AUSTRALIAN JOURNAL OF BIOMEDICAL RESEARCH
Australian Journal of Biomedical Research
(eISSN 3083-4708)
Australasia Publishing Group

Original Article

A Comprehensive Review of *Candida auris* Infections in Saudi Hospitals: Risk Factors, Resistance, and Mortality: A Systematic Review

Waleed Abdullah Almalki[1,2]

[1]*Department of Clinical Laboratory Sciences, College of Applied Medical Sciences, Taif University, Taif, Saudi Arabia*
[2]*Department of Botany and Microbiology, College of Science, King Saud University, Riyadh, Saudi Arabia*

Received: Mar 27, 2026
Accepted: May 16, 2026

Corresponding author's email:
walmalki234@gmail.com

Citation: Almalki WA. A Comprehensive Review of Candida auris Infections in Saudi Hospitals: Risk Factors, Resistance, and Mortality: A Systematic Review. Australian Journal of Biomedical Research. 2026;2(2):aubm021. https://doi.org/10.63946/aubiomed/18581

ABSTRACT

Candida auris is an emerging multidrug-resistant pathogen that represents a major global health threat. It readily colonizes the skin, spreads efficiently in healthcare settings, and causes severe infections in critically ill patients. Cases of *C. auris*, including bloodstream infections, urinary tract infections, and co-infections with bacteria such as *Acinetobacter baumannii, Pseudomonas aeruginosa, Klebsiella pneumoniae, and Staphylococcus aureus*, have been documented across Saudi Arabian hospitals. The pathogen has also been associated with worse outcomes in COVID-19 patients. However, data on antifungal resistance mechanisms and disease epidemiology in the Kingdom remain limited. This review synthesizes documented cases from Saudi Arabian hospitals, with a focus on clinical features, risk factors, antifungal susceptibility, and patient outcomes, to improve healthcare awareness, guide infection control strategies, and support effective management of *C. auris* infections in the region.

Keywords *Candida Auris*; Saudi Arabia; Multidrug-Resistant Fungi; Healthcare-Associated Infections; COVID-19; Nosocomial Transmission; Antifungal Resistance

Introduction

C. auris is a yeast-forming member of the genus Candida. Morphologically, *C. auris* is a budding yeast with cells grouped singly, in pairs, or in small clusters, ranging in size from 2.5 to 5.0 micrometers. It grows optimally at 40°C, with reduced growth at 42°C. *C. auris* does not produce hyphae or pseudohyphae under standard conditions; however, pseudohyphae-like structures may form under high-salt stress and heat-shock protein depletion. On Sabouraud dextrose agar, colonies appear smooth and white to cream-colored, while on CHROMagar, they range from light to deep pink. It was first isolated from the ear canal of a patient at the Tokyo Metropolitan Geriatric Hospital in Japan in 2009. Since then, it has spread to over 35 countries on all continents except Antarctica, with cases reported in South Korea in 2011 and the United States in 2013 (1). In 2017, *C. auris* was identified in blood and pleural tissue samples from tertiary care hospitals in Dammam and Riyadh, Saudi Arabia. Multiple publications and case series have since documented hospital-based outbreaks, underscoring the growing clinical and epidemiological significance of *C. auris* in the Kingdom (2). The pathogen persists on hospital surfaces for up to 14 days, including plastic, and spreads primarily through direct or indirect contact with contaminated surfaces and healthcare workers, causing nosocomial infections. *C. auris* has caused severe harm in patients worldwide, including fatal invasive bloodstream infections (1). Candidemia remains one of the most common hospital-acquired bloodstream infections, with *C. auris* emerging as a particularly dangerous causative pathogen due to its high morbidity and mortality (2). Treatment is complicated by an unfavorable resistance profile: fluconazole resistance exceeds 90%, amphotericin B resistance surpasses 35%, and combined multidrug resistance is observed in over 40% of isolates. The COVID-19 pandemic further accelerated its global spread, driving a substantial increase in reported outbreaks. Published data on *C. auris* infections in Saudi Arabia remain limited (3). This review aims to systematically summarize available evidence on *C. auris* in Saudi hospitals, with a focus on epidemiology, risk factors, antifungal resistance, and patient outcomes.

Materials and Methods

Study Design and Search Strategy:

A systematic literature review was conducted to identify relevant studies on *C. auris* infections in Saudi Arabia. In February 2026, a comprehensive search was conducted across the major electronic databases, namely PubMed, Web of Science, and Google Scholar. The following keywords and Boolean operators were used in the search strategy: ("*Candida auris*" AND "Saudi Arabia"), ("*Candida auris*" AND "hospital"), ("*Candida auris*" AND "mortality"), and ("*Candida auris*" AND "antifungal resistance").

