

Transcriptomic and proteomic analyses of the *Aspergillus fumigatus* hypoxia response using an oxygen-controlled fermenter.

Barker BM, Kroll K, Vödisch M, Mazurie A, Kniemeyer O, Cramer RA (2012) Transcriptomic and proteomic analyses of the *Aspergillus fumigatus* hypoxia response using an oxygen-controlled fermenter. *BMC Genomics* 13, 62-62.

[Details](#)



Abstract

Aspergillus fumigatus is a mold responsible for the majority of cases of aspergillosis in humans. To survive in the human body, *A. fumigatus* must adapt to microenvironments that are often characterized by low nutrient and oxygen availability. Recent research suggests that the ability of *A. fumigatus* and other pathogenic fungi to adapt to hypoxia contributes to their virulence. However, molecular mechanisms of *A. fumigatus* hypoxia adaptation are poorly understood. Thus, to better understand how *A. fumigatus* adapts to hypoxic microenvironments found in vivo during human fungal pathogenesis, the dynamic changes of the fungal transcriptome and proteome in hypoxia were investigated over a period of 24 hours utilizing an oxygen-controlled fermenter system.

Beteiligte Forschungseinheiten

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

Leibniz-HKI-Autor*innen



Olaf Kniemeyer

[Details](#)



Kristin Kroll

[Details](#)



Martin Vödisch

[Details](#)

Identifier

doi: 10.1186/1471-2164-13-62

PMID: 22309491