

Global transcriptome sequencing identifies chlamydospore specific markers in *Candida albicans* and *Candida dubliniensis*.

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Abstract

Candida albicans and *Candida dubliniensis* are pathogenic fungi that are highly related but differ in virulence and in some phenotypic traits. During in vitro growth on certain nutrient-poor media, *C. albicans* and *C. dubliniensis* are the only yeast species which are able to produce chlamydospores, large thick-walled cells of unknown function. Interestingly, only *C. dubliniensis* forms pseudohyphae with abundant chlamydospores when grown on Staib medium, while *C. albicans* grows exclusively as a budding yeast. In order to further our understanding of chlamydospore development and assembly, we compared the global transcriptional profile of both species during growth in liquid Staib medium by RNA sequencing. We also included a *C. albicans* mutant in our study which lacks the morphogenetic transcriptional repressor Nrg1. This strain, which is characterized by its constitutive pseudohyphal growth, specifically produces masses of chlamydospores in Staib medium, similar to *C. dubliniensis*. This comparative approach identified a set of putatively chlamydospore-related genes. Two of the homologous *C. albicans* and *C.*

dublinsiensis genes (CSP1 and CSP2) which were most strongly upregulated during chlamydospore development were analysed in more detail. By use of the green fluorescent protein as a reporter, the encoded putative cell wall related proteins were found to exclusively localize to *C. albicans* and *C. dubliniensiensis* chlamydospores. Our findings uncover the first chlamydospore specific markers in *Candida* species and provide novel insights in the complex morphogenetic development of these important fungal pathogens.

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