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Original Research Paper

Epidemiology, Risk Factors, and Molecular Identification of Burn-Associated Fungal Pathogens in Thi-Qar General Hospital, Southern Iraq

Ahmed K. M. Al-Khafaji[1], Ibtisam T. Jaaez[2]

[1,2] Department of Biology, College of Education, University of Al-Qadisiyah, Iraq.

Correspondence: mtqr86@gmail.com , edu.bio.posta2@qu.edu.iq , ebtesam.jeaz@qu.edu.iq

Abstract

Background: Burn-associated fungal infections have become an increasingly important cause of morbidity and mortality worldwide. The destruction of the skin barrier, prolonged hospitalization, extensive antibiotic exposure, and burn-induced immunosuppression create favorable conditions for fungal colonization and invasion. Despite the growing clinical significance of these infections, comprehensive epidemiological and molecular studies from Iraq remain limited. This study investigated the prevalence, demographic distribution, species diversity, and molecular characteristics of fungal pathogens isolated from burn patients admitted to Thi-Qar General Hospital, Southern Iraq.

Materials and Methods: A cross-sectional study was conducted between March and September 2025 and included 95 hospitalized burn patients with a minimum stay of seven days. Burn wound swabs were collected and cultured on standard mycological media. Fungal isolates were identified using conventional phenotypic methods and confirmed by Internal Transcribed Spacer (ITS) sequencing. Phylogenetic relationships were reconstructed using the Maximum Likelihood method in MEGA software. Statistical analyses were performed to determine associations between fungal positivity and demographic or clinical variables.

Results: Overall fungal culture positivity reached 76.8% (73/95). Male patients represented 56.8% of the study population, while females accounted for 43.2%. Eight fungal species were identified. *Aspergillus fumigatus* was the predominant isolate (31.5%), followed by *Candida albicans* (21.9%) and *Rhizopus arrhizus* (16.4%). Significant associations were observed between fungal positivity and gender ($p = 0.003$), age group ($p = 0.039$), and total body surface area burned (TBSA%) ($p = 0.030$). ITS sequencing confirmed species-level identification and corrected several preliminary morphological classifications. Phylogenetic analysis demonstrated close clustering of local isolates with international clinical strains.

Conclusions: Burn patients in Southern Iraq exhibit a high burden of opportunistic fungal infections. Molecular identification significantly improves diagnostic accuracy and supports epidemiological surveillance. *A. fumigatus*, *C. albicans*, and *R. arrhizus* represent the most clinically relevant fungal pathogens in this setting.

***Corresponding Author:**

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1. Introduction

Burn injuries remain among the most severe forms of trauma encountered in modern clinical practice. Beyond local tissue destruction, burns initiate a complex systemic response involving metabolic disturbances, inflammatory dysregulation, and profound immunological impairment. Consequently, burn patients become highly susceptible to opportunistic infections that substantially increase morbidity, mortality, and healthcare costs (Jeschke et al., 2020; Ferrari et al., 2024).

The skin functions as the primary protective barrier against microbial invasion. Following thermal injury, disruption of this barrier facilitates colonization by bacteria and fungi, while necrotic tissue provides a nutrient-rich environment that promotes microbial growth. Simultaneously, burn-induced immunosuppression impairs neutrophil activity, macrophage function, and adaptive immune responses, thereby increasing vulnerability to invasive fungal infections (Gupta et al., 2022; Hoenigl et al., 2022).

Historically, bacterial pathogens such as *Staphylococcus aureus*, *Streptococcus pyogenes*, and *Pseudomonas aeruginosa* dominated burn wound infections. However, advances in antibacterial therapy and widespread use of broad-spectrum antibiotics have altered the microbial ecology of burn units, leading to a progressive rise in opportunistic fungal infections (Lachiewicz et al., 2020; Rodríguez-Arrondo et al., 2021). Today, fungal infections are recognized as major contributors to delayed wound healing, prolonged hospitalization, graft failure, sepsis, and death among burn patients (Legrand et al., 2021).

