



Candida Bloodstream Infection and Antifungal Susceptibility Over Three Years in a Single Center from Medinah, Saudi Arabia

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Authors' contributions

This work was carried out in collaboration among all authors. Authors listed have made a substantial, direct and intellectual contribution to the work and approved it for publication.

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ABSTRACT

In the healthcare setting, *Candida* bloodstream infections significantly increase morbidity and mortality. There is little proof that invasive infections in Saudi Arabia are brought on by *Candida* spp. To identify *Candida* species that cause bloodstream infections and ascertain the clinical outcome and risk factors for mortality in a Saudi Arabian tertiary hospital. This retrospective analysis covered all instances in which patients hospitalized to Ohud hospital, a tertiary care facility in Madinah, Saudi Arabia, between January 2019 and December 2021, had positive blood cultures for *Candida*. Anaerobic and aerobic Bactec bottles were inoculated with blood samples and then incubated at 35°C for five days. Identification-YST card kits from VITEK II (BioMerieux, France) for yeast and yeast-like organisms. Testing for antifungal susceptibility was done using AST YS07. A

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total of 78 patients (71% men, 29% women) were found to have candidemia. *Candida albicans* (51.3%), *Candida parapsilosis* (16.7%), and *Candida tropicalis* (16.7%) were the three *Candida* spp. that were most frequently isolated. Those with Saudi (51%; P = 0.500), leukopenia (40%; P = 0.001), neutrophilia (92%; P = 0.638), and thrombocytopenia (42%; P = 0.374) had a higher incidence of candidemia. Fluconazole sensitivity in non-*albicans Candida* species was 39.5%. Nonetheless, caspofungin was effective against all species. This study discovered an epidemiological shift toward more non-*albicans Candida* spp. in Saudi Arabia as well as a changing pattern in the *Candida* spp. causing bloodstream infections.

Keywords: *Candidemia*; *Candida albicans*; *candida non-albicans*; *antifungal*; *echinocandins*.

1. INTRODUCTION

Although *Candida* spp. is a normal component of human skin and mucosa, reports of it as a pathogen have increased as a result of risk factors like excessive use of a wide range of antibiotics, prolonged hospital stays, organ transplantation, HIV infection, underlying malignant diseases, and exposure to invasive procedures [1,2]. One of the pillars of goal-directed sepsis management is early infection control with the right administration of antibiotics, as the survival rate of untreated sepsis patients drops by the hour [3].

Bloodstream infections (BSIs) and disseminated candidiasis are just two of the many illnesses that *Candida* spp. can cause. Despite improvements in the identification and management of candidiasis, *Candida* ranks fourth in the United States and seventh in Europe among the infections responsible for BSI [3,4]. Only a few studies from India have documented candidemia rates (6–18%) and an increase in the isolation of *non-albicans Candida* from BSIs [5-8].

A recent study found that 7.5% of ICU patients taking antifungal medication also had a candidemia incidence rate of 6.9 per 1000 patients in the critical care unit (ICU) [9,10]. Nosocomial candidiasis is linked to a crude mortality rate of over 60%, while the attributable mortality rate may be as high as 49% [11,12]. Despite these findings, there are still many unresolved issues surrounding the treatment of candidiasis.

Azole, allylamine, polyene, and echinocandin are the only antifungal medications approved to treat systemic and invasive candidiasis. Healthcare providers should be extremely concerned about the dramatic rise in *Candida* spp. resistance to antifungal treatment over the past few decades.

Clinical management solutions for this issue can be determined with the use of research on infection prevalence and antifungal susceptibility testing. Our goals were to identify the *Candida* spp. that cause bloodstream infections and to look into the antifungal susceptibility patterns of these species.

2. MATERIALS AND METHODS

2.1 Patients

This retrospective, observational study was carried out from January 2019 to December 2021 in the Ohud hospital's microbiology lab in Madinah, Saudi Arabia. Prior to the study, permission from the ethics committee was obtained (IRB 22-070). Only 78 *Candida* spp. were recovered from blood cultures out of a total of 1256 positive blood cultures. Hospitalized patients with a fever (>37°C), a respiratory rate (>20 breaths/minute), and a white blood count (WBC) of more than 12,000/mm³ or less than 4000/mm³ were all required for the study. Patient demographic data, such as age, nationality, and gender.

