Identifying infection-associated genes of *Candida albicans* in the postgenomic era.

Wilson D, Thewes S, Zakikhany K, Fradin C, Albrecht A, Almeida R, Brunke S, Grosse K, Martin R, Mayer F, Leonhardt I, Schild L, Seider K, Skibbe M, Slesiona S, Waechtler B, Jacobsen I, Hube B (2009) Identifying infection-associated genes of *Candida albicans* in the postgenomic era. *FEMS Yeast Res* 9(5), 688-700. (Review)

Details

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Abstract

The human pathogenic yeast Candida albicans can cause an unusually broad range of infections reflecting a remarkable potential to adapt to various microniches within the human host. The exceptional adaptability of C. albicans is mediated by rapid alterations in gene expression in response to various environmental stimuli and this transcriptional flexibility can be monitored with tools such as microarrays. Using such technology it is possible to (1) capture a genome-wide portrait of the transcriptome that mirrors the environmental conditions, (2) identify known genes, signalling pathways and transcription factors involved in pathogenesis, (3) identify new patterns of gene expression and (4) identify previously uncharacterized genes that may be associated with infection. In this review, we describe the molecular dissection of three distinct stages of infections, covering both superficial and invasive disease, using in vitro, ex vivo and in vivo infection models and microarrays.

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Topics

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