



Research Article

Evaluation of Automated Platforms for Accurate Identification of Post-COVID-19 *Candida auris* Isolates

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Abstract | During the worldwide spread of coronavirus disease 2019 (COVID-19), outbreaks of *Candida auris*-multidrug-resistant (MDR) yeast have been reported. The aim of this study was to provide comprehensive detection methods for *C. auris*. Accurate and timely identification is important for antifungal therapy. This retrospective cohort study was conducted on several microbial cultures. Thirty-seven isolates were identified, where 56.8% were obtained from blood specimens, sputum (21.6%), bronchoalveolar lavage (16.2%), and urine (5.4%). These isolates were identified using MALDI-TOF MS compared to VITEK 2 and BioFire® Blood Culture Identification 2 (BIOFIRE BCID2). The identification included 37 *C. auris* isolates and 20 non-*C. auris* controls. MALDI-TOF MS identified 37 isolates as *C. auris*, whereas 20 control isolates belonging to other species were misidentified as *C. auris* by VITEK 2. BIOFIRE BCID2 evaluated 21 *C. auris*-positive blood cultures and 20 non-*C. auris* controls. BIOFIRE BCID2 identified all 21 isolates as *C. auris* derived from blood specimens. Antifungal susceptibility test, minimum inhibitory concentration (MIC), minimum inhibitory concentrations of 50% of the isolates (MIC₅₀) and minimum inhibitory concentrations of 90% of the isolates (MIC₉₀) were evaluated. The findings of this study demonstrate a substantial limitation of automated identification of *C. auris* with VITEK 2. Meanwhile, identification of isolates using BIOFIRE BCID2 and MALDI-TOF MS improved the species recognition. The observed results of fluconazole-resistance (100%) and flucytosine-resistance (91.9%) of *C. auris* isolates indicated that they were MDR and reinforced the urgent need for a reliable species-level identification and antifungal susceptibility testing for use in clinical practice and infection-control strategies.

Received | July 21, 2026; **Revised** | September 15, 2026; **Accepted** | September 22, 2026; **Published** | October 06, 2026

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Citation | Ahmed, F., I.M. El-Kholy, N.A. Elkady, A.A. El-Mehalawy and D.A.M. Abdou. 2026. Evaluation of automated platforms for accurate identification of post-COVID-19 *Candida auris* isolates. *Novel Research in Microbiology Journal*, 10(5): 498-518.

DOI | <https://dx.doi.org/10.17582/journal.nrmj/2026/10.5.498.518>

Keywords | *Candida auris*, Post-COVID-19, MALDI-TOF MS, Biofire, AFST



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Introduction

Candida auris has become an important global health threat because of several concerning

properties, including resistance to multiple classes of antifungal agents, tendency to cause outbreaks in clinical settings, ability to persist on environmental surfaces, and tolerance to several commonly used

disinfectants (Bhargava *et al.*, 2025). In 2009, *C. auris* was first identified in Japan and is known as a multidrug-resistant (MRD) yeast with great potential to be acquired as a nosocomial infection (Schaefer *et al.*, 2024). In 2019, it was designated as an urgent public health threat by the Centers for Disease Control and Prevention (CDC) due to its growing risk and by the World Health Organization (WHO) as one of the most important fungal pathogens in severely ill people. A higher number of *C. auris* cases have been attributed to the degree of thermotolerance, ability of transmission among individuals, and lack of infection control practices (Khairat *et al.*, 2021; Bhargava *et al.*, 2025).

Coronavirus disease 2019 (COVID-19) caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first recorded in Wuhan, China, in December 2019, and has risen from an epidemic to a global pandemic. This viral infection has exerted a remarkable impact on the lives of the public health systems, resulting in a large amount of disease burden and millions of cases occurring in China. The first case was identified in Egypt in February 2020 (Gamal *et al.*, 2022; Yassin and Abo-Elyazeed, 2023).

The emergence of new fungal infections appeared in the post pandemic period, with post-COVID-19 infection resulting in a new threat of fungal infectious disease (Melinte *et al.*, 2024). Given the pervasive emergence and spread of *C. auris* around the world and the global increasing concern over invasive candidiasis, in depth epidemiological aspects and mechanisms of resistance of *Candida* species in different geographical areas, including Egypt need further research and investigation (Spruijtenburg *et al.*, 2025). This is also relevant in previously infected COVID-19 patients who often have longer hospital stays, receive broader-spectrum antimicrobials and steroids, or may be immunosuppressed, with a consequently increased risk of getting invasive opportunistic infections such as *C. auris* (Melinte *et al.*, 2024). The spread and incidence of *C. auris* infections have been dramatically affected by the COVID-19 pandemic, which has caused an exponential surge in cases (Schaefer *et al.*, 2024). There have been reports of a tremendous growth in the number of *C. auris* cases after the pandemic, with values > 200% in some regions. For example, more than 300 clinical cases have been reported in 10 province- level regions in China by the end of 2023 (Bing *et al.*, 2025).

The mortality associated with *C. auris* infections is exceptionally high, particularly in patients with predisposing risk factors (Bhargava *et al.*, 2025). Host and pathogen factors of COVID-19 combined with inadequate hospital care have created opportunities for the emergence and spread of this fungal global threat with acquired resistance to the mainstream medical antifungals (Schaefer *et al.*, 2024). The global spike in *C. auris* infections following the COVID-19 pandemic necessitates better surveillance, more knowledge on the pathogenic traits, and innovative preventive methods to counter the two widespread risks (Rahman *et al.*, 2024).

When identifying emerging pathogens such as *C. auris*, accurate identification of *C. auris* in the microbiology laboratories is challenging and requires a variety of advanced molecular and automated techniques. Molecular diagnostic tools, such as BioFire FilmArray panels, offer a streamlined sample-to-result approach for the detection of clinically significant *Candida* species directly from the positive samples (El-Sherif *et al.*, 2022; Widyasari *et al.*, 2023). Automated platforms such as VITEK 2 are valuable as initial screening tools for *C. auris* isolates (Huma *et al.*, 2023; Patwardhan *et al.*, 2024). As technology continues to progress rapidly, matrix-assisted laser desorption/ionization time-of flight mass spectrometry (MALDI-TOF MS) has become a top-tier method for the direct identification of *Candida* species from the routine cultures. It is frequently used as a benchmark approach for assessing the accuracy of other diagnostic techniques (Bhargava *et al.*, 2025; Park *et al.*, 2025). In addition, healthcare providers often routinely use chromogenic medium, including CHROMagar *Candida*, for the selection of *Candida* species, which allows for their discrimination from each other using unique colonies (CDC, 2026). Additionally, *C. auris*' ability to grow at 42°C due to its innate natural thermotolerance is one of the differential diagnostic criteria used during their identification procedure (Khairat *et al.*, 2021; Bhargava *et al.*, 2025; CDC, 2026). The addition of these rapid molecular assays to the standard and automated approaches provides an improved diagnostic spectrum for *C. auris* and allows rapid intervention in acute clinical situations (El-Sherif *et al.*, 2022).

The objective of this study was to critically evaluate and identify the most suitable and cost-effective

methodologies and techniques used for the accurate and timely detection of *C. auris* recovered from diverse laboratory microbial cultures, with a particular emphasis on post-COVID-19 *C. auris* isolates, given their observed increased prevalence during the pandemic.

Materials and Methods

Study design

This study was conducted as a retrospective observational microbiological study including post-COVID-19 *Candida auris* isolates collected from routine laboratory microbial cultures at Ain Shams University Specialized Hospital (ASUSH), a tertiary care center in Cairo, Egypt. *Candida auris* isolates associated with several microbiological records that documented a COVID-19 diagnosis were eligible for inclusion. These isolates were considered eligible when the associated microbiological record indicated that the cultures were processed during the period of active COVID-19 diagnosis or within one month following the documented diagnosis, in accordance with previously published studies ([Goravey et al., 2021](#); [Erturk Sengel et al., 2023](#); [El-Zakhem et al., 2023](#)). Only microbiologically confirmed *C. auris* isolates were included in the study. Isolates identified as *Candida* species other than *C. auris* and those isolates where the required microbiological information was incomplete were excluded. Duplicate isolates were excluded according to the predefined study protocol to avoid repeated inclusion of the same isolate.

