

Abstract

The objective of this thesis was to investigate how cocultures of *Candida albicans* and *Candida guilliermondii* change overtime under control conditions and under the influence of fluconazole. These species are opportunistic fungal pathogens but widely differ in their susceptibility to antimycotic of interest – fluconazole.

After a brief introduction to special commonalities, the mechanism of pathogenesis, and the treatment of infection, this work explores each organism's growth curves under selected conditions and the process of artificial evolution using the model of passaging of cocultures. Afterwards, these populations of *C. albicans* and *C. guillieromondii* were investigated using qPCR and chromogenic media.

qPCR analysis revealed that under control conditions, *C. albicans* (CA) prevails; the possible reason behind this is a 20% shorter generation time, as revealed by the growth curve. In the presence of fluconazole, two trends occurred. One is related to the innate resistance of *C. guilliermondii* (CG), where CG was dominant by the end of passaging. The second trend led to CA being the dominant one, despite its susceptibility. This is a result of a heightened resistance, where minimal inhibitory concentration 50 (MIC₅₀) increased almost 10-fold, possibly due to mutations.

The change in populations investigated using chromogenic media (CHROMagar) follows and supports the trends found by qPCR; however, their interpretation proves to be rather tricky and more data are needed to conclude.

Key words: *Candida albicans*, *Candida guilliermondii*, fluconazole, passaging, drug resistance, MIC₅₀