CHARACTERIZATION OF Candida SPECIES FROM CLINICAL SOURCES IN NAIROBI, KENYA

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ABSTRACT

Candida is a yeast of economic importance as it causes infections of the esophageal, oral, anorectal, vaginal mucosa; eyes, nails as well as life threatening fungemia. They are among emerging opportunistic pathogens especially due to HIV / AIDS. Emerging resistance to commonly used antifungal drugs has further complicated their management resulting in increased morbidity and mortality. The present study analyzed phenotypic and molecular characteristics of Candida strains from clinical sources in Nairobi. Drug susceptibility profiles of all the Candida isolates were also analyzed. A total of one hundred and fifty (150) Candida species isolated since 1997 at Kenya Medical Research Institute (KEMRI), Mycology laboratory were characterized. Preliminary identification was done using germ tube test, CHROMagar Candida, Corn meal agar, and confirmed using Analytical profile index (API 20 C aux). Genotypic analysis was done using primer pairs that span the site of the transposable intron in the 25S rDNA. Antifungal drug susceptibility to Fluconazole, Nystatin, Clotrimazole and Amphotericin B was performed using broth microdilution techniques.

The isolates were recovered from swabs 37.3 %, urine 33.3 %, sputum 16.7 %, aspirates 8 %, blood 3.3 %, CSF and others 0.7 %. Out of the 150 isolates 86.7 % were Candida albicans whereas 13.3 % were non albicans Candida as confirmed by API 20 C aux. Non albicans Candida included; C. parapsilosis 4 %, C. tropicalis 2.7 %, C. krusei 2.7 %, C. guilliemondii 1.3 %, C. glabrata 1.3 % and C. famata 1.3 %. Germ tube positive C. albicans were 96.1 % whereas only 3.8 % were germ tube negative. All the 130 isolates identified as C. albicans formed chlamydospores and all grew at both 37 °C and 45 °C ruling out the possibility of Candida dubliniensis. Genotypic analysis indicated that most of the C. albicans were genotype A (60 %) with one band of 450 base pairs followed by genotype C (16 %) with two bands of 450
and 650 base pairs and B (8 %) with 1 band of 650 base pairs. In this study 4 % of the C. albicans isolates were categorized as genotype F that had one band of 550 base pairs. The isolates were fairly susceptible to commonly used antifungal drugs. C. albicans susceptibility to Fluconazole (MIC ≤ 8 µg/ml) was 73.1 %, susceptible dose-dependent (MIC 16-32 µg / ml) 14.6 % and resistant (MIC ≥ 64 µg / ml) 12.3 %. The MIC$_{50}$ and MIC$_{90}$ to Fluconazole were 1 µg / ml and 64 µg / ml respectively. At 1 µg / ml of Amphotericin B, most of the isolates were inhibited with 90.3 % having an MIC of ≤ 1 µg / ml. The MIC$_{50}$ and MIC$_{90}$ to Amphotericin B were 0.25 µg / ml and 1.0 µg / ml respectively. Elevated MIC ≥ 4 µg / ml to Clotrimazole and Nystatin were demonstrated in 80.5 % and 90.5 % respectively. The MIC$_{50}$ and MIC$_{90}$ of Clotrimazole and Nystatin were 1.0 µg / ml, 0.29 µg / ml and 16 µg / ml, 18.5 µg / ml respectively. The rest (20) non-albicans Candida were fairly susceptible to all the four drugs with reduced susceptibility reported on very few isolates. From the study C. albicans was the most prevalent and hence the most common cause of candidiasis. The result has demonstrated some evidence of emerging resistance to commonly used antifungal drugs. For management of Candida infection, there is need to identify all the yeast from clinical sources as some have intrinsic resistance to commonly used antifungal drugs. There is also need to constantly carry out in-vitro antifungal susceptibility testing in order to establish any emerging resistance. This is essential in the management of Candida infections especially in HIV / AIDS where recurrent candidiasis is common.