

***In vivo* transcript profiling of *Candida albicans* identifies a gene essential for interepithelial dissemination.**

Zakikhany K, Naglik JR, Schmidt-Westhausen A, Holland G, Schaller M, Hube B (2007) *In vivo* transcript profiling of *Candida albicans* identifies a gene essential for interepithelial dissemination. *Cell Microbiol* 9(12), 2938-2954.

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Abstract

Candida albicans is the most common oral fungal pathogen of humans, but the mechanisms by which *C. albicans* invades and persists within mucosal epithelium are not clear. To understand oral pathogenesis, we characterized the cellular and molecular mechanisms of epithelial-fungus interactions using reconstituted human oral epithelium (RHE). We observed that hyphal formation facilitates epithelial invasion via both active (physical penetration) and passive (induced endocytosis) processes. Genome wide transcript profiling of *C. albicans* experimental RHE infection was compared with that from 11 patient samples with pseudomembranous candidiasis to identify genes associated with disease development in vivo. Expression profiles reflected the morphological switch and an adaptive response to neutral pH, non-glucose carbon sources and nitrosative stress. We identified several novel infection-associated genes with unknown function. One gene, upregulated in both RHE infection and patients, named EED1, was essential for maintenance of hyphal elongation. Mutants lacking EED1 showed transient cell elongation on epithelial tissue, which enabled only superficial invasion of epithelial cells. Once inside an epithelial

cell, Deltaeed1 cells could proliferate as yeasts or pseudohyphae but remained trapped intracellularly. Our results suggest that the adaptive response and morphology of *C. albicans* play specific roles for host-fungal interactions during mucosal infections.

Beteiligte Forschungseinheiten

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