2.2 Sample Collection

2.2.1 Isolation and identification of *Candida*

The automated blood culture system Bactec FX (Becton Dickinson, Sparks, MD) was used to collect clinical isolates of *Candida* spp. from blood cultures. Anaerobic and aerobic (adult patient) and neonate and pediatric (only one bottle) Bactec bottles were inoculated with blood samples and then incubated at 35°C for five days. If positive blood culture bottle was prepared Gram-stained and afterward, subcultures sabouraud dextrose agar (SDA) were created. Standard SDA culture were used to identify yeast isolates from positive bottles [5].

2.2.2 Antifungal susceptibility testing

Identification-YST card kits from VITEK II (BioMerieux, France) for yeast and yeast-like organisms. Testing for antifungal susceptibility was done on VITEK II using AST YS07 Kits. The Clinical and Laboratory Standards Institute approach was used to establish minimum inhibitory concentrations and resistance rates. Control organisms included *C. albicans* (ATCC 1023), *C. tropicalis* (ATCC 13803), and *C. glabrata* (ATCC 2001). Guidelines from the Clinical and Laboratory Standards Institute (CLSI) were used to interpret the data [13].

2.3 Data Analysis

The statistical analysis was carried out using the statistical package for the social sciences (SPSS) version 24.0 software from SPSS Inc. in Chicago, Illinois, USA. All nominal variables, including demographic information, were calculated as frequencies and percentages. We used the Chi-square test χ^2 and Fisher's exact test to compare the *C. albicans* and *Candida non-albicans* groups on all nominal variables. Results with a p-value less than 0.05 ($P < 0.05$) will be considered significant.

3. RESULTS

Ages of the patients ranged from one year to 72 years. both cases *Candida albicans* and non-albicans patients older than 60 had the highest frequency of *Candida*-positive cultures in both the *C. albicans* and non-albicans groups, followed by patients between the ages of 41 and 50 and those aged 1 to 10, while patients between the ages of 11 and 20 had the lowest frequency of *Candida*-positive samples. Only the age group older than 60 years ($P=0.026$) had

significant differences according to statistical analysis (Chi-square test and Fisher's exact test) (Table 1).

Of the 40 patients with *C. albicans* isolates, 14 (or 35%) were female and 26 (or 65%) were male. Although 29 (76.3%) of the patients with non-albicans *Candida* isolates were men and 9 (23.7%) were women. In addition, the risk variables for positive candidemia mentioned in Table 2 were examined. Blood culture positives for the *C. albicans* group and the *Candida non-albicans* group were found in 40 and 38 specimens, respectively (Table 2). These results show that white blood cells from patients with *C. albicans* are more likely to be *Candida* positive in cultures than from patients with *Candida non-albicans*; and that this difference is statistically significant ($P=0.001$) The incidence of *Candida*-positive cultures was also greater (72–92%) among neutrophilic individuals than neutropenic individuals (6–8%), however, this difference was not statistically significant ($P=0.638$). The incidence of *Candida* blood culture-positive bacterial infection and platelet count (27.52% versus 21.24%, $P=0.146$) did not differ significantly, as reported in Table 2.

On both blood agar and Sabouraud dextrose agar, all 78 *Candida* spp. that tested positive for the presence of *Candida* spp. by microscopy and culture were taken into consideration. *Candida non-albicans* were present in 38 (48.7%) of the 78 samples, of which *C. albicans* was recovered from 40 (51.3%). The remaining *Candida non-albicans* isolates are shown in Table 3, with the highest frequency being shared by *Candida parapsilosis* 13 (16.7%) and *Candida tropicalis* 13 (16.7%), followed by *Candida glabrata* 3 (3.8%).

Table 1. Shows the prevalence of *Candida* species other than *C. albicans* in various age groups

	Total number (n = 78)	Percent	<i>C. albicans</i> (n = 40)	non-albicans <i>Candida</i> species (n = 38)	p-value
1-10 years	11	14.1 %	5 (12.5 %)	6 (15.8 %)	0.677
11-20 years	1	1.3 %	1 (2.5 %)	0 (0 %)	0.513
21-30 years	2	2.6 %	0 (0 %)	2 (5.3 %)	0.234
31-40 years	5	6.4 %	2 (5 %)	3 (7.9 %)	0.475
41-50 years	11	14.1 %	5 (12.5 %)	6 (15.8 %)	0.677
51-60 years	10	12.8 %	3 (7.5 %)	7 (18.4 %)	0.135
>61 years	38	48.7 %	24 (60.0 %)	14 (36.8 %)	0.041
Total	78	100 %	40 (100 %)	38 (100 %)	

