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.

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Keywords: Candida glabrata, biofilms, antifungal drug resistance, fluconazole, alternative carbon sources

SPB 2016

BOOK OF ABSTRACTS

XIX NATIONAL CONGRESS OF BIOCHEMISTRY

UNIVERSITY OF MINHO
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Escola de Ciências

SPB2016

BOOK OF ABSTRACTS

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GUIMARÃES

SPB2016 Book of Abstracts

Published by

SPB – Sociedade Portuguesa de Bioquímica
Universidade de Coimbra
Departamento de Bioquímica
Apartado 3126
3001 - 401 Coimbra, Portugal

CBMA – Centro de Biologia Molecular e Ambiental
Universidade do Minho
Departmento de Biologia
Campus de Gualtar
4710 - 057 Braga, Portugal

Editor: Miguel Pinheiro
Proofreader: Lina Kakoulidou
Editing Services: SY4SCI Events, Lda.
Production Services: Copissaurio, Lda.

Interior Designer: Miguel Pinheiro
Cover Designer: Tomás Capa
Illustrator: Tomás Capa

November 2016: First edition (Print)
December 2016: Second edition (Web)