Criteria for Inclusion and Exclusion:

Studies that satisfied the following requirements were included:

(1) reported cases of *C. auris* colonization or infection within Saudi healthcare facilities.

(2) offered information on at least one important outcome, such as patient demographics, risk factors, antifungal susceptibility, or mortality.

(3) were published in English between 2017 and 2025.

Studies that reported instances outside of Saudi Arabia, lacked primary patient data (such as editorials or commentaries), or had redundant or insufficient clinical information were all omitted.

Data extraction and study selection:

Every record identified was screened for relevance and duplicates. After title and abstract screening, eligible articles were retrieved in full and assessed against the predefined inclusion criteria. Data were extracted on the number of infected or colonized patients, mortality rates, antifungal susceptibility patterns (fluconazole, amphotericin B, and echinocandins), patient comorbidities, and associated risk factors. Where the same patient cohort appeared in multiple publications, data were counted only once to avoid duplication.

Visualization and Synthesis of Data:

The retrieved material was synthesized using both narrative descriptions and summary tables. Crude mortality rates and antifungal resistance percentages were calculated by pooling data across the included studies. A formal meta-analysis was not performed due to heterogeneity in study designs and reporting formats. Data visualization was performed using Datawrapper (https://www.datawrapper.de) to produce a choropleth map illustrating the geographic distribution and epidemiological outcomes of *C. auris* in the chosen Saudi Arabian locations.

PRISMA Flow Diagram:

The study selection process followed PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines. Presents the PRISMA flow diagram (Fig. 1). A total of 1,183 records were identified across all three databases (PubMed: n = 8; Web of Science: n = 15; Google Scholar: n = 1,160). After removal of 33 duplicate records, 1,150 records were screened by title and abstract, of which 1,125 were excluded as they did not meet the inclusion criteria. The remaining 25 full-text articles were assessed for eligibility; 15 were subsequently excluded due to insufficient clinical data, duplicate patient reporting, or scope outside Saudi Arabia. A final set of 10 studies was included in the qualitative synthesis.

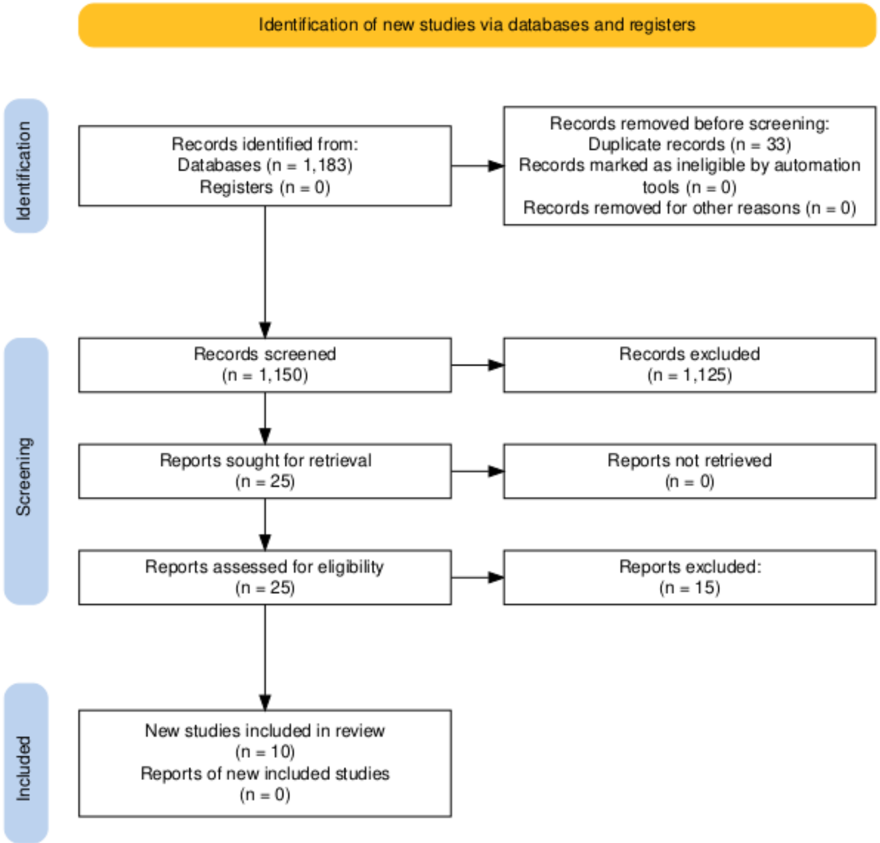

Figure 1. PRISMA flow diagram illustrating the study selection process.

