

Prevalence, associated factors and antifungal susceptibility patterns of *Candida auris* bloodstream infection among adult intensive care unit patients at a tertiary hospital in Tanzania: a cross-sectional study

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Abstract

Background

Candida auris is an emerging multidrug-resistant yeast associated with healthcare-associated invasive infections, particularly among critically ill patients. Data describing *C. auris* bloodstream infection in Tanzania are limited. This study determined the prevalence, associated factors, and antifungal susceptibility patterns of *C. auris* bloodstream infection among adult patients in the general intensive care unit (ICU) of Benjamin Mkapa Hospital (BMH), Tanzania.

Methods

A hospital-based cross-sectional study was conducted from January to April 2026 among 186 adults admitted to the general ICU for more than 48 hours with clinical suspicion of bloodstream infection. Blood cultures were processed using the BACTEC automated system. Yeast isolates were identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). Antifungal susceptibility testing was performed using the VITEK 2 Compact system with a yeast susceptibility card. Minimum inhibitory concentrations (MICs) were interpreted using Centers for Disease Control and Prevention (CDC) tentative *C. auris* breakpoints. Data were analysed in R version 4.4.0 using Fisher's exact test and Firth-penalized logistic regression.

Results

C. auris was identified in 4 of 186 participants, giving a prevalence of 2.15%. All four isolates were resistant to fluconazole (MIC 32–64 mg/L). Amphotericin B showed variable activity, with two isolates susceptible (MIC 0.5–1 mg/L) and two resistant (MIC 2 mg/L). Three isolates were susceptible to caspofungin (MIC 0.25–0.50 mg/L), while one was resistant (MIC 2 mg/L). In multivariable analysis, ICU stay ≥ 7 days (adjusted odds ratio [AOR] 6.09, 95% confidence interval [CI] 1.12–21.30; $p = 0.033$) and immunosuppression (AOR 8.34, 95% CI 1.07–32.09; $p = 0.043$) were independently associated with *C. auris* infection.

Conclusion

C. auris bloodstream infection was detected among adult ICU patients at BMH at a prevalence of 2.15% and demonstrated substantial antifungal resistance, particularly to fluconazole. Prolonged ICU stay and immunosuppression were independently associated with infection. Strengthening fungal diagnostic capacity, antifungal susceptibility testing, infection prevention and control, surveillance, and antifungal stewardship is warranted in this setting.

Introduction

Candida species are important causes of healthcare-associated infections and can produce invasive disease and bloodstream infection, particularly in critically ill patients. *Candida auris* has emerged as a major

healthcare-associated fungal pathogen because of its ability to persist in healthcare environments, transmit between patients and healthcare personnel, and exhibit resistance to multiple antifungal classes [1–4]. *C. auris* was first described in 2009 and has subsequently been reported on multiple continents, with invasive infection and colonization occurring disproportionately in high-dependency and intensive care settings [4, 5].

Patients in intensive care are exposed to several factors that may facilitate *C. auris* acquisition and progression to invasive infection, including prolonged hospitalization, invasive devices, broad-spectrum antimicrobial exposure, severe underlying disease and immunosuppression [1, 4, 6]. Accurate identification is also important because *C. auris* may be misidentified by conventional phenotypic methods. MALDI-TOF MS and other advanced identification methods can improve species-level recognition [1, 7, 8].

Antifungal resistance further complicates management. Fluconazole resistance is particularly common, while resistance to amphotericin B and echinocandins occurs less frequently but remains clinically important. CDC currently provides tentative MIC breakpoints because species-specific clinical breakpoints have not been established by CLSI for *C. auris* [9].

Evidence from Africa indicates that *C. auris* is increasingly recognized but remains underreported, with substantial variation in detection capacity and antifungal resistance profiles across countries [10, 11]. Reports from Kenya and South Africa demonstrate that *C. auris* can cause invasive infections and outbreaks in critical care environments [12, 13]. However, published evidence from Tanzania remains limited. Local data are needed to quantify the burden of infection, identify associated clinical factors, and characterize susceptibility patterns relevant to patient management and infection prevention.