The study included previously recovered *C. auris* isolates from positive leftover laboratory cultures, with the associated microbiological records documenting a post-COVID-19 diagnosis. COVID-19 status was determined from the documented laboratory diagnosis accompanying the microbiological record, and the infection was considered as confirmed when a positive SARS-CoV-2 polymerase chain reaction (PCR) result was documented from a respiratory specimen obtained *via* a nasopharyngeal or an oropharyngeal swab. Isolate's inclusion and exclusion criteria were predefined before the selection and analysis of the microbiological records and isolates.

Phenotypic screening of the recovered isolates

The obtained yeast isolates were initially screened for presumptive identification as *C. auris* based on their ability to grow at an elevated temperature (42

°C) and their characteristic colony morphology on a chromogenic agar medium (Brilliance™ *Candida* Agar) following the U.S. Centers for Disease Control and Prevention (CDC) guidelines for *C. auris* identification ([CDC, 2026](#)). Yeast isolates that grew at 42 °C and exhibited chromogenic features suggestive of *C. auris* were subjected to further identification ([CDC, 2026](#)).

Culture processing and Candida auris isolation

For all platforms, BACTEC™ culture bottles were incubated in the automated BACTEC™ FX system (BD Diagnostics, Franklin Lakes, NJ, USA) for up to five days, or until a positive growth signal was detected, according to the laboratory's routine procedures and previously published protocols ([Ulrich et al., 2022](#); [Posteraro et al., 2023](#)). Positive BACTEC™ cultures were subsequently processed for *C. auris* isolation and identification using the diagnostic platforms described below.

VITEK 2® system

Positive BACTEC™ culture bottles were subcultured onto Sabouraud's Dextrose Agar (SDA) for *C. auris* recovery. Following growth, the isolates were subjected to identification using the VITEK® 2 Compact system (version 8.01, bioMérieux, Marcy-L'Etoile, France), following the manufacturer's instructions ([Ambaraghassi et al., 2019](#); [CDC, 2024c](#)).

MALDI-TOF mass spectrometry

Following obtained positive signals in the BACTEC™ system, the cultures were subcultured onto SDA. The recovered yeast isolates were subsequently identified by Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, LT2 plus, SAI, UK) using the updated reference database BactoScreen-ID version 2.4 including *C. auris* spectra as a reference library ([Abdolrasouli and Fraser, 2022](#)).

BioFire FilmArray BCID2

For BioFire® FilmArray® BCID2 (bioMérieux, Marcy-l'Étoile, France), the positive cultures detected by the BACTEC™ FX system were processed according to the manufacturer's instructions. Following a positive signal, 200 µl aliquots were directly withdrawn from the positive BACTEC™ culture bottles and transferred to the pre-hydrated BCID2 pouch, followed by the addition of the sample buffer. The pouch was then inserted into the FilmArray instrument (Release Version 2, Software

Module Version 2.1.273.0). This system performs an automated nucleic acid extraction, multiplex PCR amplification and DNA melting where curve analysis-complete results become available within two hours. The BCID2 system includes *C. auris* isolates among the array of yeast targets, allowing a rapid identification *via* molecular means (Zhang *et al.*, 2020; Caméléna *et al.*, 2023; Puumala *et al.*, 2025).

Inclusion of non-Candida auris controls and comparison of the identification platforms

The identification analysis included 37 eligible *C. auris* isolates and an individual comparison panel of 20 non-*C. auris* isolates, comprising six *C. albicans*, six *C. tropicalis*, four *C. famata*, and four *Nakaseomyces glabratus* (formerly *C. glabrata*). Non-*C. auris* isolates were included specifically as identification controls and were analyzed separately from the main post-COVID-19 *C. auris* group. VITEK 2 and MALDI-TOF MS results were compared for all the 57 isolates, whereas BIOFIRE FilmArray BCID2 results were evaluated for 41 positive blood-culture broths, comprising 21 corresponding *C. auris*-positive cultures and 20 non-*C. auris* controls. The procedure for each platform is described above.

MALDI-TOF MS was used as the comparator for species assignment. The primary comparison assessed the agreement in classification as *C. auris* or non-*C. auris*. Pairwise agreement was calculated as the number of concordant classifications divided by the number evaluated by both platforms and was expressed as a percentage. Species-level agreement was additionally assessed among the VITEK 2, MALDI-TOF MS, and BIOFIRE BCID2 microorganisms included in the panel's target list. BIOFIRE results reported as *C. glabrata* were considered equivalent to *N. glabratus*. Because *C. famata* is not a BCID2 target, its four isolates were included in the assessment of *C. auris* detection/non-detection but were excluded from the assessment of a species-level agreement with BIOFIRE. Discordant results were described by the platform and comparator-assigned species. Performance was reported as an observed agreement within the selected collection rather than as an independently established diagnostic accuracy.

Antifungal susceptibility testing

Antifungal susceptibility testing (AFST) of all recovered isolates were performed using the VITEK 2® Compact System (bioMérieux, France) with the

AST-YS08 test card according to the manufacturer's instructions. Isolates were subcultured on SDA and incubated at 35–37 °C for 24 h prior to testing. A standardized suspension of a yeast equivalent to a 0.5 McFarland standard was prepared in sterile saline and run on the VITEK 2 system for automated minimum inhibitory concentration (MIC) determination. The panels ran included several antifungals of major therapeutic classes, namely fluconazole, voriconazole (azoles), caspofungin, micafungin (echinocandins), flucytosine and amphotericin B.

With no formal breakpoints established for *C. auris*, the antifungals were reported using tentative MIC breakpoints provided by the Centers for Disease Control and Prevention together with previously derived derivatisation method-based epidemiological cutoff values (dECOFFs) as well as extrapolated from other species (Ahmed *et al.*, 2025). The CDC tentative breakpoints that implemented included Fluconazole ≥ 32 µg/ml, amphotericin B ≥ 2 µg/ml, micafungin ≥ 4 µg/ml, and caspofungin ≥ 2 µg/ml (CDC, 2024a). The dECOFFs breakpoints were used for identifying the non-wild-type isolates for voriconazole (1 µg/ml) (Arendrup *et al.*, 2017; Bohner *et al.*, 2023). Flucytosine MICs were interpreted using the Clinical Laboratory Standards Institute (CLSI) breakpoint for other *Candida* spp. (≥ 32 µg/ml) (CLSI, 2017).

Minimum inhibitory concentrations of 50% of the isolates (MIC₅₀) and Minimum inhibitory concentrations of 90% of the isolates (MIC₉₀) were determined from MIC values ordered from the lowest to the highest, using the observations at ranks $[0.50 \times n]$ and $[0.90 \times n]$, respectively. MIC summaries for small source-specific groups were considered exploratory.

Statistical analysis

Jamovi software (version 2.6) was used for statistical analysis. Categorical data are expressed as frequencies and proportions. Antifungal MIC values (both determined values and interpreted in categories) were summarized by reporting the range, MIC₅₀ (the lowest concentration where at least 50% of the isolates show inhibition), and MIC₉₀ (the lowest concentration where at least 90% of the isolate display inhibition). Values falling below or above the testing limits were reported using the original inequality signs. Antifungal susceptibility classifications were presented as numbers and percentages of resistant

and susceptible isolates. The distributions of resistant and susceptible isolates for the individual antifungal agents were evaluated using the chi-square goodness-of-fit test against equal expected frequencies. An agreement between the identification platforms was evaluated only among the isolates tested by the corresponding platforms and was reported as the number and percentage of concordant classifications. All tests were two-sided, and a p -value <0.05 was considered statistically significant, values below 0.001 were considered highly significant.