Quality Assessment of Included Studies:

The methodological quality of all included studies was assessed independently using the JBI (Joanna Briggs Institute) Critical Appraisal Tools, with the checklist selected according to each study's design: JBI Checklist for Textual Evidence: Narrative for editorial or narrative review (n = 1), JBI Checklist for Prevalence Studies for retrospective cohort and descriptive studies (n = 3), JBI Checklist for Case Series (n = 2), and JBI Checklist for Case Reports (n = 3). One study (Almajid et al., 2025) was assessed using the JBI Checklist for Prevalence Studies as a comprehensive observational review. Each criterion was scored as Yes, No, or Unclear. Studies meeting ≥70% of applicable criteria were rated high quality; those meeting 50–69% were rated moderate quality. Summarizes (Table 1) the quality assessment results. Seven studies were rated as high quality and two as moderate quality, supporting the overall reliability of the synthesized evidence.

Table 1 Quality assessment of included studies using JBI Critical Appraisal Tools.

Quality	%	Score	Appraisal Tool	Study Design	Study (Year)
High	100%	6/6	JBI Textual Evidence: Narrative	Editorial/Narrative	Shariq et al. (2023)
High	100%	8/8	JBI Prevalence Studies	Genomic Cohort	Guan et al. (2025)
High	90%	9/10	JBI Case Series	Cross-sectional	Alshahrani et al. (2025)
High	87.5%	7/8	JBI Prevalence Studies	Retrospective Cohort	Kaki (2023)
High	87.5%	7/8	JBI Prevalence Studies	Observational Review	Almajid et al. (2025)
Moderate	67%	6/9	JBI Case Series	Case Series	AlJindan et al. (2021)
High	75%	6/8	JBI Case Report	Retrospective Multicenter	Alanazi et al. (2025)
High	87.5%	7/8	JBI Case Report	Case Report	Elsawy et al. (2019)

Quality	%	Score	Appraisal Tool	Study Design	Study (Year)
High	100%	8/8	JBI Case Report	Case Report	Alashqar et al. (2021)
Moderate	67%	6/9	JBI Case Series	Case Series	Al-Jindan & Al-Eraky (2021)

Abbreviations: *JBI, Joanna Briggs Institute. High quality: ≥70% of criteria met; Moderate quality: 50–69% of criteria met.*

Results

Epidemiology of *C. auris* in Saudi Arabia

As illustrated in (Fig. 2), a total of 110 cases were identified across the included studies. It should be noted that this figure represents cases with available geographic data from regional studies only and does not include cases reported at the national level by the ministry of health and other healthcare facilities across the kingdom. The majority of included studies were conducted in three regions Riyadh, the Western Region (Jeddah and Makkah city) and the Eastern Province (Al-Khobar) with no published data available from other regions of the Kingdom. This geographic gap in literature likely reflects a reporting bias rather than a true absence of disease, as *C. auris* may be present but undetected or unreported in centers with limited diagnostic capacity or surveillance infrastructure. Within the three documented regions, cases were heavily concentrated in Riyadh (77 cases, approximately 70% of the total), yet the city recorded a comparatively low number of deaths despite this high case burden. This discrepancy may partly reflect the concentration of specialized tertiary care facilities in the capital, which may afford superior clinical management resources and more aggressive infection control protocols. However, this remains a hypothesis that requires deeper investigation through well-designed prospective studies before any definitive conclusions can be drawn. The Western Region reported 28 cases (25.5%), consistent with its role as a major healthcare hub, while the Eastern Province reported only five cases (4.5%), a figure that may similarly underestimate the true local burden.

