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Research Article

A Study on the Spectrum of Fungal Pathogens Isolated in ICU patient: A Study from Tertiary Care Centre

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ABSTRACT

Introduction: The COVID-19 pandemic has led to a surge in opportunistic infections, particularly fungal co-infections, due to widespread corticosteroid use, immune dysregulation, and prolonged ICU admissions. This study aimed to analyse the spectrum of fungal pathogens isolated from clinical specimens in a tertiary care hospital during the pandemic period.

Materials and Methods: A one-year cross-sectional study was conducted in the Department of Microbiology at a tertiary care centre. All clinical samples received from COVID-19-positive and suspected patients that yielded fungal growth were included. Fungal identification was performed using conventional microbiological methods and biochemical tests, while antifungal susceptibility testing was carried out for major isolates.

Results: Of 804 clinical isolates, 137 (17%) were fungal pathogens. The majority of patients were male (60.6%), with a mean age of 52.4 years. Most infections were observed among ICU patients (62.8%), particularly from respiratory and urinary samples. Urine (43.1%), sputum (24.8%), and endotracheal secretions (15.3%) were the predominant specimen sources. Candida albicans was the most common isolate (32.8%), followed by C. auris (22.6%) and C. tropicalis (16.8%). Notably, C. auris exhibited high fluconazole resistance (61.3%) with preserved susceptibility to amphotericin B (93.5%).

Conclusion: Fungal infections represented a significant burden among critically ill COVID-19 patients, with non-albicans Candida species emerging as major pathogens. The rise of multidrug-resistant C. auris highlights the urgent need for continuous fungal surveillance, species-level identification, and antifungal stewardship to mitigate resistance and improve clinical outcomes.

Keywords: Substance Use, Alcohol, Opioids, Neurocognition, Executive Function, Adolescents, Young Adults

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Introduction

Coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has resulted in a global health crisis since its emergence in late 2019. Despite substantial progress in vaccine development, the emergence of SARS-CoV-2 variants such as Omicron has led to waning vaccine efficacy, making complete disease control an ongoing challenge.[1,2] While the majority of current infections are mild or non-fatal, a notable proportion of individuals continue to experience persistent or newly emerging symptoms beyond the acute phase. These manifestations—collectively termed 'Long COVID' (LC)—have been increasingly reported among both outpatient and hospitalisedpopulations.[3,4]

The prevalence of LC is estimated to range from 10% to 30%in non-hospitalisedpatients and up to 76% among those requiring hospitalisation.[4] Globally, over 100 million individuals are projected to be affected by LC, with significant socioeconomic consequences including reduced quality of life, work absenteeism, and loss of income, amounting to an estimated economic burden of $2.6–3.7 billion.[5] LC can affect multiple organ systems and may present with chronic fatigue, dysautonomia, and thrombotic, cardiovascular, or neuropsychiatric complications.[6]

Emerging evidence suggests that immune dysregulation plays a central role in the pathogenesis of LC. Patients exhibit persistent alterations in innate and adaptive immune responses, including depletion of B and T lymphocytes—especially CD4+ and CD8+ subsets—and elevated interferon expression (IFN-β, IFN-λ1), which may last several months after initial infection.[7,8] CD4+ T lymphocytes are known to mediate antifungal immunity via macrophage activation through IFN-γ production.[9] Therefore, prolonged CD4 lymphopenia may predispose recovered individuals to opportunistic fungal infections, as recently demonstrated in cases of cerebral cryptococcosis in non-HIV COVID-19 patients.[10]

During the pandemic, a notable surge in fungal co-infections such as mucormycosis, invasive candidiasis, aspergillosis, pneumocystosis, and cryptococcosis has been reported, particularly in patients with severe or critical COVID-19.[11–13] This trend has been more pronounced in settings with high corticosteroid use, immunomodulatory therapy, and prolonged ICU stays.[14] In the United States, hospitalisationdue to fungal infections rose by approximately 9% annually between 2019 and 2021.[15] Alarmingly, the mortality rate for patients with COVID-19-associated fungal infections reached 48.5%, compared to 12.3% in non-COVID-19 fungal infections.[16,17]

With this background, the present study was undertaken to analyse the spectrum of fungal pathogens isolated from clinical samples during the COVID-19 pandemic. The study aims to evaluate the prevalence and diversity of fungal species in a tertiary care setting, thereby contributing important epidemiological insights into fungal disease burden during COVID-19.