Results

Distribution of Candida auris isolates by culture source

A total of 37 *C. auris* isolates recovered from routine laboratory cultures were included in this study. Blood cultures accounted for the largest proportion of isolates (21/37, 56.8%), followed by sputum cultures (8/37, 21.6%), bronchoalveolar lavage cultures (6/37, 16.2%), and urine cultures (2/37, 5.4%) (Table 1). Collectively, the isolates recovered from the non-blood cultures represented 43.2% (16/37) of the collection.

Table 1: Distribution of included *Candida auris* isolates by original culture source.

Culture source	Isolates, n (%)
Blood	21 (56.8)
Sputum	8 (21.6)
Bronchoalveolar lavage	6 (16.2)
Urine	2 (5.4)
Total	37 (100)

Phenotypic characteristics of the recovered isolates

All 37 *C. auris* isolates (100%) expressed growth at 42°C. On Brilliance™ *Candida* Agar, the isolates produced colonies with colors ranging from white or pale pink to lavender. These obtained results supported the presumptive identification of *C. auris*, with a species identification that was subsequently established using the identification platforms described below (Figure 1).

Identification findings and inter-platform agreement

The identification analysis included 37 *C. auris* isolates and 20 non-*C. auris* controls. All 57 isolates were evaluated using VITEK 2 and MALDI-TOF MS, while BIOFIRE FilmArray BCID2 evaluated 41 corresponding positive blood-culture broths, comprising 21 *C. auris*-positive cultures and 20 non-*C. auris* controls.

All 37 isolates in the main study group were identified as *C. auris* by both VITEK 2 and MALDI-TOF MS, demonstrating a complete observed agreement within this group (37/37, 100%). BIOFIRE BCID2 detected *C. auris* in all 21 corresponding positive blood-culture broths, with concordant identification by VITEK 2 and MALDI-TOF MS for the recovered isolates. Among the 20 non-*C. auris* controls, MALDI-TOF MS identified six isolates as *C. albicans*, six as *C. tropicalis*, four as *C. famata*, and four as *Nakaseomyces glabratus*. VITEK 2 reported all 20 controls as *C. auris*, resulting in no agreement with MALDI-TOF MS within the control group (0/20, 0%). Across the combined 57-isolate collection, VITEK 2, and MALDI-TOF MS agreement was 37/57 (64.9%). All discordances involved a VITEK 2 identification of *C. auris* and a non-*C. auris* identification by MALDI-TOF MS.

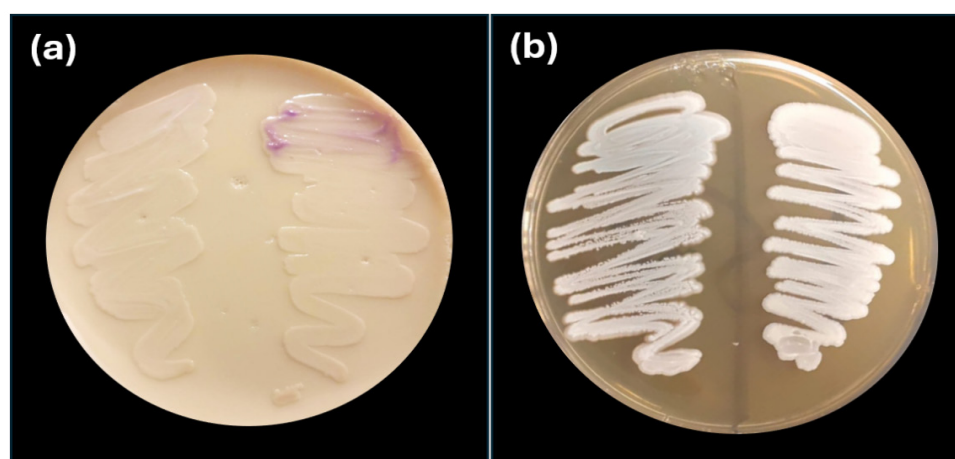


Figure 1: Phenotypic characteristics of *Candida auris*. (a) Colony appearance on chromogenic media, color ranging from pale or white to lavender. (b) Robust growth at 42°C, demonstrating *C. auris* thermotolerance.

Table 2: Identification results of VITEK 2 and BIOFIRE FilmArray BCID2 compared to MALDI-TOF MS.

MALDI-TOF classification	VITEK 2	BIOFIRE BCID2
<i>Candida auris</i> (n = 21)	21/21 concordant	21/21 concordant
<i>Candida albicans</i> (n = 6)	6/6 reported as <i>C. auris</i>	6/6 concordant
<i>Candida tropicalis</i> (n = 6)	6/6 reported as <i>C. auris</i>	6/6 concordant
<i>Nakaseomyces glabratus</i> (n = 4)	4/4 reported as <i>C. auris</i>	4/4 concordant as <i>C. glabrata</i>
<i>Candida famata</i> (n = 4)	4/4 reported as <i>C. auris</i>	<i>C. auris</i> not detected*

Where; *Species not targeted.

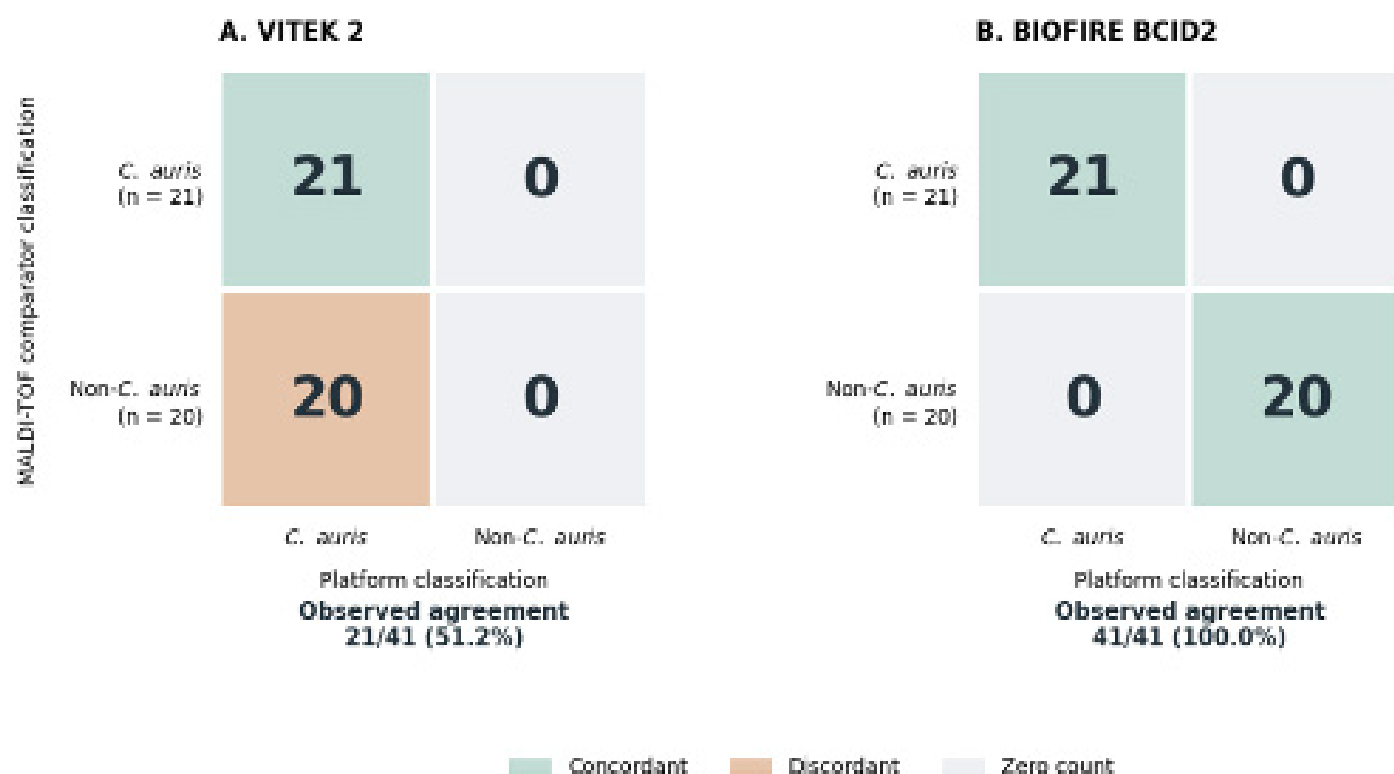


Figure 2: Agreement of VITEK 2 and BIOFIRE FilmArray BCID2 with MALDI-TOF MS for *Candida auris* classification. Matrices represent the shared subset of 41 cultures, comprising 21 *C. auris*-positive cultures and 20 non-*C. auris* controls. Rows indicate MALDI-TOF comparator classifications and columns display classifications by (A) VITEK 2 and (B) BIOFIRE BCID2. Cell values represent culture counts. Observed agreement was calculated as the sum of diagonal counts divided by 41. The four *C. famata* controls were assessed for *C. auris* non-detection, not species-level identification, because *C. famata* was not a BCID2 target.

