



Prevalence, Distribution, and Antifungal Susceptibility Patterns of Yeast Isolates at the Nairobi South Hospital

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DOI: <https://dx.doi.org/10.4314/ajhs.v37i4.7>

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Abstract

BACKGROUND

Yeast infections significantly impact global morbidity and mortality but remain underdiagnosed and underreported. Treatment failure due to antifungal resistance, particularly in critically ill patients, limits treatment options. The aim of this study was to retrospectively describe the proportion and distribution of yeast isolates recovered from inpatient records at The Nairobi South Hospital over five years and to describe the isolates' antifungal drug susceptibility patterns.

METHODOLOGY

We reviewed inpatient records from 2018 to 2022, focusing on 308 fungal culture records that met the inclusion criteria. Clinical data included age, sex, ward, and year of admission. Laboratory data included sample type, yeast species, and antifungal susceptibility. Identification and antifungal susceptibility testing were performed using VITEK-2, and interpreted as per the Clinical and Laboratory Standards Institute guidelines (CLSI).

RESULTS

Out of 2006 records, 308 (15%) yielded yeast isolates. Distribution was: *Candida albicans* (38%), non-*albicans Candida* (NAC) species (50%), *Cryptococcus* species (10%), and *Trichosporon* species (2%). The yeasts demonstrated reduced susceptibility to all tested antifungal agents. Based on Minimum Inhibitory Concentration (MIC) data and CLSI breakpoints, 90% of the isolates exhibited high MICs and were classified as resistant to amphotericin B, 70% to itraconazole, and 61% to fluconazole. In contrast, 74% and 44% of the isolates had low MICs and were susceptible to flucytosine and voriconazole, respectively.

CONCLUSION AND RECOMMENDATIONS

Candida albicans remained the most common yeast species, although non-*albicans Candida* species are on the rise. Widespread antifungal resistance necessitates tracking yeast profiles and susceptibility patterns for effective patient management.

Keywords: *Candida*, non-*albicans Candida*, *Cryptococcus*, Yeast infections, Antifungal Susceptibility and Resistance

[*Afr. J. Health Sci.* 2024 37 (4):441-452]

Introduction

Fungal infections are a significant and often underestimated global health challenge, with approximately 300 of 5 million fungal species linked to human disease (1). Africa alone faces an estimated 47.6 million annual cases, with

1.7 million severe (2,3), though these figures are likely understated due to diagnostic and data collection limitations (4). In Kenya, yeast infections affect an estimated 7% of the population, although research is insufficient to truly understand the prevalence (5).

The WHO prioritises key yeast pathogens such as *Candida auris*, *C. albicans*, *C. glabrata*, *C. parapsilosis*, and *Cryptococcus neoformans* due to escalating antifungal resistance and high mortality rates (6). *C. auris* is a multidrug-resistant pathogen causing global hospital outbreaks, while *C. neoformans* is a leading cause of meningitis in immunocompromised patients (6–8).

Yeast infections, particularly from *Candida* species, are a major public health concern. Rising morbidity and mortality are exacerbated in sub-Saharan Africa by limited antifungal access and high HIV co-infection rates (9,10). Systematic reviews emphasise the urgent need for revised antifungal therapy guidelines and robust regional surveillance due to significant variations in yeast species prevalence and resistance (9). A global meta-analysis showed *C. parapsilosis* fluconazole resistance at 15.2%, with a concerning rise in Africa from 2016–2022 (10). Many laboratories rely on basic phenotypic approaches, hindering understanding of yeast diversity and underreporting crucial species like multidrug-resistant *C. auris* in Kenya (11). While *C. albicans* causes most human yeast infections, other yeasts like *C. glabrata* and *Cryptococcus* species are gaining clinical interest due to increasing incidence and varied antifungal susceptibility (12).

Antifungal treatments face growing challenges from resistance mechanisms. Azole resistance, driven by mutations and efflux pump overexpression, reduces fluconazole efficacy against *Candida* species (13). Echinocandin resistance in *C. glabrata* and *Trichosporon* is due to FKS gene mutations (14). Polyene resistance such as amphotericin B stems from ergosterol changes and biofilm formation, while flucytosine resistance often requires combination therapies (15).