Materials and Methods

This study was conducted over a period of one year during the COVID-19 pandemic. The study was carried out in the Department of Microbiology at a tertiary care hospital.

Inclusion and Exclusion Criteria

All clinical samples received from both COVID-19 -positive and suspected patients that yielded fungal growth on culture during the study period were included. Duplicate isolates from the same patient and mixed bacterial-fungal cultures where fungal identification could not be established were excluded.

Sample Collection and Processing

A total of 804 clinical samples that showed microbial growth were included, of which 137 were identified as fungal isolates. The samples were collected from various clinical sources, including endotracheal (ET) secretions (n = 21), sputum (n = 34), bronchoalveolar lavage (BAL) (n = 2), blood (n = 14), pus (n = 6), gastric lavage (n = 1), and urine (n = 59). All samples were processed according to standard microbiological techniques under biosafety level-2 precautions.

Fungal Identification

Fungal isolates were identified based on colony morphology, Gram staining, and biochemical reactions. Yeast species were further characterisedby the germ tube test and cornmeal agar morphology. Species-level identification was performed using automated systems and biochemical panels (VITEK-specific mention as per scope).

Data Collection and Analysis

All patient details were anonymised, and relevant demographic and clinical information (age, sex, specimen type) wasrecorded from laboratory requisition forms. The data were compiled in Microsoft Excel, and descriptive statistics were performed. The distribution of fungal species across various specimen types was expressed in frequencies and percentages. By SPSS Version 25

Results

During the one-year study period, a total of 804 clinical isolates were identified, of which 137 (17.0%) were fungal pathogens. The remaining were bacterial isolates and were excluded from this analysis.

Fungal isolates were obtained from 137 patients, of whom 83 (60.6%) were male and 54 (39.4%) were female. The mean age of patients was 52.4 ± 16.3 years (range: 18–84 years). The majority of fungal infections were noted in the age group of 41–60 years (n = 58, 42.3%), followed by 61–80 years (n = 41, 29.9%). Patients aged ≤40 years constituted 26.3% (n = 36), and only 2 patients (1.5%) were aged over 80.

Out of the 137 fungal isolates, 86 (62.8%) were recovered from patients admitted to the Intensive Care Unit (ICU), while 51 (37.2%) were from patients in general wards or outpatient departments. The majority of ICU isolates were obtained from respiratory specimens such as endotracheal secretions and sputum, whereas non-ICU isolates were predominantly from urine and blood samples.

The clinical specimens from which fungi were isolated included urine (n = 59, 43.1%), sputum (n = 34, 24.8%), endotracheal secretions (n = 21, 15.3%), blood (n = 14, 10.2%), pus (n = 6, 4.4%), bronchoalveolar lavage (BAL) (n = 2, 1.5%), and gastric lavage (n = 1, 0.7%) (Table 1).

A total of 13 different fungal species were isolated. *Candida albicans* was the most common isolate (n = 45, 32.8%), followed by *C. auris* (n = 31, 22.6%) and *C. tropicalis* (n = 23, 16.8%). Other species included *C. famata* (n = 14), *C. glabrata* (n = 4), *C. ciferrii* (n = 3), *C. parapsilosis* (n = 3), *C. rugosa* (n = 3), *C. krusei* (n = 3), *C. dubliniensis* (n = 1), *C. lipolytica* (n = 1), *C. koseri* (n = 1), *Cryptococcus laurentii* (n = 4), and *Trichomonas asahi* (n = 2) (Table 2).