The epidemiology of fungal infections varies considerably across geographical regions. Globally, *Candida* species remain the most frequently isolated fungal pathogens from burn patients, followed by filamentous fungi such as *Aspergillus* species and members of the order Mucorales (Guo et al., 2020; Rodríguez-Arrondo et al., 2021). The World Health Organization (WHO) recently identified *Candida albicans* and *Aspergillus fumigatus* among the highest-priority fungal pathogens due to their increasing clinical impact and emerging antifungal resistance (WHO, 2022; Denning, 2024).

Among filamentous fungi, *Aspergillus fumigatus* possesses several biological characteristics that contribute to its pathogenicity, including thermotolerance, airborne dissemination, biofilm formation, and immune-evasion mechanisms mediated by surface hydrophobins and galactosaminogalactan production (Earle et al., 2023). Similarly, *Candida albicans* remains the most important opportunistic yeast pathogen because of its ability to switch between yeast and hyphal forms, form biofilms, and express multiple adhesion molecules involved in tissue invasion (Oh & Hoyer, 2022; Schena et al., 2023).

Members of the order Mucorales, particularly *Rhizopus arrhizus*, have attracted increasing attention following the emergence of COVID-19-associated mucormycosis. Although less frequently

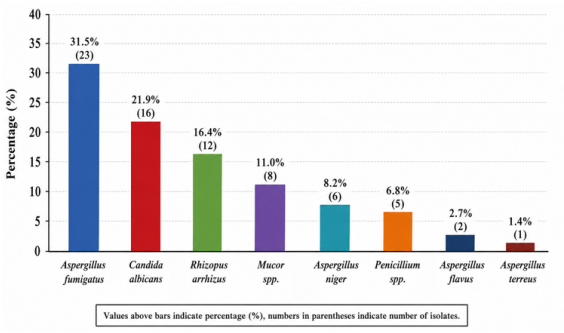

Figure 1. Show Pathogenesis of fungal infections in burn patients.
Adapted from Jeschke et al. (2020), Rodríguez-Arrondo et al. (2021), and Gupta et al. (2022).

2. Materials and Methods

2.1 Study Design and Ethical Approval

A cross-sectional hospital-based study was conducted in the Burn Unit of Thi-Qar General Hospital (Nasiriyah Teaching Hospital), Thi-Qar Province, Iraq, between March and September 2025. The study was approved by the Thi-Qar Health Directorate under official authorization and was conducted in accordance with the principles of the Declaration of Helsinki (2013 revision). Patient confidentiality was maintained throughout the study through anonymous coding of all clinical and microbiological data.

2.2 Study Population

A total of 95 burn patients were enrolled. Inclusion criteria consisted of:

1. Hospital admission to the burn unit.
2. Burn wound presence requiring inpatient management.
3. Hospital stay of at least seven days.
4. Availability of complete demographic and clinical information.

Patients discharged before seven days were excluded to minimize inclusion of transient

isolated than *Candida* or *Aspergillus*, these fungi are associated with extremely high mortality rates due to their angioinvasive behavior and rapid tissue destruction (Cornely et al., 2019; Alqarihi et al., 2023). In Iraq, investigations focusing specifically on fungal pathogens associated with burn wounds remain limited. Most available studies have concentrated on bacterial infections, leaving significant gaps regarding fungal prevalence, species distribution, and molecular epidemiology. Furthermore, no comprehensive molecular survey had previously been conducted among burn patients in Thi-Qar Province. Therefore, establishing baseline epidemiological data is essential for improving diagnostic and therapeutic strategies.

Traditional morphological identification remains useful in clinical mycology; however, molecular methods based on sequencing of the Internal Transcribed Spacer (ITS) region provide superior accuracy and have become the gold standard for fungal identification (Tamura et al., 2024). Molecular epidemiological investigations can further clarify phylogenetic relationships among isolates and facilitate surveillance of clinically important fungal pathogens.

Accordingly, the present study aimed to investigate the epidemiology of fungal infections among burn patients admitted to Thi-Qar General Hospital, determine species distribution, evaluate demographic and clinical risk factors, and characterize isolated fungi using molecular identification and phylogenetic analysis.

Culture media were prepared according to manufacturer instructions.

Table 1. Culture Media Used in the Study

Medium	Purpose
SDA	Primary fungal isolation
PDA	Colony characterization
BHI	Enrichment culture
CHROMagar Candida	Candida differentiation

2.5.2 Macroscopic Examination

Colonies were evaluated for:

- Growth rate
- Texture
- Pigmentation
- Surface appearance
- Reverse colony morphology

Species identification was initially based on standard taxonomic descriptions (de Hoog et al., 2020).