Table 2. Association of various candidemia risk factors

Risk factor	<i>C. albicans</i> (n = 40)	non-albicans <i>Candida</i> species (n = 38)	p-value
Gender			
Male	26 (65 %)	29 (76.3 %)	0.273
Female	14 (35 %)	9 (23.7 %)	
Nationality			
Saudi	22 (55 %)	18 (47.4 %)	0.500
Non-saudi	18 (45 %)	20 (52.6 %)	
WBCs			
<3000/mm	2 (5 %)	5 (13.2 %)	0.001
3000-5000/mm	25 (62.5 %)	5 (13.2 %)	
1500/mm	13 (32.5 %)	18 (47.4 %)	
Neutrophil			
<1500 cells/mm	3 (7.5 %)	3 (7.9 %)	0.638
>1500 cells/mm	37 (92.5 %)	35 (92.1 %)	
Bacterial infection			
Positive	25 (62.5 %)	14 (36.8 %)	0.305
Negative	15 (37.5 %)	14 (36.8 %)	
Platelet			
<20000	3 (7.5 %)	3 (7.9 %)	0.374
20000-100000	11 (27.5 %)	16 (42.1 %)	
>100000	26 (65 %)	19 (50.0 %)	

Table 3. The frequency (%) of isolated *Candida* spp. according to Vitak II's identification

<i>Candida</i> spp.	Total number (78)	Percent
<i>C. albicans</i>	40	51.3 %
<i>C. glabrata</i>	3	3.8 %
<i>C. parapsilosis</i>	13	16.7 %
<i>C. auris</i>	6	7.7 %
<i>C. tropicalis</i>	13	16.7 %
<i>C. krusei</i>	1	1.3 %
<i>C. famata</i>	2	2.6 %
Total	78	100 %

Table 4. Gram stain method and direct method sensitivity, specificity, and positive predictive value of direct blood culture investigation

Types of test	sensitivity	Specificity	Positive predictive value
Direct method	97.4 % (76/78)	100 %	76 (100 %)
Gram stain	98.7 % (77/78)	100 %	77 (100 %)

Table 5. Shows the microorganisms found using the direct gram stain microscopic method

Organisms	Direct examination (78)	Percent
<i>Candida</i> only	29	37.2 %
<i>Candida</i> with bacteria (gram-positive)	31	39.7 %
<i>Candida</i> with bacteria (gram-negative)	18	23.1 %

As shown in Table 5, Gram stain examination of 78 blood cultures revealed *Candida* only form in 29 (37.2%), *Candida* with bacteria Gram positive in 31 (39.7%), and *Candida* with bacteria Gram negative in 18 specimens (23.1%), with no special observations.

Candida spp. susceptibility pattern to fluconazole (FLU), voriconazole (VOR), flucytosine (5FC), amphotericin B (AMP), micafungin (MIC), and caspofungin is shown in Table 6. (CAS). Fluconazole resistance was found in 7.5% of all *C. albicans*. *C. albicans* was found to be completely sensitive to VOR, 5FC, AMP, MIC, and CAS.

Table 6. Compares *C. albicans* and *Candida non-albicans* susceptibilities to fluconazole, voriconazole, flucytosine, amphotericin B, micafungin, and caspofungin

Antifungals	Susceptibility patterns	<i>C. albicans</i> (n = 40)	non-albicans <i>Candida</i> species (n = 38)	p-value
Fluconazole	S	37 (92.5 %)	23 (60.5 %)	0.001
	I	0 (0 %)	0 (0 %)	
	R	3 (7.5 %)	15 (39.5 %)	
Voriconazole	S	40 (100 %)	33 (86.8 %)	0.024
	I	0 (0 %)	0 (0 %)	
	R	0 (0 %)	5 (13.2 %)	
Flucytosine	S	40 (100 %)	32 (84.2 %)	0.011
	I	0 (0 %)	0 (0 %)	
	R	0 (0 %)	6 (15.8 %)	
Amphotericin B	S	40 (100 %)	34 (89.5 %)	0.052
	I	0 (0 %)	0 (0 %)	
	R	0 (0 %)	4 (10.5 %)	
Micafungin	S	40 (100 %)	37 (97.4 %)	0.487
	I	0 (0 %)	0 (0 %)	
	R	0 (0 %)	1 (2.6 %)	
Caspofungin	S	40 (100 %)	38 (100 %)	0.999
	I	0 (0 %)	0 (0 %)	
	R	0 (0 %)	0 (0 %)	

S, susceptible; I, intermediate; R, resistant

Resistance to FLU, VOR, 5FC, AMP, MIC, and was found in 39.5%, 13.2%, 15.8%, 10.5%, and 2.6% of *Candida non-albicans* cases, respectively. *C. albicans* had the highest number of sensitive cases to FLU, which is statistically significant (P=0.001), whereas *Candida non-albicans* spp. have 100% sensitivity to caspofungin, which may help healthcare professionals treat *Candida* infections caused by *Candida non-albicans* in the near future.