BIOFIRE BCID2 yielded no *C. auris* detections among the 20 non-*C. auris* controls. A species-level identifications agreed with MALDI-TOF MS for all 16 controls belonging to species targeted by BIOFIRE BCID2: *C. albicans* (n= 6), *C. tropicalis* (n= 6), and *N. glabratus*, reported as *C. glabrata* (n= 4). The four *C. famata* controls were evaluated for the absence of false-positive *C. auris* detection but were excluded from species-level agreement calculations because *C. famata* was not a BIOFIRE BCID2 target. Within the shared 41-culture subset, BIOFIRE BCID2 and MALDI-TOF MS displayed a complete observed agreement for *C. auris* versus non-*C. auris*

classification (41/41, 100%), whereas VITEK 2 agreed with each platform for 21/41 classifications (51.2%). Restricting the BIOFIRE BCID2–MALDI-TOF MS species-level comparison to microorganisms targeted by BIOFIRE BCID2 yielded an agreement for all the 37 eligible cultures (37/37, 100%) (Table 2, Figure 2).

Antifungal susceptibility profiles and MIC distributions

Antifungal susceptibility testing was performed on all 37 *C. auris* isolates. The overall and culture-source-specific MIC distributions are summarized in Table 3. Fluconazole MICs were 32 µg/ml for

all isolates, yielding MIC₅₀ and MIC₉₀ values of 32 µg/ml. All isolates therefore met the CDC tentative resistance threshold for fluconazole (37/37, 100%). Voriconazole MICs ranged from ≤0.12 to 1 µg/ml, with MIC₅₀ and MIC₉₀ values of 0.25 and 0.5 µg/ml, respectively. These results were reported descriptively without assigning clinical susceptibility categories. Amphotericin B MICs ranged from 0.125 to 0.75 µg/ml, with MIC₅₀ and MIC₉₀ values of 0.5 and 0.75 µg/ml, respectively; none of the isolates reached the CDC tentative resistance threshold of ≥2 µg/ml (Figure 3). Flucytosine MICs were ≥64 µg/ml in 34 isolates (91.9%) and ≤1 µg/ml in three isolates (8.1%),

resulting in both MIC₅₀ and MIC₉₀ values of ≥64 µg/ml. The 34 isolates with elevated MICs exceeded the exploratory threshold of ≥32 µg/ml specified in the study methodology. This classification was not interpreted as resistance established using a validated *C. auris*-specific clinical breakpoint. Caspofungin MICs ranged from 0.25 to 2 µg/ml, with MIC₅₀ and MIC₉₀ values of 0.25 and 1 µg/ml, respectively. Three isolates (8.1%) met the CDC tentative resistance threshold of ≥2 µg/ml. Micafungin MICs ranged from 0.12 to 4 µg/ml, with MIC₅₀ and MIC₉₀ values of 0.12 and 4 µg/ml, respectively. Four isolates (10.8%) met the tentative resistance threshold of ≥4 µg/ml.

Table 3: Overall antifungal minimum inhibitory concentration (MIC) distributions and recorded antibiotics susceptibility categories of *Candida auris* isolates (n = 37).

Antifungal	MIC range (µg/ml)	MIC ₅₀ (µg/ml)	MIC ₉₀ (µg/ml)	Resistant n (%)	Susceptible n (%)	p value
Fluconazole	32	32	32	37 (100)	0 (0)	<0.001
Voriconazole ^a	≤0.12–1	0.25	0.5	0 (0)	37 (100)	<0.001
Amphotericin B	0.125–0.75	0.5	0.75	0 (0)	37 (100)	<0.001
Flucytosine ^b	≤1 to ≥64	≥64	≥64	34 (91.9)	3 (8.1)	<0.001
Caspofungin	0.25–2	0.25	1	3 (8.1)	34 (91.9)	<0.001
Micafungin	0.12–4	0.12	4	4 (10.8)	33 (89.2)	<0.001

Where; R/S columns reproduce the recorded classifications, which should not all be interpreted as validated clinical susceptibility categories. ^aVoriconazole's recorded susceptible category does not establish a clinical susceptibility; an epidemiological cutoff distinguishes wild-type from non-wild-type isolates. ^bFlucytosine classification uses the exploratory ≥32 µg/ml threshold specified in the Methods, not a validated *C. auris*-specific breakpoint. For the other agents, resistance counts agree with the stated Centers for Disease Control and Prevention (CDC) tentative thresholds; values below those thresholds do not independently establish a clinical susceptibility. Highly significant (p <0.001).

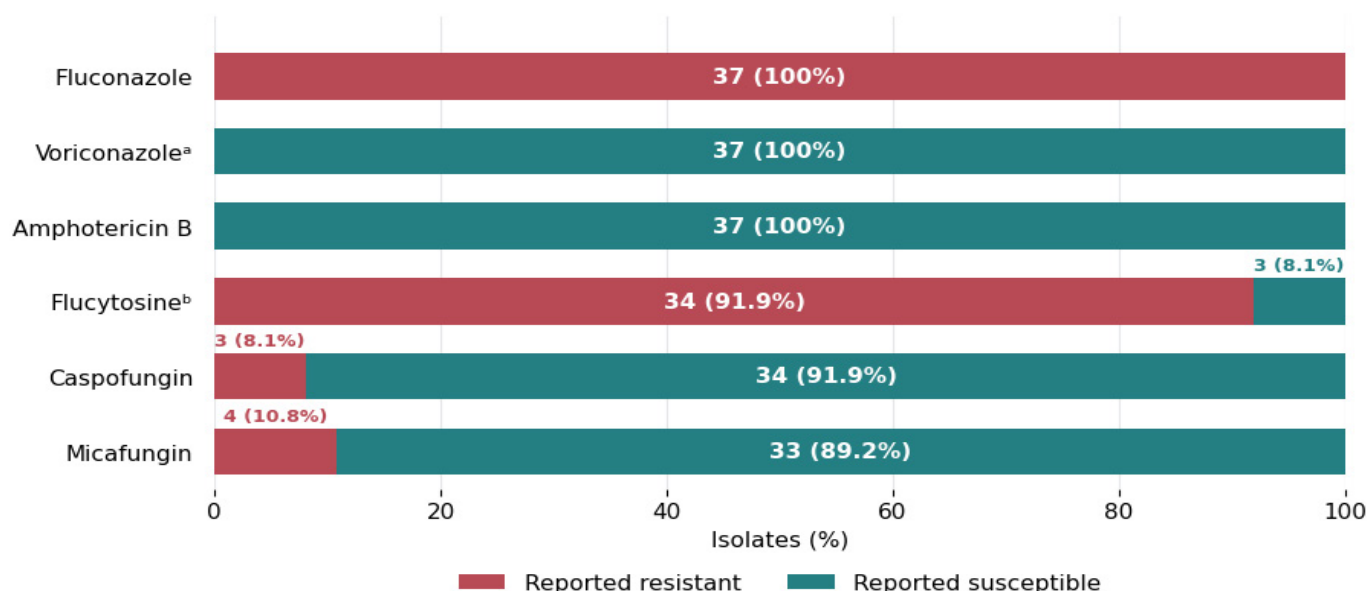


Figure 3: Antifungal susceptibility profiles of 37 *Candida auris* isolates. Stacked bars show the number and percentage of isolates in each reported susceptibility category. ^aVoriconazole categories represent non-wild-type/wild-type under the stated derivatization method-based epidemiological cutoff values (dECOFF) criterion. ^bFlucytosine classification uses the stated breakpoint extrapolated from the other *Candida* species.

