

**Impact of alternative carbon sources and antifungal treatment on *Candida glabrata* biofilms' transcription profile****[P9/05]**

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*Candida glabrata* is considered a major opportunistic fungal pathogen of humans and has emerged as a leading cause of nosocomial fungal infections. The capacity of this yeast species to cause infections is dependent on the ability to grow within the human host environment and to assimilate the carbon sources available. Previous studies have suggested that *Candida* can encounter glucose-poor microenvironments during infection and that the ability to use alternative non-fermentable carbon sources, such as carboxylic acids, contributes to the virulence of these fungi. Our recent study (Mota et al., 2015) supported this view by demonstrating that acetic acid influences *C. glabrata* behavior in biofilm formation, antifungal drug resistance and phagocytosis; and suggesting a potential role of putative carboxylate transporters on these processes. In order to extend our studies and provide a comprehensive view of the *C. glabrata* biofilms' response to alternative carbon sources and antifungal treatment, we performed comparative transcriptomics analyses using RNA-sequencing. Our data support the view that adaptative responses of *Candida* cells to the types of carbon source present in host niches affects the virulence of these fungal cells through multifarious mechanisms (Brown et al., 2014). Finally, elucidating the effect of local nutrients and pH environment on drug resistance can potentially provide new and effective treatment strategies for *C. glabrata* infections such as vaginal candidiasis.

## References:

1. Brown AJ, Brown GD, Netea MG, and Gow NA (2014). Metabolism impacts upon *Candida* immunogenicity and pathogenicity at multiple levels. *Trends Microbiol.* 22, 614–622.

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