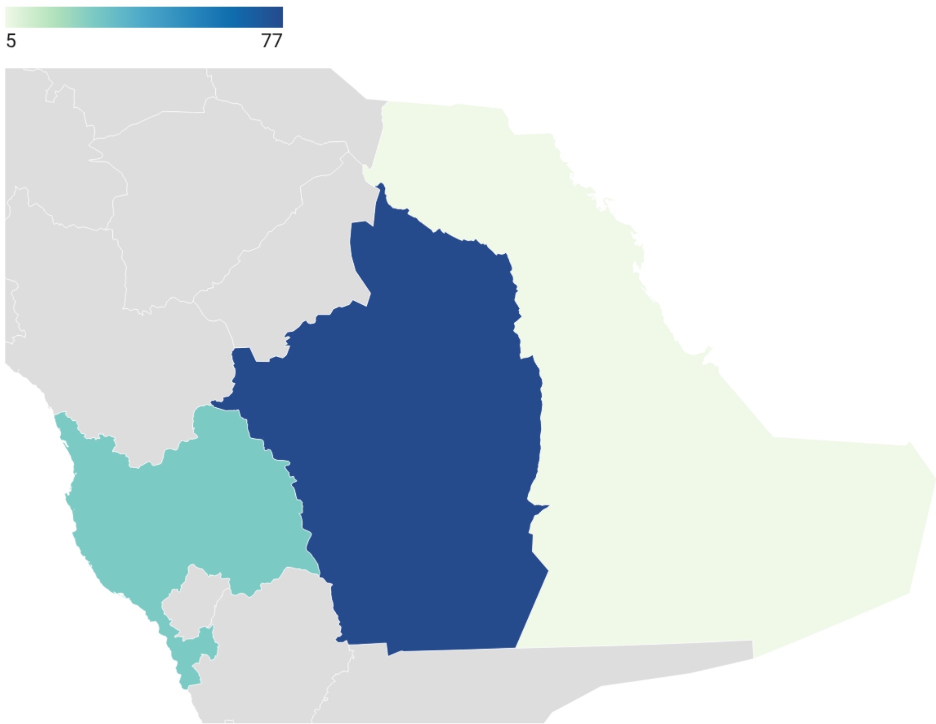

Figure 2. Geographical distribution of study cases across selected regions in Saudi Arabia.

The color coded map illustrates the variation in infection cases: the cream (pale) hue indicates 5 cases in the Eastern Province (specifically Al-Khobar). The light green represents the Makkah Region (including Jeddah and Makkah city) with 28 cases, and the dark blue signifies the highest incidence in the Riyadh Region with 77 cases.

***C. auris* in Saudi Hospitals: Cases and Mortality:**

A pooled analysis of published Saudi Arabian literature identified 252 patients with *C. auris* infection across the included studies, of whom 118 died, yielding a crude all-cause mortality rate of 46.8%; 80.5% of deaths occurred within the first 30 days. Ninety *C. auris* isolates were evaluated for antifungal susceptibility.

Echinocandin activity remained high: 95.5% of isolates were susceptible to caspofungin, 96.4% to anidulafungin, and 96.3% to micafungin. In contrast, only 14.4% of isolates were susceptible to fluconazole, while 76.6% were susceptible to amphotericin B (2).

King Fahad Medical City hospital in Riyadh, Saudi Arabia:

A genomic investigation at King Fahad Medical City (KFMC) in Riyadh identified 23 *C. auris* isolates from 20 patients between August 2018 and May 2019; 80% had invasive infections. All isolates, initially misidentified as Candida spp., were confirmed by ITS sequencing and WGS. Universal fluconazole resistance was detected, along with resistance to voriconazole, itraconazole, and posaconazole; amphotericin B and echinocandin resistance were absent. Phylogenomic analysis assigned all isolates to Clade I, with a mean pairwise SNP distance of 17, consistent with at least two independent hospital introductions (Table 2). The K143R mutation in *ERG11* conferred azole resistance across all isolates, while the CIT1 V213A mutation was implicated in 5-flucytosine resistance in one isolate. Transmission network analysis identified super-spreader patients (4).

Table 2 summarizes the King Fahad Medical City Study's findings regarding genetic mutations in *C. auris* and related antifungal resistance.

Gene	Associated drug resistance
ERG11	Azoles
FCY1	5-flucytosine
CIT1	5-flucytosine
FUR1	5-flucytosine
FCY2	5-flucytosine

Abbreviations: *C. auris, Candida auris; ERG11, FCY1, CIT1, FUR1, and FCY2 are genes associated with antifungal resistance.*

Risk Factors for *C. auris* Infection in Riyadh Hospitals:

A descriptive cross-sectional study at a tertiary hospital in Riyadh examined 53 *C. auris* positive patients (33 males, 20 females; age range 15–98 years) between 2020 and 2022. Key risk factors included at least one comorbidity (85%), prior hospitalization (50.9%), and ICU admission (35%). Additional factors included wounds (34%), indwelling devices (32.1%), and recent antibiotic use (28.3%). Multivariate analysis identified prior hospitalization, indwelling devices, and comorbidity as independent predictors of *C. auris* colonization or infection, while advanced age showed a marginally significant association. Sex, recent surgery, and antibiotic exposure were not independently significant (5).

King Abdulaziz University Hospital in Jeddah, Saudi Arabia:

A retrospective study at King Abdulaziz University Hospital in Jeddah reviewed 27 patients with invasive *C. auris* infections from 2015 to 2022. The median age was 58 years and 66.7% were male. Central line-associated bloodstream infection was the most common source (63%), followed by catheter-associated urinary tract infection (12%). All patients had indwelling devices, and 81% required ICU admission. The most prevalent comorbidities were diabetes mellitus and heart disease (48.1% each) (Table 3). The median hospital stay was 78 days, and the 90-day mortality rate was 66.7% despite antifungal treatment. All isolates were susceptible to voriconazole, caspofungin, and amphotericin B, while only 11.1% were susceptible to fluconazole (3).

Table 3 Clinical risk factors and major comorbidities in individuals infected with *C. auris*.