Table 4: Antifungal resistance of *Candida auris* isolates by source.

Isolate source	Fluconazole (FLU)	Voriconazole (VORI)	Amphotericin B (AB)	Flucytosine (FCT)	Caspofungin (CASP)	Micafungin (MCF)
Blood	21/21 (100%)	0/21 (0.0%)	0/21 (0.0%)	19/21 (90.5%)	2/21 (9.5%)	2/21 (9.5%)
Urine	2/2 (100%)	0/2 (0.0%)	0/2 (0.0%)	2/2 (100%)	1/2 (50.0%)	2/2 (100%)
Sputum	8/8 (100%)	0/8 (0.0%)	0/8 (0.0%)	8/8 (100%)	0/8 (0.0%)	0/8 (0.0%)
BAL	6/6 (100%)	0/6 (0.0%)	0/6 (0.0%)	5/6 (83.3%)	0/6 (0.0%)	0/6 (0.0%)
Total	37/37 (100%)	0/37 (0.0%)	0/37 (0.0%)	34/37 (91.9%)	3/37 (8.1%)	4/37 (10.8%)

BAL: bronchoalveolar lavage.

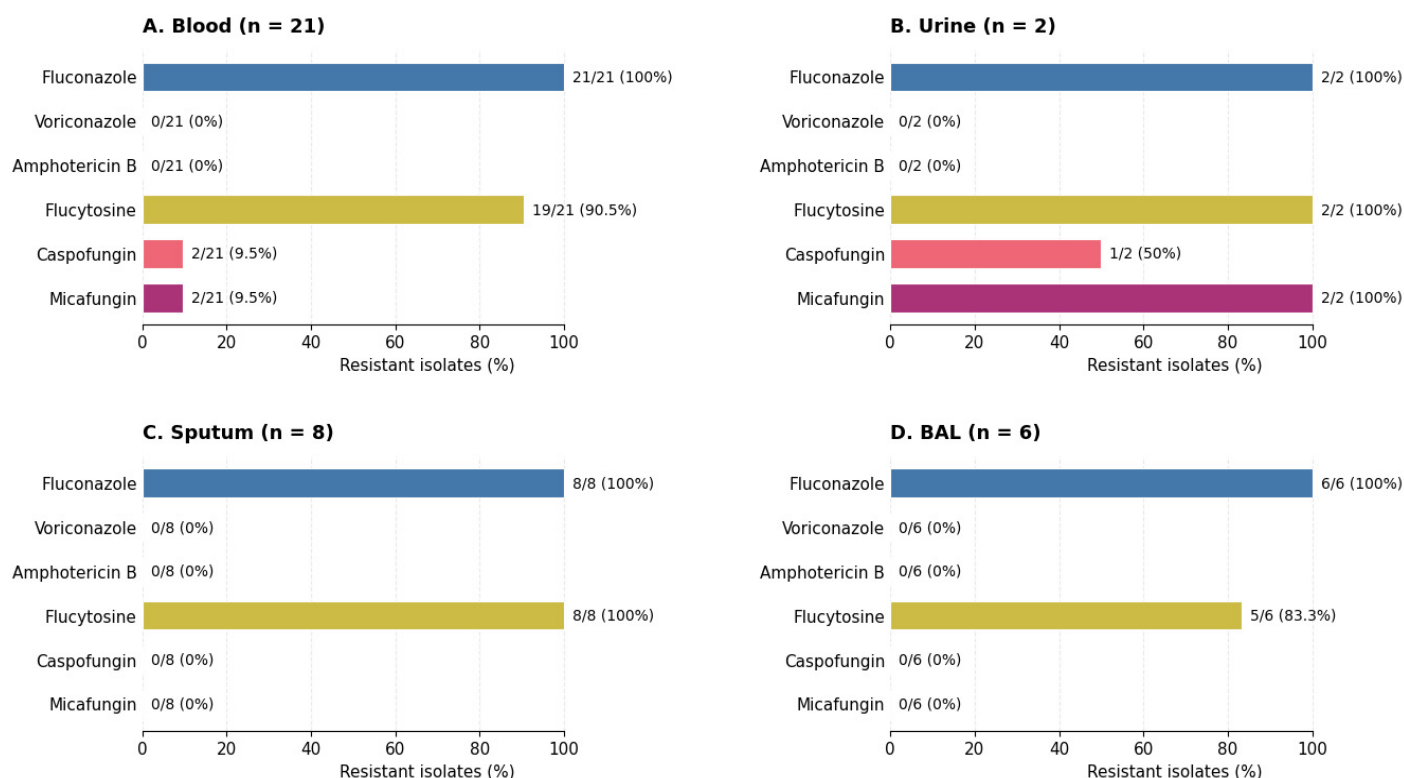


Figure 4: Antifungal resistance of *Candida auris* isolates by source. Panels represent (A) blood, (B) urine, (C) sputum, and (D) bronchoalveolar lavage (BAL). Bars indicate resistance percentages within each source, while labels show the resistant/total isolates (%).

By culture source, the isolates meeting the caspofungin resistance threshold were recovered from blood cultures (2/21, 9.5%) and urine cultures (1/2, 50.0%). Isolates meeting the micafungin resistance threshold were also recovered from blood cultures (2/21, 9.5%) and urine cultures (2/2, 100%). No sputum- or bronchoalveolar lavage (BAL)-derived isolates had reached the tentative resistance thresholds for either caspofungin or micafungin. Flucytosine MICs of ≥ 64 $\mu\text{g/ml}$ were observed in 19/21 blood-derived isolates (90.5%), 2/2 urine-derived isolates (100%), 8/8 sputum-derived isolates (100%), and 5/6 BAL-derived isolates (83.3%). The source-specific findings were interpreted descriptively, particularly for the small non-blood culture groups (Table 4 and Figure 4).

Discussion

This study included collected post-COVID-19 *C. auris* isolates, which describes the distribution of *C. auris* isolates by culture source, phenotypic characteristics, identification results, platform concordance, antifungal susceptibility patterns and MIC distributions. All these findings highlight the importance of rapid molecular diagnosis for prompt initiation of a suitable antifungal therapy and timely infection prevention measures. *C. auris* was one of the most important MDR yeasts owing to its ability to persist in healthcare environments, cause healthcare-associated outbreaks, and rapidly develop resistance to multiple antifungal agents (Bing *et al.*, 2026). *C. auris* infection has increased worldwide since the

development of COVID-19 pandemic, mainly due to its stay for long time in intensive care unit (ICU), excessive use of broad-spectrum antibiotics, corticosteroid therapy, invasive supportive care, and missing the rules of infection prevention (Ismail *et al.*, 2026). Several studies have also reported a marked increase in the transmission of *C. auris* during the pandemic, pointing out to the combined effect of overwhelmed healthcare systems and the rise of highly vulnerable patient populations (Jordan *et al.*, 2026; Parnell *et al.*, 2026).

In the present study, *C. auris* isolates were recovered from different laboratory cultures, confirming its ability to colonize and infect multiple anatomical sites. Blood cultures accounted for more than half of all cases (56.8%), followed by respiratory cultures (37.8%), whereas urinary isolates were relatively uncommon. Many previous reports are in accordance with the current distribution, which have shown that candidemia is the most frequent invasive *C. auris* infection and remains the main cause of its associated morbidity and mortality (Pappas *et al.*, 2016; Lockhart *et al.*, 2017). Similar epidemiological trends have demonstrated that *C. auris* has become a very important cause of bloodstream infections in critically ill patients (Caceres *et al.*, 2019; Wang *et al.*, 2024).

