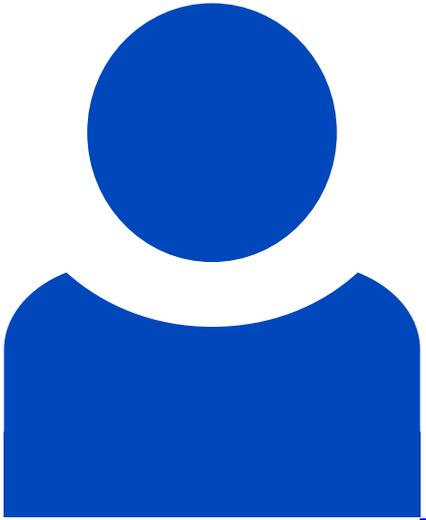
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