4. DISCUSSION AND CONCLUSION

The sixth most prevalent isolated microbial genere at Ohud hospital was *Candida*. According to Sheevani et al. [14], *C. albicans* is the sixth most common cause of nosocomial infections. Age, gender, country, and laboratory tests (Tables 1 and 2) that determined which patients were infected were the variables taken into account in this study. Patients aged > 60 and under 1 year old frequently experienced it. Accept the findings of other researchers despite blood cultures demonstrating *Candida* infection [15]. According to the study by Furnaleto et al. [16], it was generally found that ICU patients, elderly people, and people under one year old were more likely to get a *Candida* spp. infection. Our study's age and gender distribution are consistent with other Saudi Arabian researchers' observations [13,17].

Following *C. albicans* (40, 51.2%), *C. parapsilosis* (13, 16.7%), *C. tropicalis* (13, 16.7%), *C. auris* (6, 7.7%), and other species (6, 7.7%), *C. albicans* was the most frequently isolated species. Thus, 48.7% of non-albicans species were present overall. These results support earlier studies from another researcher [13]. Similar to Saudi Arabia, Italy, and Sir Lanka [15], *C. parapsilosis* and *C. tropicalis* were the second most prevalent species there as well [13].

In our study, *C. albicans* infection is on the rise, despite the fact that it has historically been the primary cause of candidemia worldwide. According to another study, non-albicans *Candida* infections of the bloodstream were more prevalent than those caused by *C. albicans*, particularly in Asia, South Europe, South America, and the Indian subcontinent [18,19,20]. *C. parapsilosis* and *C. tropicalis* are non-albicans that account for 33.4% of instances of candidemia in those over 60 and in newborns. It was prevalent in our study among newborns, where the prevalence was comparable to that of *C. albicans*.

Also prevalent in the ICU were *C. parapsilosis* cases in both children and adults. Neoplastic patients and adults both frequent contract *C. tropicalis* [21]. Similar to that, it was kept separate from patients with malignancies in our study. Contrarily, patients with leukemia and

those who are neutropenic are more likely to contract *C. tropicalis* [21]. After *C. albicans*, *C. tropicalis* was more prevalent in our study among neutropenic individuals. *C. parapsilosis* is a prevalent pathogen in catheter-related infections and has the potential to produce epidemics since it colonizes the skin.

Particularly concerning is the high prevalence of antifungal resistance among clinical isolates of *Candida* that are non-albicans. Fluconazole resistance was present in all strains of non-albicans *Candida* generating candidemia in our cohort (39.5%), while amphotericin B resistance was virtually 2.6%. Since none of the isolates exhibited caspofungin resistance from the outset, it is clear that this class of antifungals is frequently still a viable option for treating invasive *C. glabrata* and *C. auris* infections. However, our discovery of an instance of emerging caspofungin resistance is concerning and should spur additional studies to prevent jeopardizing viable treatment choices for this potentially multidrug-resistant yeast.

The majority of the discovered resistant strains, according to Saha et al. [22] study, are non-albicans, highlighting their greatest propensity to develop fluconazole resistance for all *Candida* isolates despite their high amphotericin B susceptibility, which is consistent with our findings. Caspofungin has a 100% sensitivity pattern to non-albicans spp. in the current investigation, which may be helpful for medical professionals to treat the *Candida* infection brought on by non-albicans *Candida*. The primary factor leading to non-albicans *Candida* dominance over *C. albicans* is the widespread use of fluconazole in a variety of clinical situations (Kothavade et al., 2010).

According to Kothavade et al. [23] findings, all yeast isolates were susceptible to caspofungin, and there was no discernible difference in susceptibility between *C. albicans* and non-albicans species.

DATA AVAILABILITY

All datasets generated or analyzed during this study are included in the manuscript.

CONSENT

As per international standard or university standard, patient(s) written consent has been collected and preserved by the author(s).

ETHICS APPROVAL

This study was approved by the Institutional Review Board of the General Directorate of Health Affairs in Madina, KSA, with reference number IRB-22-070.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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