2.5.3 Microscopic Examination

Microscopic examination was performed using Lactophenol Cotton Blue (LPCB) staining.

The following characteristics were evaluated:

- Hyphal morphology
- Septation
- Conidiophore structure
- Vesicle morphology
- Phialide arrangement
- Sporangial characteristics

These criteria were used to establish preliminary identification of filamentous fungi and yeasts.

2.6 Molecular Identification

2.6.1 DNA Extraction

microbial colonization and to ensure adequate exposure to hospital-associated fungal flora (Gupta et al., 2022).

2.3 Demographic and Clinical Data Collection

The following variables were recorded for each participant:

- Age
- Sex
- Burn degree
- Total Body Surface Area burned (TBSA%)
- Duration of hospitalization
- Fungal culture results

TBSA% was calculated according to standard burn assessment protocols. Burn severity was classified into second-degree and third-degree burns based on clinical examination performed by attending physicians.

2.4 Sample Collection

Burn wound swabs were collected aseptically from wound margins using sterile cotton swabs. Samples were transported immediately to the microbiology laboratory and processed within the same working day.

The sampling strategy was designed to maximize recovery of viable fungal pathogens while minimizing contamination from environmental microorganisms (Lachiewicz et al., 2020).

2.5 Fungal Isolation and Phenotypic Identification

2.5.1 Culture Media

Primary isolation was performed using:

- Sabouraud Dextrose Agar (SDA)
- Potato Dextrose Agar (PDA)
- Brain Heart Infusion Agar (BHI)
- CHROMagar Candida

Species identification was accepted when similarity exceeded accepted taxonomic thresholds (Nilsson et al., 2019).

2.7 Phylogenetic Analysis

Phylogenetic relationships were reconstructed using MEGA software.

Maximum Likelihood analysis was performed using:

- Local Iraqi isolates
- Reference GenBank sequences
- Bootstrap validation (1000 replicates)

Phylogenetic trees were generated separately for:

- Aspergillus fumigatus
- Candida albicans
- Rhizopus arrhizus

(Tamura et al., 2024).

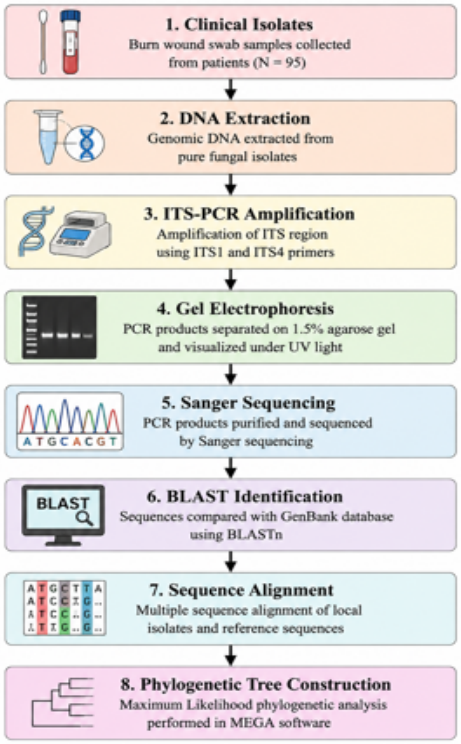

Figure 2. Show Workflow of Molecular Identification and Phylogenetic Analysis

2.8 Statistical Analysis

Data were analyzed using statistical software.

Genomic DNA was extracted using the HiPure Fungal DNA Kit (Magen, China) according to the manufacturer's instructions.

DNA purity and concentration were measured spectrophotometrically before PCR amplification.

2.6.2 PCR Amplification of the ITS Region

The Internal Transcribed Spacer (ITS) region was selected because it represents the accepted universal barcode for fungal identification (Schoch et al., 2012).

PCR reactions were performed in a final volume of 25 µL using:

- PCR Master Mix
- Forward primer ITS1
- Reverse primer ITS4
- Template DNA

Amplification was performed in a thermal cycler under standardized cycling conditions.