The limited availability of antifungals complicates management of drug-resistant strains, increasing morbidity and mortality (16).

In Kenya, despite Ministry of Health approval for echinocandins, polyenes, and azoles, rising treatment resistance to traditional antifungals like amphotericin B and fluconazole highlights the need for better options (17). These issues underscore the critical need for improved surveillance, continuous antifungal susceptibility testing, and new treatment strategies (12). This study analysed hospital records from 2018–2022 to determine yeast isolate distribution and antifungal susceptibility at a Kenyan tertiary healthcare facility.

Methodology

Study area, design and population

The study was conducted at The Nairobi South Hospital (TNSH), Kenya. We conducted a retrospective study utilising inpatient records from 2018 to 2022 to describe the prevalence, distribution, and antifungal susceptibility patterns of yeast isolates.

Selection criteria

We selected and anonymised the records of yeast-positive samples from the inpatient files. Records were excluded if they contained microorganisms other than yeast or had missing information. To control for selection bias, we employed proportionate stratification of yeast isolate records per species (5,10).

Sampling technique

Fisher's formula was applied to calculate the sample size for a population of 2006 inpatient records, yielding an initial sample size of 385 for an infinite population, which was adjusted to 323 for the finite population. Of these, 308 yeast isolates met the inclusion criteria and were stratified based on existing literature indicating that *Candida* constitutes 80%, *Cryptococcus* 14%, and *Trichosporon* 6% of isolates (18). This stratification resulted in a final sample of 246 *Candida*, 43 *Cryptococcus*, and 19 *Trichosporon* isolates, ensuring balanced representation while minimising potential bias (18).

Data collection instruments and procedures

Clinical and laboratory data, including age, sex, sample type, admission ward, year of admission, yeast isolated, and antifungal susceptibility, were extracted from the anonymised records of yeast-positive samples using a data abstraction tool.

Microbiological, antifungal drug susceptibility testing and quality assurance

From selected patient records, we obtained microbiological and antifungal susceptibility testing reports. Fungal

identification and susceptibility to five antifungals (amphotericin B, flucytosine, fluconazole, itraconazole, and voriconazole) were performed by the hospital laboratory using the Bio-Mérieux VITEK-2 system and DL-96 cards. For quality control, we used ATCC *C. albicans* 90028, *C. parapsilosis* 22019, and *C. krusei* 6258. MICs were classified (sensitive, intermediate, resistant) following CLSI guidelines (19). For *Trichosporon* species, interpretations relied on CLSI M60 Epidemiological Cut-Off Values (ECVs) since clinical breakpoints aren't available. See Table A1 for full breakpoint details (19).

Table 1

Demographic and Clinical Characteristics of Inpatients with Yeast Isolates at Nairobi South Hospital (2018–2022)

Categories		Overall samples for Culture and Susceptibility n (%)	Patients with yeast isolates (n, % of total isolates)	p-value
Age Distribution (Yrs)	<0-5	25 (1.2)	3 (1.0)	0.87
	6-17	127 (6.3)	15 (4.9)	
	18-64	1454 (72.5)	226 (73.4)	
	>65	400 (19.9)	64 (20.8)	
Sex	Female	1293 (64.5)	196 (63.6)	0.75
	Male	713 (35.5)	112 (36.4)	
Ward Type	Covid-19	168 (8.4)	42 (13.6)	0.04*
	General	1280 (63.8)	126 (40.9)	
	ICU/HDU	315 (15.7)	117 (38.0)	
	Maternity	81 (4.0)	18 (5.8)	
	NICU/Pediatric	162 (8.1)	5 (1.6)	
Sample Type	A&P Fluids	30 (1.5)	20 (6.5)	0.01*
	Blood	419 (20.9)	24 (7.8)	
	CSF	26 (1.3)	9 (2.9)	
	CVC-Tip	156 (7.8)	20 (6.5)	
	Sputum & Tissue	53 (2.6)	24 (7.8)	
	Stool	37 (1.8)	9 (2.9)	
	Urine & UC	1177 (58.7)	175 (56.8)	
	Wound Pus Swab	108 (5.4)	27 (8.8)	
Year	2018	46 (2.3)	6 (1.90)	0.92
	2019	274 (13.7)	37 (12.0)	
	2020	391 (19.5)	51 (16.6)	
	2021	1188 (59.2)	166 (53.9)	
	2022	107 (5.3)	48 (15.6)	
Proportion at 95% CI			15.4% (13.8 – 17.1)	0.01*