Category	Factor	Percentage %
Comorbidity	Diabetes mellitus	48.1
Comorbidity	Heart disease	48.1
Clinical factor	ICU admission	81
Medical factor	Presence of indwelling medical devices	100
Infection type	Central line-associated bloodstream infection	63
Infection type	Catheter-associate urinary tract infection	12

Abbreviations: *C. auris, Candida auris; ICU, Intensive Care Unit.*

Hospital in Al Khobar, Saudi Arabia:

A study at a tertiary care hospital in Al Khobar analyzed *C. auris* isolates from five patients between November 2018 and April 2019. Six clinical specimens were collected from blood, urine, ear swabs, and groin samples, and isolates were confirmed by MALDI-TOF MS and 18S rRNA/ITS sequencing. All isolates were resistant to fluconazole; 50% were resistant to voriconazole and 50% to amphotericin B, while flucytosine, micafungin, and caspofungin retained activity. Molecular analysis identified two *ERG11* mutations (F132Y and K143R) conferring azole resistance, with no *FKS1* alterations detected (Table 4). Three of the five patients died within one month of *C. auris* identification, all with multiple comorbidities (6).

Table 4 Gene targets and primers utilized for *C. auris* molecular identification and resistance study.

Gene Target	Primer Name	Primer Sequence (5'–3')	Purpose
18S rRNA	NS1	GTAGTCATATGCTTGTCTC	Molecular identification of fungal isolates
18S rRNA	NS8	TCCGCAGGTTCACCTACGGA	Amplification of the 18S rRNA gene for phylogenetic analysis
ITS region	ITS1	TCCGTAGGTGAACCTGCGG	Amplification of ITS region for species confirmation
ITS region	ITS4	TCCTCCGCTTATTGATATGC	Sequencing and identification of fungal species
ERG11	ERG11-F	ATGGCTATTGTTGAAACTGTC	Detection of mutations associated with azole resistance
ERG11	ERG11-R	TTAGTAAACACAAGTACCAAC	Amplification of *ERG11* gene for mutation analysis
FKS1	FKS1-F	TTGGTGGTGTTGTTGTTGTT	Screening for echinocandin resistance mutations

Abbreviations: *C. auris, Candida auris; rRNA, ribosomal RNA; ITS, internal transcribed spacer; ERG11 and FKS1 are genes associated with antifungal resistance; F, forward primer; R, reverse primer.*

Al Noor Specialist Hospital, Makkah, Saudi Arabia:

The second confirmed case of *C. auris* in Saudi Arabia was reported in 2019 from Al Noor Specialist Hospital in Makkah. A 68-year-old diabetic man admitted following severe head trauma developed multiple hospital-acquired infections during a prolonged hospitalization, including urinary tract infection, hospital-acquired pneumonia, and infected pressure ulcers. *C. auris* was isolated from two blood cultures and the femoral catheter tip and confirmed by MALDI-TOF MS with 99.9% certainty. The isolate was resistant to both fluconazole and amphotericin B; caspofungin therapy was initiated but the patient deteriorated rapidly and died within days. This case highlights the critical importance of molecular confirmation of all Candida isolates (7).

Two Cases in a university hospital, Saudi Arabia:

First case:

Due to infected pressure sores, an 85-year-old man with multiple comorbidities including prior stroke, pressure ulcers, and cellulitis was readmitted. Initial bacterial co-infections caused by *Propionibacterium acnes, Klebsiella pneumoniae, Morganella morganii, and Acinetobacter baumannii* were treated with meropenem and vancomycin. *C. auris* was isolated from urine on day 27, confirmed by VITEK-2 and MALDI-TOF MS with growth at 42°C. Empirical therapy included tigecycline, followed by caspofungin and colistin. Despite treatment, the patient deteriorated, and one month after *C. auris* was identified, he died (8).

Second case:

A 62-year-old man with multiple comorbidities (peripheral vascular disease, diabetes, hypertension, dyslipidemia, coronary artery disease, below-elbow amputation, and prior stroke) was admitted with fever of unknown origin. During hospitalization he developed sequential bacterial infections including *Staphylococcus epidermidis*, MRSA, *K. pneumoniae*, and *Pseudomonas aeruginosa*. These were managed with a sequence of antibiotics including ceftriaxone, piperacillin/tazobactam, clindamycin, ceftazidime, gentamicin, meropenem, and colistin. *C. auris* was isolated from urine on day 47 after admission using the VITEK-2 system and verified by MALDI-TOF MS. Colonies grew well at 42°C. Caspofungin was planned; however, three weeks after *C. auris* isolation, the patient's condition worsened, and he died before antifungal therapy could begin (8).

