

Infection-associated genes of *Candida albicans*.

Hube B (2006) Infection-associated genes of *Candida albicans*. *Future Microbiol* 1(2), 209-218. (Review)

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Abstract

Advances in the medical treatment of life-threatening disorders have increased the population of patients that are more susceptible to opportunistic microbial infections, such as those caused by the *Candida* species, in particular *Candida albicans*. This fungus normally belongs to the microbial flora but may cause a range of diseases from superficial to disseminated. What exactly causes the transition from commensalism to pathogenesis is not clear and how this fungus switches from a commensal mode of growth to a parasitic lifestyle remains unknown. Identifying the genes and factors essential for the different stages of *C. albicans* infections will not only help understanding of the infection process but also provide information about those fungal factors that have to be inhibited, and those parts of the immune system that have to be stimulated, in order to control or prevent infections. Furthermore, knowledge of those genes whose expression is associated with infection but not commensalism may provide valuable information to improve our diagnostic tools. A number of methodologies and models have already been used to identify infection-associated genes. In addition to genes encoding classical virulence determinants, such as those involved in interactions with the immune system and immune evasion, scientists have monitored the expression of genes involved in nutrient acquisition, metabolism, stress response, physical interaction and hyphal formation in infection models and have begun to elucidate the roles of these

genes.

Beteiligte Forschungseinheiten

[Mikrobielle Pathogenitätsmechanismen](#) [Bernhard Hube](#) [Mehr erfahren](#)

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