This study therefore determined the prevalence, associated factors, and antifungal susceptibility patterns of *C. auris* bloodstream infection among adult patients admitted to the general ICU at BMH, Dodoma, Tanzania, between January and April 2026.

Methods

Study design and setting

A hospital-based quantitative cross-sectional study was conducted from January to April 2026 in the general ICU of Benjamin Mkapa Hospital, Dodoma, Tanzania. BMH is a level III public zonal referral and teaching hospital established in 2015 and serving approximately 14 million people, including patients referred from neighbouring regions. The general ICU provides care to critically ill adult patients and was purposively selected because of its referral role and availability of microbiology and critical care services.

Study population and eligibility

The study population comprised adults aged ≥ 18 years admitted to the general ICU. Patients were eligible if they had been admitted for more than 48 hours, had clinical suspicion of bloodstream infection, and provided informed consent or proxy consent from a close family member. Patients who had received systemic antifungal therapy for more than 48 hours before blood specimen collection, those transferred out of the ICU within 24 hours, and patients re-admitted after having already been enrolled were excluded.

Sample size and sampling

The minimum sample size was calculated using the single-population proportion formula with an anticipated prevalence of 12.42%, a 95% confidence level, and a 5% margin of error. The anticipated prevalence was derived from available African evidence used during protocol development [14]. The initial sample size was 167 participants and, after adjustment for a 10% non-response rate, the minimum required sample was 186. A non-probability convenience sampling approach was used to recruit eligible patients during the study period.

Data collection

A structured, coded, and pre-tested questionnaire adapted from previously published *C. auris* risk-assessment and infection-control tools was used to collect demographic and clinical information. Variables included age, sex, education, occupation, admission diagnosis, prior hospitalization, recent antibiotic and corticosteroid use, comorbidities, immunosuppression, malignancy, recent surgery, blood transfusion, duration of ICU stay, and use of invasive devices. Relevant clinical information was supplemented from hospital electronic records.

Blood specimen collection and culture

After informed consent, blood was collected using aseptic technique. Two blood culture bottles were labelled using a unique laboratory identifier. Approximately 10 mL of blood was collected, avoiding sampling through an existing cannula when possible. The venipuncture site was disinfected using 70% isopropyl alcohol followed by 2% chlorhexidine or povidone-iodine, allowing the antiseptic to dry before venipuncture. Blood culture bottles were transported to the microbiology laboratory within 30 minutes at room temperature and incubated in the BACTEC automated blood culture system for up to five days.

Candida isolation and species identification

Positive blood cultures were processed under appropriate biosafety practices and subcultured onto Sabouraud dextrose agar and blood agar. Plates were incubated aerobically at 38 °C for 24 hours. Creamy yeast colonies were assessed microscopically. A germ-tube test was performed in human serum at 37 °C for 2 hours; isolates that were germ-tube negative were subjected to further species identification. Isolates were identified to species level using MALDI-TOF MS (Bruker Daltonics; Flex Control software version 3.0 and BioTyper 3.0). A well-isolated colony was applied to a target plate, treated with formic acid and matrix solution, and analysed against the instrument reference database. Identification was based on the established log-score thresholds used by the laboratory [15].

Antifungal susceptibility testing

Confirmed *C. auris* isolates underwent antifungal susceptibility testing using the bioMérieux VITEK 2 Compact system with a yeast susceptibility card. A standardized yeast suspension equivalent to a 2.0 McFarland standard was prepared from a pure culture and inoculated into the card. Fluconazole, amphotericin B, and

caspofungin were tested, and MICs were obtained after automated incubation and reading. Quality-control strains *Candida parapsilosis* ATCC 22019 and *Candida albicans* ATCC 90028 were used. Because CLSI has not established *C. auris*-specific clinical breakpoints, MIC interpretations followed CDC tentative breakpoints: fluconazole ≥ 32 mg/L, amphotericin B ≥ 2 mg/L, and caspofungin ≥ 2 mg/L were considered resistant [9].

Statistical analysis

Data were entered, cleaned, coded, and analysed using R version 4.4.0 (R Foundation for Statistical Computing, Vienna, Austria). Continuous variables were summarized using medians and interquartile ranges (IQR), while categorical variables were summarized using frequencies and percentages. Prevalence was calculated as the number of laboratory-confirmed *C. auris* bloodstream infections divided by the total number of participants analysed, multiplied by 100.

