Molecular identification and antifungal susceptibility profiles of Candida dubliniensis and Candida africana isolated from vulvovaginal candidiasis: A single-centre experience in Iran

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Abstract

Background Vulvovaginal candidiasis (VVC) is a common and debilitating long-term illness affecting million women worldwide. This disease is caused mainly by Candida albicans and a lesser extent by other species, including the two phylogenetically closely related pathogens Candida africana and Candida dubliniensis.

Objectives In this study, we report detailed molecular epidemiological data about the occurrence of these two pathogenic yeasts in Iranian patients affected by VVC, or its chronic recurrent form (RVVC), and provide, for the first time, data on the antifungal activity of two new drugs, efinaconazole (EFN) and luliconazole (LUL).

Methods A total of 133 vaginal yeast isolates, presumptively identified as C albicans by phenotypic and restriction analysis of rDNA, were further analysed by using a specific molecular method targeting the HWP1 gene. All C africana and C dubliniensis isolates were also tested for their in vitro susceptibility to a panel of modern and classical antifungal drugs.

Results and Conclusions Based on the molecular results, among 133 germ-tube positive isolates, we identify 119 C albicans (89.47%), 11 C africana (8.27%) and 3 C dubliniensis (2.26%) isolates. C africana and C dubliniensis showed low MIC values for most of the antifungal drugs tested, especially for EFN and LUL, which exhibited a remarkable antifungal activity. High MIC values were observed only for nystatin and terbinafine. Although C albicans remains the most common Candida species recovered from Iranian VVC/RVVC patients, our data show that its prevalence may be slightly overestimated due to the presence of difficult-to-identify closely related yeast, especially C africana.

Keywords

Author Keywords: Candida africana; Candida dubliniensis; efinaconazole; HWP1 gene; luliconazole; vulvovaginal candidiasis