2.6.3 Agarose Gel Electrophoresis

PCR products were separated using 1.5% agarose gel electrophoresis stained with ethidium bromide and visualized under ultraviolet illumination.

Successful amplification was confirmed by the presence of single DNA bands of expected size.

2.6.4 DNA Sequencing and BLAST Analysis

Representative PCR products were subjected to Sanger sequencing.

Obtained sequences were:

1. Edited and assembled.
2. Compared against GenBank databases using BLASTn.
3. Assigned to species based on highest sequence similarity.

13–17 years	6	6.3
18–39 years	33	34.7
40–59 years	9	9.5
≥60 years	5	5.3

TBSA Distribution

TBSA values ranged from:

5%–100%

Mean TBSA:

30.41 ± 25.28%

The most common category was 10–19% TBSA (32.6%).

Table 4. Show Distribution According to TBSA

TBSA (%)	Number	Percentage (%)
<10	9	9.5
10–19	31	32.6
20–29	19	20.0
30–49	19	20.0
50–69	5	5.3
≥70	12	12.6

3.2 Overall Fungal Culture Positivity

Among the 95 burn wound samples collected during the study period, 73 yielded positive fungal cultures, corresponding to an overall positivity rate of **76.8%**, while 22 samples (23.2%) showed no fungal growth. This finding indicates a substantial burden of fungal colonization and/or infection among hospitalized burn patients in Thi-Qar General Hospital.

The observed prevalence exceeds many rates reported in neighboring countries and may reflect the combined influence of prolonged hospitalization, extensive antibiotic exposure, climatic conditions, and the severity of burn injuries (Rodríguez-Arrondo et al., 2021; Gupta et al., 2022).

Normality was assessed using the Shapiro–Wilk test.

Comparisons were performed using:

- Pearson Chi-square test
- Fisher's Exact test
- Mann–Whitney U test

Results were considered statistically significant at:

$p < 0.05$

(Field, 2022).

3. Results

3.1 Demographic Characteristics of Burn Patients

A total of 95 burn patients were enrolled in the study.

Males accounted for 56.8% (54/95), whereas females represented 43.2% (41/95), yielding a male-to-female ratio of approximately 1.3:1.

Table 2. Show Gender Distribution of Burn Patients

Gender	Number	Percentage (%)
Male	54	56.8
Female	41	43.2
Total	95	100

Age Distribution

Patient age ranged from one month to 93 years.

The overall mean age was:

20.21 ± 20.51 years

The largest age group was 18–39 years (34.7%), followed by children aged 1–4 years (29.5%).

Table 3. Show Age Distribution of Participants

Age Group	Number	Percentage (%)
<1 year	6	6.3
1–4 years	28	29.5
5–12 years	8	8.4

18–39 years	90.9
40–59 years	88.9
≥60 years	80.0

$\chi^2 = 13.298$, p = 0.039

3.3.3 Association with TBSA%

The frequency of fungal positivity increased with burn extent. Statistical analysis revealed a significant relationship between TBSA category and fungal positivity ($\chi^2 = 12.408$, p = 0.030).

Table 7. Show Association Between TBSA and Fungal Positivity

TBSA Category	Positive (%)
<10%	55.6
10–19%	67.7
20–29%	78.9
30–49%	84.2
50–69%	100
≥70%	100

$\chi^2 = 12.408$, p = 0.030

3.3.4 Association with Burn Degree

No statistically significant association was observed between burn degree and fungal positivity (Fisher's Exact Test, p = 1.000).

3.4 Distribution of Isolated Fungal Species

Eight fungal species were identified among the 73 positive cultures. Three species predominated and collectively accounted for approximately 70% of all isolates.

Aspergillus fumigatus represented the most frequently isolated fungus (31.5%), followed by *Candida albicans* (21.9%) and *Rhizopus arrhizus* (16.4%).