Key: Percentage indicates the proportion of total culture and susceptibility records and total yeast isolates. (N=2006, n=308). A&P = Ascitic & Peritoneal, CVC = Central Venous Catheter, CSF = Cerebral Spinal Fluid, UC = Urinary-Catheter, ICU = Intensive Care Unit, HDU = High Dependency Unit, NICU = Neonatal Intensive Care Unit, CI = Confidence Interval. P-values from chi-square tests for categorical data; * indicates statistical significance ($p < 0.05$).

Data and statistical analysis

Demographic and clinical data from inpatients at The Nairobi South Hospital were analysed using Microsoft Excel and IBM SPSS version 26. Descriptive and inferential statistics were used, with chi-square tests applied to normally distributed binary data, and a p-value set at 0.05 for comparisons.

Ethical considerations

The study was approved by the Kenyatta National Hospital-University of Nairobi Ethics Review Committee (P747/09/2022), the National Commission for Science, Technology, and Innovation (NACOSTI/P/23/25973), and The Nairobi South Hospital Administration.

Table 2a

Distribution of Yeast Isolates by Year

Yeast Isolate	2018	2019	2020	2021	2022
Total (%)	1.9	12.0	16.6	53.9	15.6
<i>Candida</i> species	1.9	10.4	14.6	47.8	13.6
<i>C. albicans</i>	0.6	5.2	5.8	20.5	5.5
Non- <i>albicans Candida</i>	1.3	5.2	8.8	27.3	8.1
<i>C. dubliniensis</i>	0.3	2.6	6.8	10.4	3.9
<i>C. glabrata</i>	0.3	1.0	0.0	4.2	1.3
<i>C. guilliermondii</i>	0.0	0.0	0.3	1.3	0.3
<i>C. lusitanae</i>	0.0	0.0	0.3	1.0	0.3
<i>C. parapsilosis</i>	0.0	0.0	0.0	3.6	0.3
<i>C. tropicalis</i>	0.6	1.3	1.0	5.2	1.3
<i>C. krusei</i>	0.0	0.3	0.3	1.6	0.6
<i>Cryptococcus</i> species	0.0	1.6	2.0	4.6	1.6
<i>C. laurentii</i>	0.0	1.6	1.0	3.6	0.6
<i>C. var. neoformans</i>	0.0	0.0	1.0	1.0	1.0
<i>Trichosporon beigeli</i>	0.0	0.0	0.0	1.6	0.3

Key: * Percentage indicates the proportion of the total number of yeast isolate records (n = 308).

Table 2b

Distribution of Yeast Isolates by Age in Years and Sex

	<0-5yrs	6-17 yrs	18-64 yrs	>65 yrs	Female	Male
Total (%)	1.0	4.9	73.4	20.8	63.6	36.4
<i>Candida</i> species	0.6	4.5	65.3	17.9	58.1	30.2
<i>C. albicans</i>	0.0	1.6	27.9	8.1	24.0	13.6
Non- <i>albicans Candida</i>	0.6	2.9	37.4	9.8	34.1	16.6
<i>C. dubliniensis</i>	0.3	1.9	15.9	5.5	16.9	6.8
<i>C. glabrata</i>	0.0	0.0	6.8	0.3	5.5	1.6
<i>C. guilliermondii</i>	0.3	0.3	1.0	0.3	1.3	0.6
<i>C. lusitanae</i>	0.0	0.0	1.3	0.3	1.6	0.0
<i>C. parapsilosis</i>	0.0	0.3	2.6	1.0	1.3	2.6
<i>C. tropicalis</i>	0.0	0.3	7.1	1.9	5.2	4.2
<i>C. krusei</i>	0.0	0.0	2.6	0.3	2.3	0.6
<i>Cryptococcus</i> species	0.3	0.3	7.1	1.9	3.6	6.2
<i>C. laurentii</i>	0.3	0.0	5.1	1.3	2.3	4.5
<i>C. var. neoformans</i>	0.0	0.3	1.9	0.6	1.3	1.6
<i>Trichosporon beigeli</i>	0.0	0.0	1.0	1.0	1.9	0.0

Key: Yrs = Year. Percentages reflect proportions of total yeast isolates (n=308). Non-uniform age groups reflect clinical relevance, ward classifications, and fungal infection susceptibilities.



