In vivo and *ex vivo* comparative transcriptional profiling of invasive and non-invasive *Candida albicans* isolates identifies genes associated with tissue invasion.

Thewes S, Kretschmar M, Park H, Schaller M, Filler SG, Hube B (2007) *In vivo* and *ex vivo* comparative transcriptional profiling of invasive and non-invasive *Candida albicans* isolates identifies genes associated with tissue invasion. *Mol Microbiol* 63(6), 1606-1628.

Details



Abstract

The human pathogenic fungus Candida albicans can cause a wide range of infections and invade multiple organs. To identify C. albicans genes that are expressed during invasion of the liver, we used genome-wide transcriptional profiling in vivo and ex vivo. By analysing the different phases of intraperitoneal infection from attachment to tissue penetration in a time-course experiment and by comparing the profiles of an invasive with those of a non-invasive strain, we identified genes and transcriptional pattern which are associated with the invasion process. This includes genes involved in metabolism, stress, and nutrient uptake, as well as transcriptional programmes regulating morphology and environmental sensing. One of the genes identified as associated with liver invasion was DFG16, a gene crucial for pH-dependent hyphal formation, correct pH sensing, invasion at physiological pH and systemic infection.

Involved units

Microbial Pathogenicity Mechanisms Bernhard Hube Read more

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Bernhard Hube

Details

Awards

Selected as “Recommended” Factor 6.0 by Faculty of 1000 and as “of outstanding interest” by Current Opinion in Microbiology (3x); European ERA-Pathogenomics Awards 2008; Forschungspreis der DGHM Fachgruppe Eukaryontische Krankeitserreger 2008

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