Fisher's exact test was used for bivariable analysis because of the small number of *C. auris*-positive cases and sparse cell counts. Firth-penalized logistic regression was used to reduce small-sample bias and address sparse-data problems. Variables with $p < 0.20$ in the bivariable/univariable analysis were considered for multivariable modelling. Crude odds ratios (CORs) and adjusted odds ratios (AORs) with 95% CIs were reported, and $p < 0.05$ was considered statistically significant.

Ethical considerations

Ethical approval was obtained from the University of Dodoma Ethical Review Committee (ethical clearance reference number MA.84/261/98/73), and permission to conduct the study was obtained from Benjamin Mkapa Hospital. Written informed consent or proxy consent was obtained before enrolment. Participant confidentiality was maintained using unique study identifiers and restricting access to study data. The study was conducted in accordance with the principles of the Declaration of Helsinki.

Results

Participant enrolment and characteristics

A total of 315 ICU patients were assessed for eligibility. Of these, 125 were excluded according to the predefined criteria, 190 met the eligibility criteria, and four declined participation, leaving 186 participants for analysis. Blood specimens were collected from all enrolled participants.

The median age was 56.5 years (IQR 39.3–68.0), and 108 (58.1%) participants were male. Participants aged ≥ 60 years accounted for 44.6% of the study population. Nearly half of the participants (91, 48.9%) had an ICU stay of ≥ 7 days. Common comorbidities included hypertension (48.4%), diabetes mellitus (26.9%), chronic kidney disease (24.7%), malignancy (16.7%), and immunosuppression (10.7%). All participants had recent antibiotic exposure. Mechanical ventilation was recorded in 18.8%, central venous catheter use in 39.2%, haemodialysis catheter use in 30.6%, and parenteral nutrition in 16.1% (Table 1).

Table 1
Demographic and clinical characteristics of the 186
adult ICU participants.

Characteristic	n (%)
Male	108 (58.1)
Female	78 (41.9)
Age < 40 years	47 (25.3)
Age 40–59 years	56 (30.1)
Age ≥ 60 years	83 (44.6)
ICU stay < 7 days	95 (51.1)
ICU stay ≥ 7 days	91 (48.9)
Diabetes mellitus	50 (26.9)
Hypertension	90 (48.4)
Chronic kidney disease	46 (24.7)
Immunosuppression	20 (10.7)
Malignancy	31 (16.7)
Mechanical ventilation	35 (18.8)
Central venous catheter	73 (39.2)
Haemodialysis catheter	57 (30.6)
Parenteral nutrition	30 (16.1)
Recent blood transfusion	54 (29.0)
Recent corticosteroid use	76 (40.9)
Recent surgery	81 (43.5)
Prior hospitalization within 90 days	95 (51.1)
Recent antibiotic use	186 (100.0)

Prevalence of *C. auris* bloodstream infection

Four of 186 participants had blood cultures from which *C. auris* was identified, corresponding to a prevalence of 2.15% during the study period. The remaining participants had either other microorganisms isolated or no laboratory-confirmed *C. auris*.

Factors associated with *C. auris* bloodstream infection

On bivariable analysis, ICU stay ≥ 7 days ($p = 0.038$), immunosuppression ($p = 0.027$), and recent blood transfusion ($p = 0.040$) were significantly associated with *C. auris* infection. Malignancy showed a borderline

association ($p = 0.085$). Other demographic and clinical variables did not show statistically significant associations.

In Firth-penalized univariable regression, ICU stay ≥ 7 days was associated with higher odds of *C. auris* infection (COR 5.00, 95% CI 1.24–21.00; $p = 0.047$), as were immunosuppression (COR 9.11, 95% CI 1.21–33.70; $p = 0.027$) and recent blood transfusion (COR 3.31, 95% CI 1.22–12.56; $p = 0.039$). In the multivariable model, ICU stay ≥ 7 days (AOR 6.09, 95% CI 1.12–21.30; $p = 0.033$) and immunosuppression (AOR 8.34, 95% CI 1.07–32.09; $p = 0.043$) remained independently associated with *C. auris* infection. Malignancy (AOR 1.71, 95% CI 0.48–11.83; $p = 0.194$) and recent blood transfusion (AOR 1.31, 95% CI 0.64–9.86; $p = 0.081$) were not statistically significant after adjustment.