Authority to access patient records was granted by the hospital, and all data anonymised to protect patient confidentiality. The requirement for written informed consent was waived by the Ethics Review Committee, and access to data restricted to the research team, in line with national guidelines and the Data Protection Act.

Results

Participant characteristics

Of 2006 inpatient records, 308 (15%) yielded yeast isolates, predominantly from the general ward (41%, n=126), urine and urinary-catheter tips (57%, n=175), female patients (64%, n=196), and the 19-45 age group.

Table 2c:

Distribution of Yeast Isolates by Ward

	General	Maternity	NICU/Pediatric	COVID-19	ICU/HDU
Total (%)	40.9	5.8	1.6	13.6	38.0
<i>Candida</i> species	36.4	5.8	1.3	13.0	31.8
<i>C. albicans</i>	17.2	1.6	0.0	4.9	14.0
Non-albicans <i>Candida</i>	19.2	34.2	1.3	8.1	17.8
<i>C. dubliniensis</i>	9.1	2.3	2.7	4.2	7.5
<i>C. glabrata</i>	2.6	1.0	0.0	1.3	2.3
<i>C. guilliermondii</i>	0.6	0.0	0.3	0.0	1.0
<i>C. lusitanae</i>	0.6	0.0	0.3	0.0	1.0
<i>C. parapsilosis</i>	0.0	0.0	1.0	1.0	1.0
<i>C. tropicalis</i>	4.5	1.0	0.0	1.0	4.5
<i>C. krusei</i>	0.6	0.0	0.0	0.3	0.6
<i>Cryptococcus</i> species	0.0	0.0	0.6	4.9	3.9
<i>C. laurentii</i>	0.0	0.0	0.3	3.9	3.9
<i>C. var. neoformans</i>	0.0	0.0	0.3	1.0	1.0
<i>Trichosporon beigeli</i>	0.3	0.0	0.0	1.3	0.3

Key: ICU = Intensive Care Unit, HDU = High Dependency Unit, NICU = Neonatal Intensive Care Unit. Percentages reflect proportions of total yeast isolates (n=308).

Table 2d

Distribution of Yeast Isolates by Sample Type

	Urine & UC	A&P Fluids	Blood	CSF	CVC-Tip	Sputum & Tissue	Stool	Wound-Pus Swab
Total (%)	56.8	6.5	7.8	2.9	6.5	7.8	2.9	8.8
<i>Candida</i> species	52.6	6.2	7.5	0.3	5.8	6.5	2.3	7.1
<i>C. albicans</i>	23.1	4.5	1.9	0.0	2.3	1.3	0.0	4.5
Non-albicans <i>Candida</i>	29.5	1.7	5.6	0.3	3.5	5.2	2.3	2.6
<i>C. dubliniensis</i>	15.0	1.0	1.6	0.0	0.0	2.9	1.6	1.6
<i>C. glabrata</i>	4.5	0.3	1.9	0.0	0.0	0.0	0.0	0.3
<i>C. guilliermondii</i>	0.3	0.0	0.6	0	0.3	0.6	0.0	0.0
<i>C. lusitanae</i>	0.3	0.3	0.3	0.0	0.0	0.0	0.6	0.0
<i>C. parapsilosis</i>	1.9	1.0	0.0	0.3	1.3	0.3	0.0	0.0
<i>C. tropicalis</i>	4.9	0.0	1.0	0.0	1.9	1.0	0.0	0.6
<i>C. krusei</i>	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0
<i>Cryptococcus</i> species	0.0	0.0	2.6	0.0	1.0	0.6	1.0	0.0
<i>C. laurentii</i>	0.0	0.0	0.0	0.0	0.6	0.6	1.6	0.0
<i>C. var. neoformans</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<i>Trichosporon beigeli</i>	0.0	0.3	0.0	0.0	0.0	0.3	0.0	0.0

Key: CVC = Central Venous Catheter, UC = Urinary Catheter, A&P = Ascitic & Peritoneal, CSF = Cerebral Spinal Fluid. Percentages reflect proportions of total yeast isolates (n=308).