The predominance of *C. auris* isolates recovered from blood cultures observed in this study is likely multifactorial. Infection of acute COVID-19 requires admission in ICU for a long time, central venous catheterization, mechanical ventilation, urinary catheterization, parenteral nutrition, and repeated usage of broad-spectrum antimicrobial agents. All these factors help in fungal colonization and subsequent dissemination in blood (Chowdhary *et al.*, 2020; Kazancioglu *et al.*, 2024). In addition, *C. auris* has the ability to still alive on hospital surfaces and medical equipment, so the prolonged hospitalization increases the chance of exposure to contaminated healthcare environments and the *C. auris* spread among the patients (Prestel *et al.*, 2021; Bing *et al.*, 2026).

Respiratory isolates recovered from sputum and bronchoalveolar lavage cultures represent another notable finding. Severe COVID-19 disrupts the local pulmonary immune defenses and causes an extensive epithelial injury, creating favorable conditions for

the opportunistic fungal colonization and infection (Salmanton-García *et al.*, 2021; Mina *et al.*, 2022). Mechanical ventilation affects the mucosal integrity and increases the risk of secondary fungal infections in the admitted patients (Bassetti *et al.*, 2020; Bergamasco *et al.*, 2021). Nosocomial transmission contributed by the presence of *C. auris* either as a colonization or an infection of the lower respiratory tract, warrants a clinical assessment (Prestel *et al.*, 2021; Salmanton-García *et al.*, 2021; Chowdhary *et al.*, 2026).

The recovered urinary isolates were 5.4%, a finding that is consistent with a previous report, which indicated that a urinary infection is less common than a bloodstream one, but it occurs primarily in those patients with a urinary catheterization for a long time and having severe diseases (Cortegiani *et al.*, 2018). Together, these findings illustrate that the combination between severe COVID-19 and the invasive procedures used for its management creates a perfect setting for the opportunistic fungal infections at different body sites (Chowdhary *et al.*, 2020; Kazancioglu *et al.*, 2024).

In this study, *C. auris* infection following recovery from COVID-19 is likely representative of different characteristics of severe COVID-19 cases, including lymphopenia, loss of CD4⁺ and CD8⁺ T-cells, functional exhaustion of immune cells, and dysregulated inflammatory responses with increased cytokine levels (interleukin-6). All these factors compromise the host defense against the opportunistic fungal pathogens (Salehi *et al.*, 2020; Nucci *et al.*, 2021; Bing *et al.*, 2026; Ismail *et al.*, 2026).

Beyond immune dysregulation, disruption of the normal microbiota and reduction in microbial competition due to excessive use of broad-spectrum antibiotic therapy contributes to fungal overgrowth facilitating *Candida* spp. colonization (Li *et al.*, 2022). The COVID-19 pandemic imposed pressure on the infection prevention programs at the healthcare system level. Overcrowded ICUs, a shortage of personnel, healthcare, and environmental persistence of both SARS-CoV-2 and *C. auris* created favorable circumstances for hospital transmission and development of many outbreaks worldwide (Eyre *et al.*, 2018; Prestel *et al.*, 2021; Bing *et al.*, 2026). Along these lines, the rates of secondary fungal coinfection—most importantly, candidemia—among COVID-19

hospitalized patients were considerably greater than the hospital-wide population, with candidemia representing one of the deadliest comorbidities because of its associated death rate and challenging treatment approaches (Mirzaei *et al.*, 2020; Jordan *et al.*, 2026; Parnell *et al.*, 2026).

In the present study, the initial laboratory screening was performed as per the CDC recommendations on chromogenic agar, where *C. auris* generally produces white to pale pink colonies (Ravichandran *et al.*, 2022). The characteristic appearance of *C. auris* was observed in all 37 isolates, which was consistent with the phenotypic descriptions reported by Ninan *et al.* (2020); Ravichandran *et al.* (2022). Though colony morphology is not sufficient to differentiate *C. auris* from the closely related yeasts, chromogenic media represent a useful and cost-effective screening tool, particularly in laboratories where advanced identification technologies are not readily available. Their values lie in facilitating early recognition and selection of those isolates that require confirmatory testing, not for a definitive identification (CDC, 2026). Furthermore, one phenotypic characteristic of all the isolates was that they all grew at 42 °C, which further emphasizes their exceptional thermostolerance, distinguishing them from most other species in the genus *Candida*. Extreme thermostolerance is the property that is most strongly associated with the *C. auris* persistence and environmental success (Borman *et al.*, 2016; Larkin *et al.*, 2017; Casadevall *et al.*, 2019; Jenks *et al.*, 2025). The capacity to grow at temperatures above the normal body temperature has also been attributed to the evolutionary adaptation, allowing *C. auris* to overcome the mammalian thermal barrier, thereby emerging as a human pathogen (Casadevall *et al.*, 2019; Di Luca *et al.*, 2019; Jackson *et al.*, 2019). Critically, the virulence-associated enzymatic activity is maintained during high temperature conditions further enabling tissue penetration and endurance. (Rossato and Colombo, 2018; Watkins *et al.*, 2022; Semenya *et al.*, 2025).

An accurate identification of a group of 20 non-*C. auris* controls was included in the identification analysis. All 57 isolates were evaluated by VITEK 2 and MALDI-TOF MS, while 41 corresponding positive blood-culture broths, comprising 21 positive *C. auris* cultures and 20 non-*C. auris* controls were evaluated by BIOFIRE FilmArray BCID2. The main study population comprised 37 isolates that were identified

by the automated system VITEK 2 system (software version 8.01). The obtained results were confirmed by MALDI-TOF MS, which becomes a standard method for yeast's identification, as it was accurate, fast, and inexpensive when *C. auris*-specific spectra were included in a commercial or a curated database (Tan *et al.*, 2019; Ivanova *et al.*, 2023; Jamalain *et al.*, 2023; Hsu and Yassin, 2025). Complete concordance among chromogenic agar, VITEK 2, and MALDI-TOF MS provides reassurance on reliable diagnostic workflow utilized herein. Similar high levels of agreement among automated identification systems and MALDI-TOF MS have been reported by other investigator, emphasizing the importance of updated reference databases for an accurate recognition of this emerging fungal pathogen (Lockhart *et al.*, 2022).

In accordance with the 20 non-*C. auris* control group, no agreement was observed between VITEK 2, which identified all the control group as *C. auris* and MALDI-TOF MS, which identified six isolates as *C. albicans*, six as *C. tropicalis*, four as *C. famata*, and four as *N. glabratus*. The misidentification may be attributed to the fact that *C. auris* shared deeply overlapping phenotypic characteristics with other *Candida* species (Ding *et al.*, 2019; Hsu and Yassin, 2025).

The traditional culture remained the reference standard method for the diagnosis of candidemia (Timsit *et al.*, 2020; El-Sherif *et al.*, 2022); however, its limitation was a turnaround time. Identification methods, using typical conventional processes, which involve cultures and subcultures for identification, followed by an antifungal susceptibility test, may take a few more days to implement a definitive treatment decision for a patient (Kang *et al.*, 2020). While automated blood culture systems have shortened the time needed to detect a microbial growth, they do not eliminate the need for subsequent identification procedures (Bruins *et al.*, 2004). Furthermore, the conventional biochemical methods have historically misidentified *C. auris* as a closely related species, potentially delaying an appropriate antifungal therapy and infection control interventions (Altun *et al.*, 2013; Salimnia *et al.*, 2016). To address these diagnostic limitations, the BIOFIRE BCID2 panel was incorporated into 41 corresponding positive blood-culture broths of the current diagnostic workflow. Detection of *C. auris* occurred in all 21 corresponding positive blood-culture broths. BIOFIRE BCID2 yielded no *C.*

auris detections among the 20 non-*C. auris* controls. BIOFIRE BCID2 is a multiplex polymerase chain reaction (PCR) assay used for identification of pathogens directly from positive blood culture bottles by simultaneously detecting 43 clinically relevant microorganisms plus relevant antimicrobial resistance genes within an hour. It is one of the first commercially available syndromic assays that received the U.S. Food and Drug Administration/ Conformité Européenne (French for European Conformity) (FDA/CE) approval for the identification of *C. auris* (Bassetti *et al.*, 2020; Chowdhary *et al.*, 2026). The value of BIOFIRE BCID2 is particularly evident with *C. auris*, since it is associated with high mortality rates, has frequent MDR rates and substantial breakout potential. Time is critical; thus every one hour that counts before appropriate antifungal treatment and infection prevention measures may be important (Lockhart *et al.*, 2022; Rhoads *et al.*, 2023; Chowdhary *et al.*, 2026).

