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

Linde J, Duggan S, Weber M, Horn F, Sieber P, Hellwig D, Riege K, Marz M, Martin R, Guthke R, Kurzai O (2015) Defining the transcriptomic landscape of *Candida glabrata* by RNA-Seq. *Nucleic Acids Res* 43(3), 1392-1406. PubMed

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Projects

Prediction of gene regulatory networks involved in the differentiation, secondary metabolism and cross talk of *Aspergillus nidulans*
Details

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.

Identifier

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