

134 : Portrait of Gene Expression in *C. glabrata* with Stress Induced by Drugs

Session D

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Candidiasis have globally increased over the last years, being a major cause of morbidity and mortality, especially in immunosuppressed and hospitalized patients. *Candida albicans* remains to be the most common species responsible in candidiasis, but *Candida glabrata* has appeared as second most common *Candida* in the USA and the third in Europe, and is described to have a substantial resistance to several antifungal drugs. With the purpose of evaluating how *C. glabrata* cells try to adjust their biofilm composition in response to an antifungal drug treatment, a series of nine genes - *BGL2*, *FKS1*, *FKS2*, *GAS2*, *KHN1*, *MNN2*, *RAM2*, *UPG1*, and *XOG1* – known to be related to the production of β -1,3, β -1,6-glucans and mannans, were selected. The genes expression was evaluated by Real Time-qPCR in three strains of *C. glabrata* (reference, urinary isolate and vaginal isolate), after fluconazole (Flu), amphotericin B (AmB), caspofungin (Csf) or micafungin (Mcf) exposure. The antifungal's concentrations were fixed through the determination of the Minimum Biofilm Eradication Concentration, according to the EUCAST guidelines. Accordingly, the biofilms were grown during 24h and then the drugs were applied for more 24h before performing the Real Time-qPCR.

Generally, the results indicated that, comparing to the control group, the expressions were considerably and statistically significantly higher after a drug stress induction, especially for *BGL2*, *FKS1*, *FKS2*, *GAS2*, *MNN2* and *XOG1* and when using Mcf. Moreover, the fallouts revealed that these expression profiles were dependent on the strain, gene and drug. This work demonstrates the plasticity of biofilm cells and the high capacity of *C. glabrata* cells to adapt and respond properly to any antifungal drug aggression, which can explain, to some degree, the particular high virulence associated to this species.

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