Prince Mohammad Bin Abdulaziz Hospital Riyadh, Saudi Arabia:

A 48-year-old woman with diabetes, hypertension, and epilepsy was admitted with fever, dyspnea, and cough and was subsequently diagnosed with severe COVID-19 pneumonia requiring intubation and ICU admission. Chronic *Acinetobacter baumannii* bacteremia developed during hospitalization, requiring prolonged antibiotic therapy. *C. auris* candidemia was identified using the VITEK-2 system on day 20 of admission and verified by growth at 42 °C. Anidulafungin was initiated but candidemia persisted. The patient required tracheostomy and prolonged mechanical ventilation, and died of sudden cardiorespiratory arrest after 90 days. Notably, *C. auris* was later discovered in two more ICU patients, indicating potential nosocomial transmission (9)

Ministry of Health hospitals, Saudi Arabia:

A national three-year retrospective study (2020–2022) across 45 Ministry of Health facilities documented 511 *C. auris* cases, of which 56.9% were classified as infections and 43.1% as colonization. Most patients were male (68.9%) and nearly one-third were older than 65 years. ICU admission was recorded in 95.5% of cases. Diabetes mellitus and hypertension were the most common comorbidities. Frequently used invasive devices included Foley catheters (85.9%), mechanical ventilators (68.5%), tracheostomies (53.8%), and central venous lines (37.7%). The overall crude mortality rate was 41.5%; infected patients had higher mortality than colonized patients, though the difference was not statistically significant. Central line use and COVID-19 were more prevalent in infected patients, while hypertension, diabetes, and peripheral lines were more common in colonized cases (10).

As appears in (Fig.3) the distribution of *C. auris* cases and associated mortality across Saudi Arabian cities and national healthcare facilities (2, 10) reveals a notable disparity between case volume and mortality burden. At the regional hospital level, 252 cases were recorded with 118 deaths, yielding an overall case-fatality ratio of 46.8%, which underscores the severe clinical impact of *C. auris* even within well-established tertiary care settings. At the city level, Riyadh recorded the highest absolute case count (77 cases) with a relatively low number of deaths (3 deaths). Jeddah, by contrast, recorded the highest case-fatality ratio among all reported cities, with 18 deaths among only 27 cases (66.7%), suggesting either greater clinical severity, a higher prevalence of advanced comorbidities in that patient population, or potentially delayed diagnosis and treatment initiation. Al-Khobar, despite its small case count (5 cases), recorded 3 deaths, yielding a case-fatality ratio of 60%, which raises concerns about the adequacy of local diagnostic and clinical response capacity. At the national level, Ministry of Health facilities documented the largest overall burden with 511 cases and 212 deaths (41.5%), a figure that substantially exceeds the regional hospital data and reflects the true breadth of the *C. auris* epidemic across the Saudi healthcare system, underscoring the urgent need for a unified national surveillance strategy, standardized diagnostic protocols, and coordinated infection control measures across all healthcare sectors .

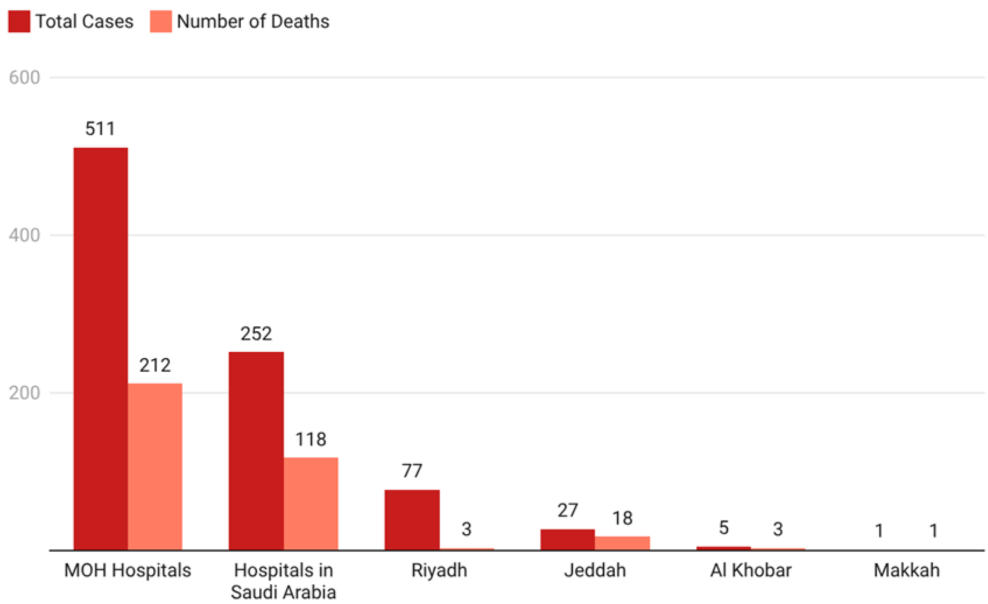

Figure 3. Presents a bar graph showing the distribution of *C. auris* cases and associated deaths across Saudi Arabian cities and healthcare sectors. MOH hospitals reported the highest burden with 511 cases and 212 deaths, while regional hospitals collectively documented 252 cases and 118 deaths. At the city level, Jeddah recorded a higher case-fatality ratio (18 deaths among 27 cases) compared with Riyadh (3 deaths among 77 cases), Makkah (1 death among 1 case), and Al-Khobar (3 deaths among 5 cases). Dark red bars represent total cases and light red bars represent deaths.

