Methods: A total of 324 clinical isolates of *Candida* species were collected. Identification of the clinical samples was determined by culturing on CHROMagar, carbohydrate assimilation and ITS sequencing methods. Antifungal susceptibility was tested using the 2-fold serial microdilution method. The ER111 genes of 42 isolates of *C. albicans* were amplified and sequenced. Results: Of the 324 isolates collected, 45.71% (145 isolates) were *C. albicans*. ER111 gene was sequenced in 42 isolates. In total, 14 missense mutations were detected in ER111 gene from 42 isolates. Among them, 4M8A and F95A substitutions were most prevalent and were known to cause fluconazole resistance.

Conclusions: A total of 14 mutations in the ER111 gene were identified in *azole-resistant* *C. albicans isolates, which indicated a possible resistance mechanism inazole resistance to azole drugs and the occurrence of *Candida* species. Finding more mutations and relevance studies require a higher number of samples.

1. **To determine the prevalence of *Candida* among all blood positive culture.
2. Isolates profiling or speciation of *Candida* sp.
3. Antifungal susceptibility testing of the *Candida* isolates.

Methods: Autamatic blood culture bottles (BD BACTEC 912) that flagged positive were taken up for azole staining. Those bottles which showed positive-blooding yeast growth with or without pseudohyphae were selected as the study isolates for *Candida* species. All such bloods were subcultured on Sabouraud’s dextrose agar and incubated aerobically at 37°C for 2-5 days. Crema, parent, white-coloured cultivations of *Candida* were further taken up for identification by gram tube testing, CHROMagar, and VITEK-MS.

Antifungal susceptibility testing was performed for all isolates by VITEK 2 against fluconazole, caspofungin, voriconazole, miconazole, flucytosine, and amphotericin B.

Results: The study population comprised 9, 2015 January 31, 2022, the microbiology laboratory received a total of 10 914 automated blood culture bottles, of which, overall, 1015 flagged positive. Blood bags were sent in 92 bottles. The prevalence of *Candida* was found to be 1.49%. Blood bags made up 8.75% of all positive blood cultures. Conventional and automated identification methods showed that the majority of *Candida* was *C. albicans* (84.87%). ER111. *Candida* tropicalis (45.43%) was the most common species overall, followed by *C. parapsilosis* (17.37%), *C. albicans* (14.15%), *C. guillermondii* (5.34%), *C. glabrata* (5.34%), and *C. krusei* (4.34%). Two isolates each of *C. krusei*, *C. albicans*, and *C. lusitaniae* were obtained.

The antifungal susceptibility testing results for the common species *C. tropicalis showed susceptibility of 90% against *C. albicans* showed 44% for anticandidal drugs, and 47.7% against amphotericin B. *C. albicans* showed 100% susceptibility to *Candida* species. Although the complete antifungal testing is not mentioned in the study, we can assume the prevalence and the susceptibility pattern of *Candida* isolates were determined. The study findings reflect a low prevalence of candidiasis, indicating adequate antifungal and antifungal stewardship practices at Jodhpur.

Objective: To determine the species distribution, compare *Candida* albicans and non-*C. albicans* candidiasis, determine indicators and antifungal susceptibility pattern of candidiasis cases in adult patients at a tertiary care hospital, New Delhi, India.

Methods and Materials: *Candida* species identification was performed by phenotypic methods, VITEK (Biomérieux, France), and DNA sequencing (PGMY-chip, SGD). The antifungal susceptibility was performed by broth microdilution method as per CLSI M27-A4 guidelines 2017.

Results: Out of 1524 blood samples, 70% samples were found to be positive. Of the 1015 flagged positive, 13.2% were *C. albicans* candidiasis patients, 12.65% *C. glabrata* and 9.7% were non-*C. albicans* candidiasis (87.4%, 10.7%) was isolated in this study. In *C. albicans* candidiasis, *C. tropicalis* (28.77%, 270) was the predominant *Candida* species followed by *C. parapsilosis* (11.86%, 109) and *C. glabrata* (14.28, 107). Rare species among *Candida* spp, included *C. auris* and *C. lusitaniae*. *C. lusitaniae* and *C. auris* were isolated. The most common predisposing factor for *C. albicans* and non-*C. albicans* candidiasis was urinary catheter (72.85%, 1070) followed by an increased period of hospitalization (42.82%, 308), diabetes mellitus (12.13, 1570), and the most significant associated risk factor associated with *C. albicans* was diabetes mellitus (P < 0.05). The overall resistance was 22.77% to all antifungal drugs. The multidrug resistance (MDR) was noted in 71.7% of isolates.

Conclusions: Early identification of risk factors for candidiasis, prompt management and timely management are crucial for the outcome of candidiasis cases. Non-albicans species were predominant over *C. albicans* depicting the change in the epidemiology and emergence of MDR *Candida* spp, like *C. auris*, *C. glabrata*, *C. parapsilosis*, *C. lusitaniae*, and *Pichia kudriavzevii* ( *C. krusei*). This warrants the need for antifungal susceptibility profiling (ASP) and dose management for *Candida* spp. Accurate species identification, and their antifungal susceptibility is crucial for overall patient management.