Yeast isolation increased significantly from 2018 (2%, n=6) to 2021 (54%, n=166). Key findings include higher yeast isolation rates in COVID-19 wards (14% vs. 8% overall, $p=0.04$), wound pus swabs (9% vs. 5% overall, $p=0.03$), and 2022 (16% vs. 5% overall, $p=0.01$), indicating higher prevalence in these specific contexts. Other demographic or sample types showed no significant differences (Table 1).

Distribution of yeast isolates by year, age group, sex, admission ward, and sample type

In 2021, yeast isolates peaked at 54%, primarily *Candida* species (48%). Both *C. albicans* and non-*albicans Candida* (NAC) also peaked before declining in 2022. *Cryptococcus* and *Trichosporon beigelii* showed brief increases, with *Cryptococcus* peaking in 2021. Yeast isolates were most common in individuals aged 19-64 years (73%) and females (64%). Prevalence was highest in the general ward (41%) and ICU/HDU (38%).

Cryptococcus was mainly isolated in COVID-19 wards (5%) and ICU/HDU (4%), while *T. beigelii* was rare (1%). Urine and urinary-catheter samples were the primary

sources (57%) of isolates. *Candida* species accounted for 88% of isolates, with NAC species comprising 50% (*C. dubliniensis* being most frequent). *Cryptococcus laurentii* was detected in urine/urinary-catheter samples (4%), while *C. var. neoformans* predominated in cerebrospinal fluid (CSF) samples (3%) (Table 2a-d).

Antifungal susceptibility pattern of yeast isolates

C. albicans, the most common isolate, showed variable resistance, particularly to fluconazole and itraconazole. Notably, *C. dubliniensis* and *C. glabrata* exhibited high MICs to amphotericin B (modal MIC = 4 $\mu\text{g/ml}$). *Cryptococcus* species also displayed high amphotericin B MICs but had low MICs to azoles and flucytosine. *C. krusei* generally had high MICs across antifungal agents, while *Trichosporon beigelii* mostly had low MICs except for amphotericin B. Overall, amphotericin B showed the highest MICs (≥ 4 $\mu\text{g/ml}$), and flucytosine the lowest (0.060 $\mu\text{g/ml}$) (Table 3). Each yeast species showed distinct sensitivity patterns to the five antifungal drugs, with overall widespread resistance.

Table 3

Summary Minimum Inhibitory Concentrations (MIC) of the Yeast Species Identified

Yeast Species	Total n (%)	Amphotericin B ($\mu\text{g/ml}$)	Flucytosine ($\mu\text{g/ml}$)	Fluconazole ($\mu\text{g/ml}$)	Itraconazole ($\mu\text{g/ml}$)	Voriconazole ($\mu\text{g/ml}$)
<i>C. albicans</i>	116 (37.7)	0.500-4.000	0.060-16.000	0.250- 64.000	0.060-4.000	0.030-8.000
<i>C. glabrata</i>	21 (6.8)	4.000	0.060-16.000	0.250- 64.000	0.030-8.000	0.030-0.500
<i>C. guilliermondii</i>	6 (1.9)	2.000-4.000	0.250-64.000	0.250- 64.000	4.000	8.000
<i>C. tropicalis</i>	29 (9.4)	0.500-4.000	0.060-64.000	0.125- 64.000	0.030-4.000	0.030-8.000
<i>C. dubliniensis</i>	74 (24.0)	0.250-4.000	0.060-16.000	0.250- 64.000	0.060-4.000	0.030-0.500
<i>C. krusei</i>	9 (2.9)	4.000	0.060-16.000	4.000- 64.000	4.000-4.000	8.000
<i>C. lusitanae</i>	5 (1.6)	4.000	0.125	4.000	4.000	8.000
<i>C. parapsilosis</i>	12 (3.9)	4.000	0.060	4.000-64.000	0.030-4.000	0.030
<i>C. laurentii</i>	21 (6.8)	4.000	0.060-0.500	4.000-64.000	0.250-4.000	0.250-8.000
<i>C. var. neoformans</i>	9 (2.9)	4.000	0.250-8.000	4.000-64.000	0.250-4.000	0.250-8.000
<i>Trichosporon beigelii</i>	6 (1.9)	4.000	0.125	4.000-64.000	4.000	8.000
Modal MIC for each yeast species to antifungals	308(100.0)	4.000	0.060	64.000	4.000	8.000

