

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.

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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.

Involved units

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