VOLUME - 15, ISSUE - 06, JUNE - 2026 • PRINT ISSN No. 2277 - 8160 • DOI : 10.36106/gjra

Original Research Paper

Microbiology

ANTIFUNGAL PROFILE OF CANDIDA SPECIES ISOLATED FROM BLOODSTREAM INFECTIONS

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KEYWORDS :

In 2022, the World Health Organization (WHO) released the first fungal priority pathogen list, categorizing Candida albicans and C. auris as critical priority pathogens, and N. glabrata, C. tropicalis, and C. parapsilosis as high-priority, and P. kudriavzevii as medium-priority [1]. Candida species are still one of the most significant pathogens in causing nosocomial fungal infections, especially in immuno-compromised patients, in patients who are critically ill in the intensive care unit setting, diabetics and in patients who have been on a long period of antimicrobial or immunosuppressive therapy [2,3]. Vulnerable patients have a high risk for invasive infections such as candidemia because they can colonize and adapt to a variety of host environments.

Many studies have reported that an epidemiological shift observed all over the world involves the emergence of non-albicans Candida (NAC) species instead of the previously repotred Candida albicans, and that the occurrence of antifungal resistance to these pathogens has also risen [2,4]. Some of these NAC are intrinsically resistant to antifungals, such as the fluconazole resistance in Pichia kudriavzevii, as well as multi drug resistance in emerging pathogens like Candida auris for which periodic epidemiological surveillance is of paramount importance [3,5]. As species distribution as well as susceptibility profile varies in different geographical regions, the present study was carried out to elucidate the distribution of species and antifungal susceptibility pattern of Candida isolates in our tertiary care centre.

One hundred nonduplicate Candida isolates obtained from blood culture samples were initially studied. Conventional methods were used and combined with the VITEK 2 Compact system (bioMérieux), for preliminary identification. Data on final species identification by Matrix assisted laser desorption ionisation- time of flight- mass spectrometry (MALDI-TOF MS) was available for 90 isolates and included in the antifungal susceptibility testing (AFST).

Candida tropicalis emerged as the most common isolate (27.78%, 25/90), trailed by Candida auris (23.33%, 21/90), Candida parapsilosis (12.22%, 11/90), Nakaseomyces glabrata (7.78%, 7/90), Candida albicans (5.56%, 5/90), Pichia kudriavzevii (5.56%, 5/90), Kodamaea ohmeri (4.44%, 4/90), Candida pelliculosa (4.44%, 4/90), Candida orthopsilosis (3.33%, 3/90), and Candida viswanathii (1.11%, 1/90), with other rare species contributing 4.44%. The percentage of NAC was seen to be overwhelming (94.44) and only 5.56 was C. albicans, which is in line with other Indian and worldwide studies [2,4,6].

Results from AFST showed that fluconazole was the most resistant antifungal, especially present among NAC isolates. The Candida species with the highest levels of fluconazole resistance was C. auris (76.19%) followed by N. glabrata (40%), C. orthopsilosis (33%), C. parapsilosis (27%) and C. tropicalis (20%). However, all C. albicans isolates were susceptible to fluconazole. Flucytosine resistance was observed in C.auris (19.05%) and C.tropicalis (4%). Sporadic resistance was observed to itraconazole, voriconazole and posaconazole, All the isolates were susceptible to amphotericin B, caspofungin, micafungin or anidulafungin.

The high rate of NAC species in our study suggests the changing epidemiology of candidemia as is being noted in India and globally [2,4]. The increase in the proportion of C.auris being isolated is noteworthy as it has been linked to many healthcare-associated outbreaks and multidrug-resistant isolates [5]. The reported high level of fluconazole resistance reported for C. auris is in line with the literature, supporting the necessity for performing routine species identification and susceptibility testing, instead of relying on an empirical therapy with fluconazole [5,7]. C.tropicalis was the most commonly isolated species in our study, owing to its virulent characteristics such as adaptability and biofilm formation which contribute to its increasing association with invasive candidiasis [4,6].

Our study is reassuring because the susceptibility to amphotericin B, echinocandins and newer azoles has remained preserved and may be due to smart fungal stewardship at our hospital, such as judicious use of the drug and avoidance of extensive prophylactic use [3,8]. But, the development of resistance to azoles among multiple NAC species is a concern.

The present study helps provide institute data to guide clinicians for tailored antifungal therapy, in view of global rise in antifungal resistance. It also highlights the vital importance of ongoing monitoring of the distribution of the species and the patterns of antifungal resistance to inform optimal antifungal stewardship and patient outcomes based on local resistance trends.

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