Key: *Percentage indicates the proportion of total number of yeast isolates records (n =308)

C. albicans had the highest resistance to amphotericin B and also exhibited significant sensitivity. Among *NAC* species, *C. dubliniensis* was the most sensitive (32%). Yeast species resistance was notable to amphotericin B (25%), itraconazole (17%), and fluconazole (20%). All *C. lusitaniae* and *C. krusei* isolates were resistant to amphotericin B, with *C. krusei* also showing 2% resistance to fluconazole. *C. tropicalis* showed the highest fluconazole resistance (7%) among the *NAC* species (Figure 1, a-f).

Discussion

We identified various yeast isolates, including *Candida*, *Cryptococcus*, and *Trichosporon* species, from patient samples. Yeast infections, especially *Candida*, are increasingly prevalent in hospitalised, immunocompromised patients or those on extended antibiotic and antifungal treatments. Our findings align with global trends showing rising *Candida* incidence due to increased hospital admissions, immunosuppressive therapies, and prolonged hospital stays, including during COVID-19. The threefold increase in

yeast isolates during the study period echoes other studies noting a growing burden of fungal infections in hospitals, especially during the pandemic period (20). A notable trend was the rising prevalence of non-*albicans Candida* (*NAC*) species such as *C. glabrata*, *C. tropicalis*, *C. parapsilosis*. This global shift from *C. albicans* to *NAC* species is well-documented, often linked to their resistance to common antifungals, especially azoles like fluconazole (21). Our finding of half of *Candida* isolates were *NAC* species, including *C. glabrata*, reflects this broader global trend (5,8). The increasing dominance of fluconazole-resistant *C. glabrata* highlights the challenge of managing *Candida* infections in hospitalised, critically ill patients requiring long-term treatment.

This study reveals critical antifungal resistance, particularly to amphotericin B. Almost all yeast isolates, particularly *C. albicans*, displayed reduced susceptibility and the highest MICs to this last-line treatment. This finding contradicts previous reports of high susceptibility (18), posing a significant challenge for empiric and targeted therapies.