Quick detection enables appropriate early escalation of antifungals and allows for the early implementation of a patient isolation and contact precautions. It also enhances antimicrobial stewardship by limiting empiric treatment and, thereby, exposure to other antimicrobials. These advantages are especially relevant in intensive care settings, where delayed recognition of *C. auris* may contribute to ongoing healthcare-associated transmission (Lockhart *et al.*, 2022; Chowdhary *et al.*, 2026).

Recently, the diagnostic performance of BIOFIRE BCID2 has been consistently demonstrated. A multicenter evaluation in the United Arab Emirates has confirmed the significance of BIOFIRE BCID2. Implementation of the BIOFIRE BCID2 yielded a median reduction in the time of diagnosis of *Candida* pathogens from 92 to 28 h. ($p < 0.0001$), increased pathogen-detection rates compared to the conventional methods (98.8% versus 87.9%), and was associated with a significantly improved rate of 30-d. survival (17.3% versus 31.6% [$p = 0.019$]) (Senok *et al.*, 2023). Other multicenter evaluations have displayed high sensitivity and specificity among most of the included microorganisms, including the challenging *C. auris*, along with an accurate identification of antimicrobial resistance mechanisms (Kim *et al.*, 2024; Aygar and Hoşbul, 2025). Comparable findings have also been reported in Egypt. El-Sherif *et al.* (2022) reported a sensitivity of 75.8% and a specificity

of 98% of identifying pathogens from central line-associated bloodstream infections with the use of BIOFIRE BCID2 compared to the VITEK 2 system. However, the sensitivity and specificity of identifying antimicrobial resistance genes were higher for the BIOFIRE BCID2 (90% and 99.6%, respectively).

Findings of this study further support the incorporation of BIOFIRE BCID2 into the diagnostic workflow with a suspected *C. auris* candidemia. Given that more than half of all isolates in the present study originated from blood cultures, rapid molecular identification provided clinically meaningful information considerably earlier than the conventional culture-based methods alone. Nevertheless, BIOFIRE BCID2 should be regarded as a complementary rather than a replacement technology. This assay detects only predefined pathogens and resistance markers but does not provide antifungal susceptibility results. Consequently, conventional culturing remains indispensable for isolate recovery, epidemiological investigations, and comprehensive antifungal susceptibility testing, particularly in view of the marked geographic variations in the *C. auris* resistance profiles (Rhoads *et al.*, 2023). These obtained diagnostic results demonstrated the higher clinical accuracy of BIOFIRE BCID2 and proteomic fingerprinting of MALDI-TOF MS than VITEK 2 in the identification of *C. auris*, preventing the constant risk of metabolic cross-reactivity. A 100% agreement was observed between BIOFIRE BCID2 panel results and those of MALDI-TOF MS in identifying *C. auris* (41/41) and identifying species-specific targets (37/37) as expected of an array designed with a gene-target amplification. This array tested the highly conserved sequences in all *C. auris* isolates.

By focusing on the highly conserved regions, *C. auris* isolates could be correctly identified; because of this, the BIOFIRE BCID2 panel has an apparent 0% false positive rate compared to the 100% rate observed with VITEK 2, representing an incorrect identification of all the non-*C. auris* controls and misidentification of the following isolates: *C. albicans*, *C. tropicalis*, *C. famata* and *N. glabratus*. The use of conventional culturing, phenotype characterization, MALDI-TOF MS, and rapid molecular testing *via* BIOFIRE BCID2 ensured a robust diagnostic strategy of the *C. auris*, which compromised species identification and enabled precise antifungal susceptibility testing. Moreover, BIOFIRE BCID2 allowed early *C. auris* detection, individual patient treatment and infection

prevention practices in high-risk environments.

Fluconazole recorded MIC ≥ 32 $\mu\text{g/ml}$ for all isolates in accordance with the CDC tentative MIC breakpoints. Resistance to fluconazole is attributed to resistance mutation in the *Erg11* gene that encodes the target enzyme of azole (CDC, 2024a). The breakpoint of flucytosine was ≥ 32 $\mu\text{g/ml}$ which was interpreted according to the other *Candida* species breakpoint (CLSI, 2017). MICs of flucytosine were ≥ 64 $\mu\text{g/ml}$ in 91.9% of the isolates and ≤ 1 $\mu\text{g/ml}$ in 8.1% of them, in consistency with a report from Africa (Osaigbovo *et al.*, 2024). MICs were above the exploratory cut-off of ≥ 32 $\mu\text{g/ml}$ which was not interpreted as an established resistance. Flucytosine MICs were observed in blood, urine, sputum and BAL-derived isolates in 90.5%, 100%, 100%, and 83.3%, respectively. Flucytosine was not effective when used as a monotherapy; however, complete growth inhibition of resistant *C. auris* was achieved on using combinations of amphotericin B-5-flucytosine and anidulafungin-5-flucytosine at concentrations of 0.25/1 mg/l and 0.008/1 mg/l, respectively (O'Brien *et al.*, 2020a, John *et al.*, 2023). Flucytosine is an anti-*Candida* drug that enters the fungal cell and inhibits the synthesis of both proteins and DNA (Chowdhary *et al.*, 2018; Osaigbovo *et al.*, 2024).

Antifungal susceptibility testing results recorded 100% resistance to fluconazole and high rates of 91.8% for flucytosine. These findings are in concordance with the global epidemiology of *C. auris* (Osman *et al.*, 2020; Khairat *et al.*, 2021; Deshkar *et al.*, 2022). Fluconazole resistance typically exceeded 90% across most of the recorded surveillance reports worldwide and was generally considered one of the most definitive features of this emergent pathogen (Ahmad and Alfouzan, 2021; Garcia-Bustos *et al.*, 2021; Ahmad and Asadzadeh, 2023). In contrast, the resistance rates of amphotericin B and echinocandins are variable regionally and amongst the clades of several circulating microorganisms (Maphanga *et al.*, 2021; Yadav *et al.*, 2021; Burrack *et al.*, 2022; Kilburn *et al.*, 2022). In accordance, data from previous surveillance studies in the United States revealed a fluconazole resistance of 90%, amphotericin B of 30%, and echinocandins of 5%. Higher rates of amphotericin B resistance have been observed in New York-New Jersey outbreak (Kilburn *et al.*, 2022). Additionally, similar trends have been documented in South Africa and India where fluconazole resistance

reached 90-95%, whereas amphotericin B and echinocandin resistance remained rare (Maphanga *et al.*, 2021; Yadav *et al.*, 2021). These discrepancies reflect the distribution of the different genetically divergent groups of *C. auris*, each was associated with a unique susceptibility profile (Maphanga *et al.*, 2021; Yadav *et al.*, 2021; Burrack *et al.*, 2022; Kilburn *et al.*, 2022).