Table 2
Firth-penalized logistic regression analysis of factors associated with *C. auris* bloodstream infection. COR, crude odds ratio; AOR, adjusted odds ratio; CI, confidence interval.

Variable	COR (95% CI)	p	AOR (95% CI)	p
ICU stay ≥ 7 days vs < 7 days	5.00 (1.24–21.00)	0.047	6.09 (1.12–21.30)	0.033
Immunosuppression vs no	9.11 (1.21–33.70)	0.027	8.34 (1.07–32.09)	0.043
Malignancy vs no	2.20 (0.78–14.95)	0.085	1.71 (0.48–11.83)	0.194
Recent blood transfusion vs no	3.31 (1.22–12.56)	0.039	1.31 (0.64–9.86)	0.081

Antifungal susceptibility patterns

All four *C. auris* isolates were resistant to fluconazole, with MICs of 32–64 mg/L. Amphotericin B demonstrated heterogeneous susceptibility: two isolates were susceptible at MICs of 0.5 and 1 mg/L, while two were resistant at 2 mg/L. Caspofungin was susceptible in three isolates at MICs of 0.25–0.50 mg/L and resistant in one isolate at 2 mg/L (Table 3). Thus, resistance was observed in all four isolates to fluconazole, in two isolates to amphotericin B, and in one isolate to caspofungin.

Table 3
Antifungal susceptibility of the four *C. auris* bloodstream isolates. MIC, minimum inhibitory concentration; S, susceptible; R, resistant. Interpretations were based on CDC tentative *C. auris* breakpoints [9].

Isolate	Fluconazole MIC (mg/L)	Interpretation	Amphotericin B MIC (mg/L)	Interpretation	Caspofungin MIC (mg/L)	Interpretation
1	32	R	0.5	S	2	R
2	64	R	2	R	0.25	S
3	32	R	1	S	0.25	S
4	64	R	2	R	0.50	S

Discussion

This study provides ICU-based evidence of *C. auris* bloodstream infection in Tanzania and demonstrates the coexistence of a measurable burden with substantial antifungal resistance. Among 186 adult ICU patients with suspected bloodstream infection, four cases were identified, corresponding to a prevalence of 2.15%. The

detection of *C. auris* in this setting is important because African data remain limited and systematic reviews indicate that the pathogen is still underrecognized in several parts of the continent [10, 11].

The observed prevalence was lower than some estimates reported in African and international studies, but direct comparison should be made cautiously because study populations, sampling strategies, definitions of infection, and diagnostic approaches differ. The present study was restricted to adults admitted to a single ICU and used blood-culture-based detection among patients with clinical suspicion of bloodstream infection. The relatively low prevalence may therefore reflect the study population and case definition rather than the absence of *C. auris* transmission or colonization. In addition, *C. auris* can be missed when laboratories rely on conventional identification systems, making access to MALDI-TOF MS particularly relevant [1, 7, 8].

Prolonged ICU stay was independently associated with *C. auris* bloodstream infection. Patients who remained in the ICU for ≥ 7 days had approximately six-fold higher adjusted odds of infection than those with shorter stays. This finding is consistent with previous evidence identifying prolonged healthcare exposure as an important factor in *C. auris* acquisition [4, 6, 10]. Longer ICU stays increase opportunities for exposure to contaminated healthcare environments, invasive devices, repeated antimicrobial administration, and contact with healthcare workers. Because this study was cross-sectional, the association should not be interpreted as proof that prolonged stay causes infection; prolonged hospitalization may also reflect greater severity of illness and cumulative healthcare exposure.

Immunosuppression was also independently associated with *C. auris* bloodstream infection. Immunocompromised patients may have impaired clearance of opportunistic fungal pathogens and may require prolonged hospitalization, invasive procedures, and repeated antimicrobial exposure [1, 6]. The finding supports heightened clinical awareness and targeted diagnostic consideration in immunosuppressed ICU patients.

