

Defining the transcriptomic landscape of *Candida glabrata* by RNA-Seq.

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Abstract

Candida glabrata is the second most common pathogenic *Candida* species and has emerged as a leading cause of nosocomial fungal infections. Its reduced susceptibility to antifungal drugs and its close relationship to *Saccharomyces cerevisiae* make it an interesting research focus. Although its genome sequence was published in 2004, little is known about its transcriptional dynamics. Here, we provide a detailed RNA-Seq-based analysis of the transcriptomic landscape of *C. glabrata* in nutrient-rich media, as well as under nitrosative stress and during pH shift. Using RNA-Seq data together with state-of-the-art gene prediction tools, we refined the annotation of the *C. glabrata* genome and predicted 49 novel protein-coding genes. Of these novel genes, 14 have homologs in *S. cerevisiae* and six are shared with other *Candida* species. We experimentally validated four novel protein-coding genes of which two are differentially regulated during pH shift and interaction with human neutrophils, indicating a potential role in host-pathogen interaction. Furthermore, we identified 58 novel non-protein-coding genes, 38 new introns and condition-specific alternative

splicing. Finally, our data suggest different patterns of adaptation to pH shift and nitrosative stress in *C. glabrata*, *Candida albicans* and *S. cerevisiae* and thus further underline a distinct evolution of virulence in yeast.

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