Abbreviations: *C. auris, Candida auris; MOH, Ministry of Health.*

Discussion

This review documents a consistent and concerning pattern of nosocomial *C. auris* spread across Saudi Arabian hospitals. The data demonstrate a strong association with advanced age, male predominance, and critical care settings, including ICU admission and mechanical ventilation (2, 10). During the COVID-19 pandemic, resource constraints such as staff shortages and reduced personal protective equipment availability compromised infection control adherence, accelerating *C. auris* transmission. Key infection control deficiencies included inadequate hand hygiene, environmental contamination, shared medical equipment, and prolonged personal protective equipment use (10). *C. auris* has also been associated with worse clinical outcomes in COVID-19 patients, and its co-infection with bacterial pathogens is documented in (Table 5). Echinocandins show the highest susceptibility rates and are recommended as first-line empirical therapy, yet high mortality persists even with appropriate and timely treatment, highlighting the formidable nature of this pathogen (2). The urban concentration of cases, with Riyadh accounting for the highest burden (4, 5, 8, 9), followed by Jeddah (3), Makkah (7) and Al-Khobar (6) reflects both the high patient density in metropolitan centers and the concentration of advanced tertiary care facilities with greater diagnostic and surveillance capacity. These findings underscore the need for a coordinated national strategy encompassing active surveillance, environmental decontamination, and standardized screening protocols to contain the spread of this multidrug-resistant pathogen across Saudi healthcare settings (10).

Table 5 *C. auris*-Related Bacterial Coinfections in Saudi Arabian Cases Reported.

Bacteria	Associate infection
S. epidermidis	Bloodstream infection
Methicillin-resistant S. aureus (MRSA)	Bloodstream infection
K. pneumoniae	Urinary tract infection
P. aeruginosa	Respiratory infection (tracheal aspirate)
A. baumannii	Bloodstream infection

Abbreviations: *C. auris, Candida auris; **S.** epidermidis, Staphylococcus epidermidis; MRSA, Methicillin-resistant Staphylococcus aureus; S. aureus, Staphylococcus aureus; **K.** pneumoniae, Klebsiella pneumoniae; **P.** aeruginosa, Pseudomonas aeruginosa; **A.** baumannii, Acinetobacter baumannii.*

Comparison with Global Trends

The epidemiological and resistance patterns documented in Saudi Arabia are broadly consistent with global trends, yet several context-specific distinctions warrant discussion. In the United States, preparedness efforts following early *C. auris* outbreaks highlighted critical gaps in hospital infection control, including delayed recognition, inadequate contact precautions, and limited diagnostic capacity outside reference laboratories (11). These challenges closely mirror the diagnostic delays encountered at Saudi tertiary centers, where initial misidentification of isolates as *C. haemulonii* was common prior to library updates in automated identification systems (4). In Europe, the first documented hospital outbreak occurred in a United Kingdom intensive care unit, establishing that *C. auris* can persist in healthcare environments for extended periods despite standard disinfection protocols, and that patient-to-patient transmission via contaminated surfaces and shared equipment is a principal mode of spread (12). The nosocomial transmission patterns identified at King Fahad Medical City, including super-spreader events with a mean pairwise genetic distance of only 17 SNPs among local isolates (4), are strikingly similar to those described in the European experience. In India, whole-genome sequencing and microsatellite typing have been used to trace colonization and transmission dynamics among patients with chronic respiratory diseases, demonstrating that colonized individuals serve as persistent reservoirs capable of driving sustained nosocomial spread (13). This resonates with the Saudi MOH national data, in which 43.1% of cases were classified as colonization rather than active infection, underscoring the importance of active surveillance cultures in high-risk units. Antifungal resistance profiles in Saudi Arabia characterized by near-universal fluconazole resistance and preserved echinocandin susceptibility align with the globally predominant Clade I (South Asian) genotype confirmed by phylogenomic analysis of Saudi isolates (4). The absence of *FKS1* mutations in locally sequenced strains is reassuring and consistent with the relatively low echinocandin resistance rates reported globally for Clade I. Collectively, these comparisons highlight that while the core biological and epidemiological features of *C. auris* are consistent across regions, the Saudi Arabian context is characterized by the same diagnostic and infection control vulnerabilities that have driven outbreaks internationally, reinforcing the urgent need for a coordinated national response.