Table 8. Show Distribution of Fungal Species Isolated from Burn Patients

Species	Number	Percentage (%)
Aspergillus fumigatus	23	31.5

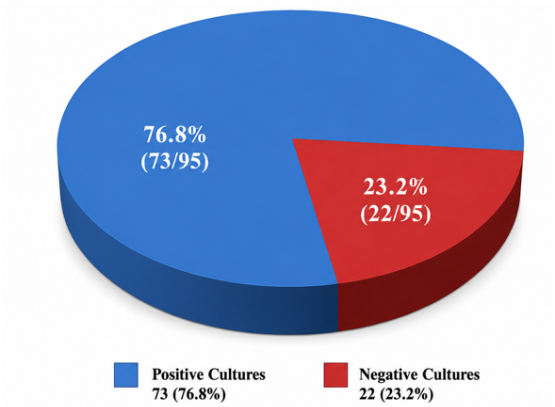

Figure 3. Overall fungal culture positivity among burn patients.

3.3 Association Between Fungal Positivity and Demographic and Clinical Variables

3.3.1 Association with Gender

A statistically significant association was observed between gender and fungal culture positivity. Positive fungal cultures were detected in 48 of 54 males (88.9%) compared with 25 of 41 females (61.0%) ($\chi^2 = 8.696$, p = 0.003).

Table 5. Show Association Between Gender and Fungal Positivity

Gender	Positive n (%)	Negative n (%)
Male	48 (88.9)	6 (11.1)
Female	25 (61.0)	16 (39.0)

$\chi^2 = 8.696$, p = 0.003

3.3.2 Association with Age

Fungal positivity differed significantly among age categories ($\chi^2 = 13.298$, p = 0.039). The highest positivity rates were generally observed among adult patients, particularly those aged 18–39 years.

Table 6. Show Association Between Age Group and Fungal Positivity

Age Group	Positive (%)
<1 year	66.7
1–4 years	67.9
5–12 years	75.0
13–17 years	66.7

characteristic rhizoids consistent with *Rhizopus* species.

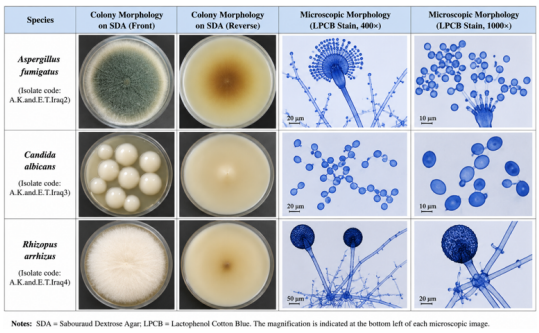

Figure 5. Show Representative morphological characteristics of the three major fungal pathogens isolated from burn patients.

3.6 Molecular Identification by ITS Sequencing

PCR amplification of the Internal Transcribed Spacer (ITS) region produced clear amplicons for representative fungal isolates.

Subsequent sequencing and BLAST analysis confirmed the identity of the three major pathogens.

Sequence similarity exceeded accepted taxonomic thresholds for species-level identification.

Importantly, molecular analysis corrected the preliminary classification of several isolates initially assigned morphologically to *Mucor* spp., demonstrating that they belonged to *Rhizopus arrhizus*. One representative isolate exhibited **96.95% sequence similarity** with reference *R. arrhizus* sequences deposited in GenBank.

Table 9. Show Summary of Molecular Identification Results

Species	Identification Method	Sequence Similarity (%)
Candida albicans	16	21.9
Rhizopus arrhizus	12	16.4
Mucor spp.	8	11.0
Aspergillus niger	6	8.2
Penicillium spp.	5	6.8
Aspergillus flavus	2	2.7
Aspergillus terreus	1	1.4
Total	73	100

3.5 Morphological Identification of the Three Target Species

Because *A. fumigatus*, *C. albicans*, and *R. arrhizus* represented the most prevalent fungal pathogens, they were selected for subsequent molecular and experimental investigations.

3.5.1 Aspergillus fumigatus

Colonies grew rapidly on SDA, producing velvety blue-green to gray-green surfaces. Microscopically, isolates exhibited septate hyphae, short conidiophores, flask-shaped vesicles, and uniseriate phialides covering the upper two-thirds of the vesicle.

3.5.2 Candida albicans

Colonies appeared smooth, creamy, convex, and white. Microscopic examination demonstrated oval budding yeast cells with characteristic blastoconidia.