Despite universal resistance to fluconazole, all isolates in the present study remained susceptible to voriconazole (breakpoint 1 $\mu\text{g/ml}$) (Arendrup *et al.*, 2017; Bohner *et al.*, 2023), which exerted its antifungal activity by inhibiting the biosynthesis of ergosterol. It selectively inhibited 14α -sterol demethylase enzyme of fungal Cytochrome P450 leading to the depletion of ergosterol, disruption of fungal cell membrane integrity, and inhibition of fungal growth (Ghannoum *et al.*, 2002). Similarly, all tested isolates were susceptible to amphotericin B antifungal (breakpoint ≥ 2 $\mu\text{g/ml}$) that targeted the fungal cell membrane by interacting with ergosterol to form ion channels, which may cause cell death by permitting the release of protons and cations from the cells (Al-Balushi *et al.*, 2018; Rybak *et al.*, 2019).

The voriconazole MICs ranged from ≤ 0.12 to 1 $\mu\text{g/ml}$ with MIC₅₀ of 0.25 and MIC₉₀ of 0.5 $\mu\text{g/ml}$. These results are described in a descriptive manner without any classification into susceptibility categories as the primary objective of the analysis was to characterize the antifungal response patterns of the tested isolates rather than determine their clinical susceptibility or resistance status. MICs of amphotericin B were between 0.125–0.75 $\mu\text{g/ml}$ (MIC₅₀, 0.5 $\mu\text{g/ml}$; MIC₉₀, 0.75 $\mu\text{g/ml}$), but no isolate attained MIC ≥ 2 $\mu\text{g/ml}$ (breakpoint [CDC value]). The echinocandin class displayed the highest susceptible percentage recording 91.8% for caspofungin (≥ 2 $\mu\text{g/ml}$ breakpoint) and 89.2% for micafungin (≥ 4 $\mu\text{g/ml}$) (CDC, 2024a). The mode of action of echinocandins was based on the inhibition of β -1,3-glucan, an essential polysaccharide in the fungal cell wall (Chen *et al.*, 2011; Perlin, 2011). Isolates derived from blood and urine cultures met the echinocandin resistance threshold by 9.5% and 50.0% for caspofungin and 9.5% and 100% for micafungin, respectively. This susceptibility pattern differed from that reported from several endemic regions and suggested that amphotericin B and echinocandins remained effective therapeutic options in our setting. These results also emphasized the importance of local

antifungal susceptibility surveillance, as treatment recommendations should be based on the resistance patterns of the region and not only on the global trends (CDC, 2024c; Wang *et al.*, 2024). Echinocandins are now the first-line therapeutic agents advised for use against invasive *C. auris* infections according to the WHO. This is based on the fact that most of the clinical isolates have demonstrated a sensitivity towards the echinocandins, in addition to the success of echinocandin-mediated treatment of invasive *C. auris* infection observed so far (Lepak *et al.*, 2017; Biagi *et al.*, 2019; Kwon *et al.*, 2019). However, a great number of emerging resistant strains has been detected for the last decade as a result of the continued, recurring use, and treatment courses with echinocandins (Biagi *et al.*, 2019). High echinocandin's susceptibility observed in the current isolates supported their use while waiting for the susceptibility results, with the use of amphotericin B as an alternative treatment. The prevalence of strains that are resistant to multidrugs or all antifungal drugs is rapidly emerging and represents the biggest challenge in terms of treatment of *C. auris*.

Even though pan-resistant strains are currently sporadic, they have been reported in several countries and leads to a high death rate due to limitations in the number of treatment alternatives (Lockhart *et al.*, 2019). The combination of antifungal drug therapy has therefore attracted considerable attention. Many antifungal combinations were reported to be synergistic, including flucytosine and amphotericin B, or echinocandins, caspofungin and posaconazole, anidulafungin and flucytosine or manogepix (O'Brien *et al.*, 2020b; Balla *et al.*, 2022; John *et al.*, 2023). Several emerging antifungals such as fosmanogepix which showed well-known effects *in vitro* and in early stages of clinical trials, and rezafungin, a long-acting echinocandin, which has favorable pharmacokinetic properties along with a high antifungal activity in clinical trials, have gained remarkable attention as prospective agents for MDR *C. auris* infection (Tóth *et al.*, 2019; Ham *et al.*, 2021; Vazquez *et al.*, 2023; CDC, 2024b).

Several strengths improve the significance of the present study. It provides one of the few detailed evaluations of post-COVID-19 laboratory-confirmed *C. auris* infection, integrating comprehensive clinical data with phenotypic identification, MALDI-TOF MS confirmation, rapid molecular diagnosis using the

BIOFIRE BCID2 panel, and antifungal susceptibility testing. This integrated diagnostic approach allowed timely identification of bloodstream infections while providing a clinically relevant susceptibility data that may help inform the local treatment strategies.

The study also has several limitations. First, the relatively small number of candidemia cases that reduced the statistical power. Second, molecular typing was not performed; thus, prevalent strains of *C. auris* and transmission of strains within the healthcare setting have not been analyzed. Follow-up research studies using advanced approaches, such as whole-genome sequencing (WGS) with comprehensive patient samples, will allow the detailed epidemiologic definition of regional patterns, routes of transmission, mechanisms of antifungal resistance and clinical outcomes (Parnell *et al.*, 2026).

Conclusions and Recommendations

Candida auris has become an important opportunistic pathogen among patients recovering from COVID-19 infection, particularly those with prolonged hospitalization and intensive care exposure. The findings demonstrate substantial differences in the performance of the evaluated identification platforms for *C. auris*. Vitek 2 correctly identified the main 37 isolates of the study as *C. auris* but misidentified all 20 non-*C. auris* control as *C. auris*. In contrast, MALDI-TOF MS showed complete discrimination between *C. auris* and non-*C. auris* isolates in the evaluated collection. BIOFIRE BCID2 demonstrated 100% agreement with MALDI-TOF MS for *C. auris* versus non-*C. auris* classification in the shared 41-culture subset and showed complete species-level agreement for microorganisms targeted by the panel. These findings indicate that BIOFIRE BCID2 and MALDI-TOF MS provided more specific identification than VITEK 2 in this study, particularly for distinguishing *C. auris* from closely related or other yeast species. The antifungal susceptibility results demonstrated a concerning pattern of reduced susceptibility among the *C. auris* isolates. The observed resistance profile, characterized by universal fluconazole resistance but with preserved susceptibility to amphotericin B and echinocandins, supported the current treatment recommendations and emphasized the importance of a continued local resistance surveillance. Overall, these findings highlight the value of integrating rapid molecular

diagnostics with conventional microbiological methods to improve patient management, strengthen infection prevention strategies, and optimize antifungal stewardship in healthcare settings where *C. auris* continues to emerge. Accordingly, confirmation of suspected *C. auris* isolates using a reliable reference method, particularly when identified by VITEK 2, is recommended. Rapid molecular blood-culture testing such as BIOFIRE BCID2 may further facilitate early recognition and appropriate infection-control responses. Routine antifungal susceptibility testing and ongoing laboratory and infection-control surveillance should be maintained to detect emerging resistance and support appropriate clinical management.

Novelty Statement

The novelty of this study lies in using a novel strategy for enabling a timely recognition of bloodstream infection using the BioFire® BCID2 panel in combination with conventional microbiological methods for the early and accurate diagnosis of *C. auris*, improvement of patient's management, infection control, and antifungal stewardship.

Author's Contributions

Fatma Ahmed: Methodology, formal analysis, resources, data curation.

Iman M. El-Kholy: Conceptualization, methodology, validation, investigation, review and editing, visualization, supervision, project administration.

Nadia A. Elkady: Methodology, formal analysis, writing original draft, writing review and editing, project administration.

Adel A. El-Mehalawy: Conceptualization, review and editing, supervision, project administration.

Dalia A.M. Abdou: Conceptualization, methodology, validation, investigation, data curation, writing original draft, writing review and editing, project administration.

All authors reviewed and approved the final manuscript.

Generative AI and AI assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of the text of the manuscript.

Ethical approval

The Institutional Research Ethics Committee of the

Faculty of Science, Ain Shams University, reviewed and approved the study protocol with an approval number ASU-SCI/MICR/2026/08/02

Conflict of interests

The authors have declared no conflicts of interest.

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