Recent blood transfusion was associated with *C. auris* infection in bivariable analysis but did not remain statistically significant after adjustment. Similarly, malignancy showed a borderline bivariable association but was not independently associated in the final model. These findings may reflect confounding by illness severity, immunosuppression, and duration of healthcare exposure. Importantly, only four *C. auris* cases were identified, resulting in wide confidence intervals and limited precision. The use of Firth-penalized regression was appropriate for reducing small-sample bias, but the estimates should nevertheless be interpreted cautiously.

The susceptibility findings demonstrated a pronounced resistance phenotype. All four isolates were resistant to fluconazole, consistent with the high prevalence of fluconazole resistance reported globally and in African surveillance [2, 10, 13]. CDC currently considers MICs ≥ 32 mg/L resistant for fluconazole in *C. auris*, while emphasizing that these are tentative breakpoints because species-specific clinical breakpoints have not been established [9]. The universal fluconazole resistance observed in this study therefore supports the importance of species-level identification and susceptibility testing when *C. auris* is suspected.

Amphotericin B susceptibility was heterogeneous, with two susceptible and two resistant isolates. This variability is consistent with the recognized diversity of *C. auris* antifungal susceptibility profiles [2, 10, 13]. The presence of amphotericin B-resistant isolates is clinically relevant because it limits the reliability of amphotericin B as a uniformly active alternative.

Caspofungin remained active against three of four isolates, although one isolate had an MIC of 2 mg/L and was classified as resistant using the CDC tentative breakpoint [9]. Echinocandins are generally the most active antifungal class against *C. auris*, but resistance can occur and should be considered when clinical response is inadequate. Therefore, susceptibility testing remains important even when an echinocandin is selected empirically.

The study has several strengths. It generated primary ICU data from Tanzania, used MALDI-TOF MS for species-level identification, and applied MIC-based antifungal susceptibility testing. The statistical analysis also incorporated Firth penalization to address sparse data associated with the small number of confirmed infections. However, the cross-sectional single-centre design limits causal inference and generalizability. Convenience sampling may have introduced selection bias, and the four confirmed cases resulted in imprecise association estimates. The study also did not include molecular characterization; therefore, strain relatedness, transmission pathways, and specific resistance mechanisms could not be assessed.

These findings support strengthening laboratory capacity for *C. auris* detection, maintaining access to reliable species-level identification, performing antifungal susceptibility testing on confirmed clinical isolates, and reinforcing infection prevention and control measures in critical care. Continued surveillance and multicentre studies are needed to determine the wider epidemiology of *C. auris* in Tanzania and to clarify transmission and resistance mechanisms.

Conclusion

C. auris bloodstream infection was identified among adult ICU patients at BMH at a prevalence of 2.15%. The four isolates showed universal fluconazole resistance, variable amphotericin B susceptibility, and predominantly preserved caspofungin activity. ICU stay ≥ 7 days and immunosuppression were independently associated with infection. Strengthened diagnostic capacity, routine antifungal susceptibility testing, infection prevention and control, surveillance and antifungal stewardship are warranted. Larger multicentre and molecular studies are recommended to define the burden, transmission dynamics and resistance mechanisms of *C. auris* in Tanzania.

Declarations

Ethics approval and consent to participate

Ethical approval was obtained from the University of Dodoma Ethical Review Committee under ethical clearance reference number MA.84/261/98/73. Permission to conduct the study was obtained from Benjamin Mkapa Hospital. Written informed consent or proxy consent was obtained from participants before enrolment. The study was conducted in accordance with the Declaration of Helsinki.

Consent for publication

Not applicable. No individual-level identifiable information is reported.

Availability of data and materials

The datasets generated and/or analysed during the current study are available from the corresponding author on reasonable request, subject to applicable institutional and ethical requirements.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

EG conceptualized the study, collected and analysed the data, interpreted the findings, and drafted the manuscript. MLM, EN, and AB supervised the study design and methodology and contributed to critical review and revision of the manuscript. All authors read and approved the final manuscript.

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