

# **Transcriptome analysis of *Aspergillus fumigatus* exposed to voriconazole.**

da Silva Ferreira ME, Malavazi I, Savoldi M, Brakhage AA, Goldman MH, Kim HS, Nierman WC, Goldman GH (2006) Transcriptome analysis of *Aspergillus fumigatus* exposed to voriconazole. *Curr Genet* 50(1), 32-44.

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## **Abstract**

For a comprehensive evaluation of genes that have their expression modulated during exposure of the mycelia to voriconazole, we performed a large-scale analysis of gene expression in *Aspergillus fumigatus* using a microarray hybridization approach. By comparing the expression of genes between the reference time and after addition of voriconazole (30, 60, 120, and 240 min), we identified 2,271 genes differentially expressed in the wild-type strain. To validate the expression of some of these genes during exposure to voriconazole, we analyzed 13 genes showing higher expression in the presence of voriconazole by real-time RT-PCR. Although the magnitudes of induction differed between the two experimental systems, in about 85% of the cases they were in good agreement with the microarray data. To our knowledge this is the first study of microarray hybridization analysis for a filamentous fungus exposed to an antifungal agent. In our study, we have observed: (i) a decreased mRNA expression of various ergosterol biosynthesis genes; (ii) increased mRNA levels of genes involved in a variety of cell functions, such as transporters, transcription factors, proteins involved in cell metabolism, and hypothetical proteins; and (iii) the

involvement of the cyclic AMP-protein kinase signaling pathway in the increased mRNA expression of several of these genes.

## Beteiligte Forschungseinheiten

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

## Leibniz-HKI-Autor\*innen



Axel A. Brakhage

[Details](#)

**Identifier**

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