3.5.3 Rhizopus arrhizus

Colonies demonstrated rapid cottony growth and eventually filled the entire culture plate. Microscopic examination revealed broad pauciseptate hyphae, sporangiophores, sporangia, and

reported from neighboring countries and international burn centers. Studies from Egypt, Iran, Turkey, and Jordan have generally reported fungal prevalence ranging between 20% and 45% among burn patients (El-Mahallawy et al., 2021; Pakshir et al., 2020; Akyildiz et al., 2021). Similarly, a recent systematic review found that fungal infection rates among burn patients typically range between 6.3% and 44% worldwide (Rodríguez-Arrondo et al., 2021).

Several factors may explain the elevated prevalence observed in the current study. First, all enrolled patients had prolonged hospitalization periods exceeding seven days, a recognized risk factor for hospital-acquired fungal colonization and infection (Gupta et al., 2022). Second, extensive use of broad-spectrum antibiotics may have altered the microbial ecology of burn wounds, reducing bacterial competition and creating favorable conditions for fungal growth (Lachiewicz et al., 2020). Third, environmental conditions in Southern Iraq, including high temperatures, dust storms, and airborne fungal spore dissemination, may increase patient exposure to opportunistic fungi (Ferrari et al., 2024).

Furthermore, the extensive tissue damage associated with severe burns creates a nutrient-rich environment that facilitates fungal adhesion, colonization, and biofilm development. Burn-induced immunosuppression may further enhance susceptibility by impairing neutrophil activity and reducing antifungal immune responses (Jeschke et al., 2020; Gupta et al., 2022).

4.2 Demographic Factors Associated with Fungal Positivity

A. fumigatus	ITS sequencing	>99
C. albicans	ITS sequencing	>99
R. arrhizus	ITS sequencing	96.95

3.7 Phylogenetic Analysis

Maximum Likelihood phylogenetic trees demonstrated close clustering of local isolates with globally reported clinical strains retrieved from GenBank.

The local *A. fumigatus* isolate (A.K.and.E.T.Iraq2) clustered within the major pathogenic lineage of *A. fumigatus*. Likewise, *C. albicans* and *R. arrhizus* isolates grouped with international clinical isolates originating from Asia, Europe, and the Middle East. These findings indicate substantial conservation of clinically important fungal lineages across geographical regions.

4. Discussion

The present study provides the first comprehensive molecular epidemiological investigation of burn-associated fungal pathogens in Thi-Qar Province, Southern Iraq. The findings revealed a remarkably high fungal culture positivity rate (76.8%), a predominance of *Aspergillus fumigatus*, and significant associations between fungal positivity and patient gender, age, and burn extent. Collectively, these results highlight the substantial burden of opportunistic fungal pathogens among hospitalized burn patients and emphasize the importance of implementing routine fungal surveillance programs in Iraqi burn units.

4.1 Overall Fungal Positivity

The overall fungal positivity rate observed in this study (76.8%) exceeds many rates

The predominance of *Aspergillus fumigatus* (31.5%) represents one of the most important findings of this investigation. Although *Candida albicans* remains the most frequently reported fungal pathogen in many burn centers worldwide, several studies have documented increasing recovery of filamentous fungi, particularly *A. fumigatus*, in environments characterized by high airborne spore concentrations (Denning, 2024; Earle et al., 2023).

The success of *A. fumigatus* as a burn-associated pathogen may be attributed to several biological characteristics. The organism produces abundant airborne conidia that readily disperse throughout hospital environments. In addition, its thermotolerance permits growth at temperatures exceeding normal body temperature, while virulence determinants such as RodA hydrophobin and galactosaminogalactan facilitate immune evasion and biofilm formation (Earle et al., 2023).

Candida albicans represented the second most common fungal isolate. This observation is consistent with numerous investigations conducted throughout the Middle East and internationally (Guo et al., 2020; Rodríguez-Arrondo et al., 2021). As a commensal organism of human skin and mucosal surfaces, *C. albicans* can rapidly exploit disruptions in epithelial integrity and alterations in normal microbiota caused by antibiotic therapy (Oh & Hoyer, 2022).

Particularly noteworthy was the relatively high prevalence of *Rhizopus arrhizus* (16.4%). Members of the order Mucorales are associated with invasive mucormycosis, a disease characterized by rapid angioinvasion, tissue necrosis, and high mortality (Cornely et al., 2019). The

A statistically significant association was observed between gender and fungal positivity. Male patients demonstrated a considerably higher positivity rate than females (88.9% versus 61.0%). Similar findings have been reported in several burn epidemiology studies, where males generally account for the majority of severe burn admissions due to occupational exposure and environmental hazards (Peck, 2020; Rodríguez-Arrondo et al., 2021; Pate; et al.,2024).

