

A core filamentation response network in *Candida albicans* is restricted to eight genes.

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Abstract

Although morphological plasticity is a central virulence trait of *Candida albicans*, the number of filament-associated genes and the interplay of mechanisms regulating their expression remain unknown. By correlation-based network modeling of the transcriptional response to different defined external stimuli for morphogenesis we identified a set of eight genes with highly correlated expression patterns, forming a core filamentation response. This group of genes included ALS3, ECE1, HGT2, HWP1, IHD1 and RBT1 which are known or supposed to encode for cell- wall associated proteins as well as the Rac1 guanine nucleotide exchange factor encoding gene DCK1 and the unknown function open reading frame orf19.2457. The validity of network modeling was confirmed using a dataset of advanced complexity that describes the transcriptional response of *C. albicans* during epithelial invasion as well as comparing our results with other previously published transcriptome studies. Although the set of core filamentation response genes was quite small, several transcriptional regulators are involved in the control of their expression, depending

on the environmental condition.

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