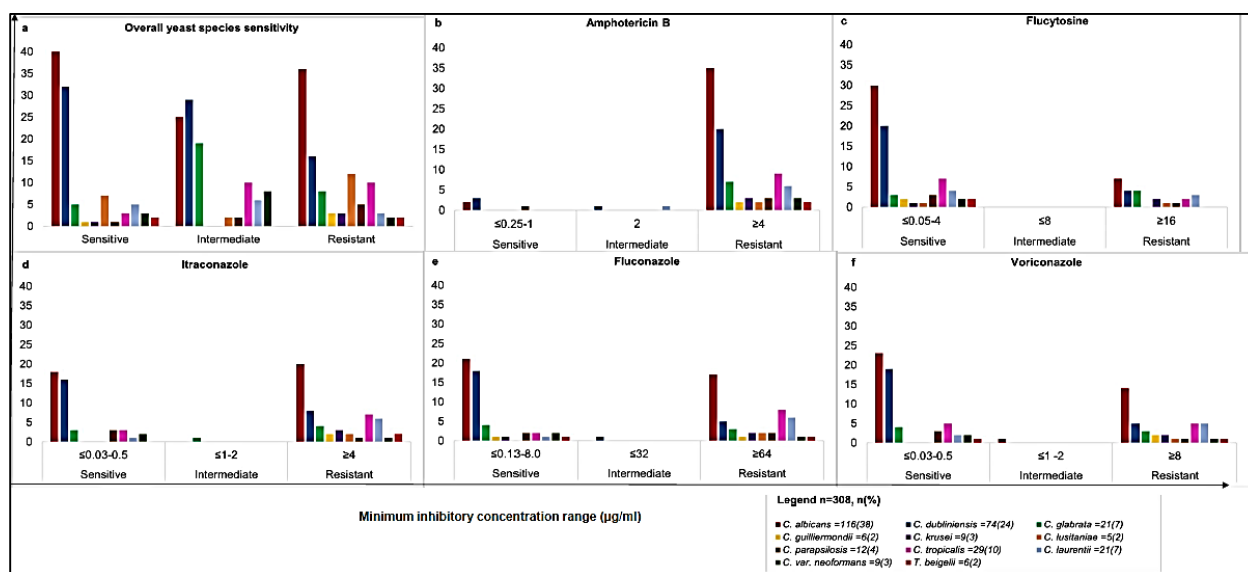


Figure 1:
Antifungal Susceptibility Patterns of Yeast Species (n=308)

Understanding underlying resistance mechanisms and optimizing dosing strategies are crucial for clinical success (28). Such high resistance poses a major challenge for empiric and targeted treatment, potentially leading to poorer patient outcomes if local susceptibility data isn't considered. Beyond *in vitro* susceptibility, understanding pharmacokinetics and pharmacodynamics (PK/PD) is crucial; optimal dosing strategies to achieve effective drug concentrations are vital for resistant isolates to ensure clinical success while minimising toxicity (22). Resistance mechanisms, including altered drug uptake and efflux, may explain this phenomenon; these need to be explored. Notably, *Trichosporon* species, particularly *T. beigelii*, also demonstrated amphotericin B resistance (23).

Conversely, isolates showed high susceptibility to flucytosine, aligning with its known synergistic effect in combination therapies (24). However, flucytosine carries significant toxicity risks, including bone marrow suppression, hepatotoxicity, and gastrointestinal side effects. This necessitates careful therapeutic drug monitoring, especially in renally impaired patients, to ensure efficacy while minimising adverse events (25). The reduced susceptibility of *C. glabrata* and *C. krusei* to flucytosine, as observed in this study, further emphasises the need for tailored antifungal therapies and more comprehensive resistance monitoring, while always considering the drug's potential for adverse effects. The widespread resistance observed in this study, especially to amphotericin B, underscores the need for exploring combination antifungal therapy for resistant infections. While our study focuses on single-agent susceptibility, combination strategies, such as fluconazole-echinocandin or amphotericin B-flucytosine, are increasingly employed to achieve synergistic effects, broaden coverage, and potentially mitigate resistance development in severe or resistant candidiasis, even if

randomised clinical trials are still limited (24). The findings from this study highlight the importance of antifungal stewardship programs, particularly in inpatient settings like The Nairobi South Hospital, to ensure the appropriate use of antifungal agents and minimise the emergence of resistance.

Demographic factors like age and gender influence yeast infection prevalence. Consistent with prior research, women of reproductive age were more affected, possibly due to hormonal changes and vaginal flora changes (26). Older adults with comorbidities like diabetes and HIV were also disproportionately affected (20,27). The immunocompromised status of patients, particularly those in ICU/HDU or with HIV and diabetes, significantly drives the prevalence of resistant strains, necessitating tailored antifungal regimens (20).

Beyond *Candida* species, this study identified rare fungi like *Cryptococcus* and *Trichosporon* species, highlighting the growing concern over opportunistic fungal infections (5). We isolated the rare non-*neoformans* species *C. laurentii*, an emerging nosocomial pathogen, in critically ill patients (5,28). The isolation of *Trichosporon* species, particularly *T. beigelii*, from ICU and central venous catheter samples is noteworthy due to their intrinsic resistance to common antifungals (23).

Our study had limitations, primarily distinguishing between yeast colonisation and true infection, especially in non-sterile samples like urine, urinary catheters, and sputum. Urine and catheter samples were the main source of yeast isolates, predominantly *Candida* species. Nosocomial infections, often linked to prolonged hospital stays and biofilm formation on medical devices (e.g., urinary catheters), are a known source of resistant yeast infections (29). The high isolation rate from urinary catheters highlights the need to consider biofilm formation, as yeasts within biofilms are more resistant to antifungals, requiring higher drug concentrations for

inhibition. This phenomenon is a critical factor in treatment failure for device-related infections (29). Future research should use molecular typing and clinical correlation to determine isolate origin (17). While in vitro susceptibility guides therapy, the absence of corresponding clinical outcome data is a limitation (17). Despite these limitations, our study offers important findings for future research and clinical practice. Additionally, we did not investigate the potential link between COVID-19 and emerging yeast infections, an area warranting further exploration, particularly regarding viral infections and fungal co-infections in immunocompromised patients (20).