Age was also significantly associated with fungal positivity. Adult patients, particularly those aged 18–39 years, exhibited the highest infection rates. This finding may reflect greater exposure to occupational burn injuries and larger burn surface areas among working-age adults. Comparable age-related trends have been reported by Legrand et al. (2021) and Sharma et al. (2022).

The significant association between TBSA and fungal positivity is biologically plausible. Larger burn areas are associated with greater tissue necrosis, prolonged wound exposure, and increased requirements for invasive medical interventions. Previous studies have consistently identified TBSA as one of the strongest predictors of fungal infection among burn patients (Gupta et al., 2022; Rodríguez-Arrondo et al., 2021).

In contrast, burn degree was not significantly associated with fungal positivity in the present study. This finding suggests that the overall extent of tissue injury may be more important than burn depth alone in determining susceptibility to fungal colonization.

4.3 Distribution of Fungal Species

The high prevalence of opportunistic fungi among burn patients has several important clinical implications.

First, routine fungal screening should be considered for patients with prolonged hospitalization and extensive burns. Early identification may facilitate timely antifungal therapy and improve patient outcomes (Lachiewicz et al., 2020).

Second, molecular diagnostic methods should be incorporated whenever feasible, particularly when Mucorales infections are suspected. Accurate species identification can significantly influence therapeutic decision-making because different fungal species exhibit distinct susceptibility profiles (Cornely et al., 2019; Sane et al.,2023; Lei et al.,2022; Qasim et al.,2025; Qasim et al.,2024; Ramaiah et al.,2024).

Third, the predominance of *A. fumigatus*, *C. albicans*, and *R. arrhizus* supports the selection of these species as targets for subsequent investigations of antifungal susceptibility, virulence factors, and nanoparticle-based therapeutic approaches.

5. Conclusions

The present study demonstrated a remarkably high prevalence of fungal colonization and infection among burn patients admitted to Thi-Qar General Hospital.

Key findings include:

1. Overall fungal positivity reached 76.8%.
2. *Aspergillus fumigatus* was the predominant fungal species.
3. *Candida albicans* and *Rhizopus arrhizus* represented additional major pathogens.

presence of this pathogen among burn patients should therefore be considered a significant clinical warning sign, especially given the increasing global recognition of mucormycosis following the COVID-19 pandemic (Alqarihi et al., 2023).

4.4 Molecular Identification and Phylogenetic Analysis

One of the major strengths of the present study was the application of molecular identification methods. Sequencing of the ITS region confirmed the identity of all major fungal isolates and demonstrated the limitations of relying solely on morphological methods.

The reclassification of several isolates initially identified as *Mucor* spp. into *Rhizopus arrhizus* illustrates the diagnostic value of molecular techniques. Morphological overlap among members of the order Mucorales often complicates species-level identification and may lead to clinically important misclassification (Cornely et al., 2019;Al-Jassani et al.,2022; Qasim et al.,2022; Zamanian et al.,2024; Gupta et al.,2022).

Phylogenetic analysis revealed close clustering between local Iraqi isolates and globally distributed clinical strains. This finding suggests substantial conservation of pathogenic fungal lineages across geographical regions and supports previous observations that many clinically important fungal species exhibit relatively limited ITS variability (Tamura et al., 2024).

The establishment of molecularly confirmed fungal sequences from Southern Iraq also contributes valuable information to regional fungal surveillance efforts and may facilitate future epidemiological investigations.

4.5 Clinical Implications

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4. Gender, age, and TBSA were significantly associated with fungal positivity.
5. ITS sequencing substantially improved diagnostic accuracy.
6. Phylogenetic analysis confirmed close relationships between local and international clinical strains.
7. The findings provide the first molecular epidemiological baseline for burn-associated fungal pathogens in Southern Iraq.

Future studies should investigate antifungal susceptibility profiles, virulence mechanisms, and novel therapeutic approaches targeting these clinically important fungal pathogens.

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