Conclusion

The emergence of *C. auris* in Saudi Arabia underscores the paucity of systematic research on this multidrug-resistant pathogen. This review consolidates available evidence from Saudi hospitals and serves as a practical reference for clinicians, researchers, and public health practitioners. It is hoped that these findings will stimulate further investigation, strengthen clinician awareness, and support effective *C. auris* infection management strategies.

Acknowledgements

Author Contributions: Conceptualization, W. A.; methodology, W. A.; formal analysis, W. A.; investigation, W. A.; resources, W. A.; data curation, W. A.; writing original draft preparation, W. A.; writing review and editing, W. A.; visualization, W. A.; supervision, W. A.; project administration, W. A. The author has read and agreed to the published version of the manuscript.

Funding: Not applicable.

Disclosure of AI Use: The author declare that no artificial intelligence (AI) tools were used in the preparation of this manuscript.

References

1. Shariq A, Rasheed Z, Alghsham RS, Al Abdulmonem W. *Candida auris*: An emerging fungus that presents a serious global health threat. Int J Health Sci. 2023;17(2). Available from: https://pub.qu.edu.sa/index.php/journal/article/view/8153
2. Almajid A, Zeidan A, Alsaihati F, Alghashmari K, Almousa Z, Ashour T, et al. A comprehensive review of epidemiology, risk factors, clinical manifestations, antifungal susceptibility, and mortality of *Candida auris* in Saudi Arabia. Cureus. 2025;17(8):e89455. doi:10.7759/cureus.89455
3. Kaki R. Risk factors and mortality of the newly emerging *Candida auris* in a university hospital in Saudi Arabia. Mycology. 2023;14(3):256–263. doi:10.1080/21501203.2023.2227218
4. Guan Q, Alasmari F, Li C, Mfarrej S, Mukahal M, Arold ST, et al. Independent introductions and nosocomial transmission of *Candida auris* in Saudi Arabia: A genomic epidemiological study of an outbreak from a hospital in Riyadh. Microbiol Spectr. 2025;13:e03260-24. doi:10.1128/spectrum.03260-24
5. Alshahrani FS, Elgujja AA, Alsubaie S, Ezreqat S, Albarrag A, Barry M, et al. Risk factors for *Candidozyma auris* among admitted patients in Riyadh, Saudi Arabia (2020–2022). Infect Drug Resist. 2025;18:3369–3381. doi:10.2147/IDR.S528127
6. Al-Jindan R, Al-Eraky DM. Two cases of the emerging *Candida auris* in a university hospital from Saudi Arabia. Saudi J Med Med Sci. 2021;9(1):71–74. doi:10.4103/sjmms.sjmms_449_19
7. Elsawy A, Alquthami K, Alkhutani N, Marwan D, Abbas A. The second confirmed case of *Candida auris* from Saudi Arabia. J Infect Public Health. 2019;12(6):907–908. doi:10.1016/j.jiph.2019.07.011
8. AlJindan R, AlEraky DM, Mahmoud N, Abdalhamid B, Almustafa M, AbdulAzeez S, et al. Drug resistance-associated mutations in *ERG11* of multidrug-resistant *Candida auris* in a tertiary care hospital of Eastern Saudi Arabia. J Fungi. 2021;7(1):18. doi:10.3390/jof7010018
9. Alashqar MB, Alabdan L, Khan M, Almakadma AH, Almustanyir S. A case report of a *Candida auris* infection in Saudi Arabia. Cureus. 2021;13(5):e15240. doi:10.7759/cureus.15240
10. Alanazi KH, Roushdy HM, Alzubaidi WI, Alanazi AS, Alanazi NM, Alamri AH, et al. An overview of healthcare-associated *Candida auris* outbreaks in Ministry of Health hospitals Saudi Arabia 2020–2022: Retrospective multicentric study. PLOS ONE.

2025;20(1):e0313589. doi:10.1371/journal.pone.0313589

11. Meyer D, Martin EK, Madad S, Dhagat P, Nuzzo JB. Preparedness and response to an emerging health threat—Lessons learned from *Candida auris* outbreaks in the United States. Infect Control Hosp Epidemiol. 2021;42(11):1301–1306. doi:10.1017/ice.2021.12
12. Ruiz Gaitán AC, Moret A, López Hontangas JL, Molina JM, Aleixandre López AI, Cabezas AH, et al. Nosocomial fungemia by *Candida auris*: First four reported cases in continental Europe. Rev Iberoam Micol. 2017;34(1):23–27. doi:10.1016/j.riam.2016.11.002
13. Yadav A, Singh A, Wang Y, Haren MHV, Singh A, de Groot T, et al. Colonisation and transmission dynamics of *Candida auris* among chronic respiratory diseases patients hospitalised in a chest hospital, Delhi, India: A comparative analysis of whole genome sequencing and microsatellite typing. J Fungi (Basel). 2021;7(2):81. doi:10.3390/jof7020081