Finally, the VITEK-2 system, a diagnostic method used, has limitations in distinguishing intrinsic from acquired resistance in *Candida* species (11). Our study, relying on phenotypic susceptibility testing, does not explore molecular resistance mechanisms. Future work should use genomic approaches; sequencing ERG11, FKS1/2, or efflux pump genes to understand resistance evolution (15). VITEK-2's identification limitations might also have underestimated emerging/cryptic fungal species like *C. auris* (7). Advanced techniques like MALDI-TOF MS are crucial for comprehensive surveillance, given the rising multidrug-resistant pathogens (7). The narrow antifungal panel tested may not fully capture resistance profiles, suggesting more comprehensive testing. Prior antifungal exposure likely contributes to observed resistance, emphasising robust antifungal stewardship programs (25). Longitudinal and multi-centre studies are vital to expand our understanding of yeast infections and resistance, especially in resource-limited settings. Future studies should include environmental surveillance for resistant yeast reservoirs, informing targeted disinfection (30).

Conclusion

We demonstrate the variety of fungal agents associated with illness in inpatients at an

urban hospital in Nairobi. *Candida albicans* was the dominant isolate, with a notable increase in the prevalence of *NAC*, *Cryptococcus*, and *Trichosporon* species. Additionally, these yeasts exhibited widespread resistance to antifungal agents, particularly to amphotericin B, highlighting the need for routine monitoring to guide effective treatment.

Acknowledgements

We thank Hassan Adam Mohamed and the Medical Microbiology laboratory staff at The Nairobi South Hospital for their support in conducting this research. We also acknowledge the training provided by the University of Nairobi's Building Capacity for Writing Scientific Manuscripts (UANDISHI) Program at the Faculty of Health Sciences, University of Nairobi.

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Authors contribution

Conceptualization, C.A.; methodology, C.A., F.M., W.M., and G.O.M.; formal analysis, C.A.; investigation, C.A.; resources, F.M., W.M., and G.O.M.; data curation, C.A. and K.O.; writing, original draft, C.A.; writing, review & editing, C.A., F.M., W.M., and G.O.M.; supervision, F.M., W.M., and G.O.M.; project administration, C.A. All authors have read and approved the final manuscript.

Source of funding. No financial support was received for this study

Competing Interests. There are no conflicts of interest to report.



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Appendix A: Antifungal Susceptibility Breakpoints

Table A1

Minimum Inhibitory Concentration (MIC) Breakpoints for Yeast Species

	Antifungal	Sensitive MIC (µg/ml)	Intermediate MIC (µg/ml)	Resistant MIC (µg/ml)
<i>Candida</i> species	Amphotericin B	≤ 1	2	>4
	Flucytosine	≤ 4	8	≥16
	Fluconazole	≤ 8	= 16-32	≥ 64
	Itraconazole	≤ 0.12-0.5	= 1-2	≥ 4
	Voriconazole	≤ 1	= 2	≥ 4
<i>Cryptococcus</i> species	Amphotericin B	≤ 1	= 2	≥ 4
	Flucytosine	≤ 8	= 16	≥ 32
	Fluconazole	≤ 8	= 16-32	≥ 64
	Itraconazole	≤ 0.12-0.5	= 1-2	≥ 4
	Voriconazole	≤ 1	= 2	≥ 4
<i>Trichosporon</i> species	Amphotericin B	≤ 1	= 2	≥ 4
	Flucytosine	≤ 4	= 8	≥ 16
	Fluconazole	≤ 8	= 16-32	≥ 64
	Itraconazole	≤ 0.12-0.5	= 1-2	≥ 4
	Voriconazole	≤ 1	= 2	≥ 4

See: *Candida* and *Cryptococcus* species breakpoints: CLSI M27. *Trichosporon* species use CLSI M60 ECVs, lacking clinical breakpoints (19).