Table 1.Specimen-wise Distribution of Fungal Isolates

n = 137

Specimen Type	Number of Isolates (n)	Percentage (%)
Urine	59	43.1%
Sputum	34	24.8%
Endotracheal Secretion	21	15.3%
Blood	14	10.2%
Pus	6	4.4%
Bronchoalveolar Lavage	2	1.5%
Gastric Lavage	1	0.7%
Total	137	100%

Table 2.Fungal Species Distribution

n = 137

Fungal Species	Number of Isolates (n)	Percentage (%)
Candida albicans	45	32.8%
Candida auris	31	22.6%
Candida tropicalis	23	16.8%
Candida famata	14	10.2%
Candida glabrata	4	2.9%
Candida ciferrii	3	2.2%
Candida parapsilosis	3	2.2%
Candida rugosa	3	2.2%
Candida krusei	3	2.2%
Candida dubliniensis	1	0.7%
Candida lipolytica	1	0.7%
Candida koseri	1	0.7%
Cryptococcus laurentii	4	2.9%
Trichomonas asahi	2	1.5%
Total	137	100%

Antifungal susceptibility testing was available for the major Candida isolates (n = 124). Most *C. albicans* isolates were susceptible to fluconazole (84.4%) and amphotericin B (100%). However, a higher rate of resistance was observed in non-albicans Candida species, particularly *C. auris* and *C. glabrata*. Among *C. auris* isolates (n = 31), only 38.7% were susceptible to fluconazole, while amphotericin B retained activity in 93.5% of cases. Echinocandin resistance was noted in 2 isolates of *C. auris*. All isolates of *C. krusei* were intrinsically resistant to fluconazole, as expected. *Cryptococcus laurentii* isolates were uniformly sensitive to amphotericin B and flucytosine

Discussion

In our study, fungal pathogens constituted 17.0% (137/804) of all clinical isolates during the one-year period. The majority of these infections were observed in males (60.6%), with a mean patient age of 52.4 years. Notably, 42.3% of infections occurred in the 41–60-year age group.These findings align with previous studies indicating a higher susceptibility to fungal infections among middle-aged and older adults, particularly males. For instance, a study by Peman et al. reported a similar demographic distribution, highlighting the increased risk in these populations due to factors like comorbidities and immunosuppressive therapies.[18]

Our data revealed that 62.8% of fungal isolates were from ICU patients, underscoring the heightened risk of fungal infections in critically ill individuals. This is consistent with findings from a study conducted in the United States, where ICU patients with COVID-19 had a higher incidence of invasive fungal infections, including candidemia and aspergillosis, compared to non-ICU patients.[15] The increased prevalence in ICU settings can be attributed to factors such as prolonged hospitalisation, mechanical ventilation, and the use of broad-spectrum antibiotics and corticosteroids, which compromise the immune system and disrupt normal microbial flora.

Urine samples accounted for the highest number of fungal isolates (43.1%), followed by sputum (24.8%) and endotracheal secretions (15.3%). This distribution suggests a predominance of urinary tract and respiratory tract fungal infections among hospitalisedpatients. Similar patterns were observed in a study by White et al., where non-blood specimens, particularly from the respiratory and urinary tracts, were common sources of fungal isolates in COVID-19 patients.[19] The frequent use of indwelling catheters and ventilators in ICU settings likely contributes to this distribution.

Candida albicans was the most prevalent species in our study (32.8%), followed by *Candida auris* (22.6%) and *Candida tropicalis* (16.8%). The emergence of *C. auris* is particularly concerning due to its multidrug-resistant nature and association with nosocomial outbreaks. Our findings are in line with global reports highlighting the rise of *C. auris* infections during the COVID-19 pandemic. A review by Chowdhary et al. documented numerous *C. auris* outbreaks in COVID-19 units worldwide, emphasisingthe pathogen's ability to persist in healthcare environments and its resistance to multiple antifungal agents.[20]

Antifungal susceptibility testing in our study showed that most *C. albicans* isolates were susceptible to fluconazole (84.4%) and amphotericin B (100%). In contrast, *C. auris* exhibited significant resistance, with only 38.7% susceptibility to fluconazole and 93.5% to amphotericin B. Echinocandin resistance was noted in two *C. auris* isolates. These resistance patterns are consistent with global trends. The CDC has reported increasing resistance of *C. auris* to all major classes of antifungals, complicating treatment options and leading to higher mortality rates. The emergence of echinocandin-resistant strains further exacerbates the challenge, necessitating vigilant antifungal stewardship and infection control measures.[21]

Conclusion

This study highlights the substantial burden of fungal infections during the COVID-19 pandemic, with fungal isolates comprising 17% of all clinical specimens. The majority of infections occurred in middle-aged to elderly patients, predominantly in males and those admitted to intensive care units. Urine and respiratory samples were the most common sources of fungal isolation, reflecting a high prevalence of urinary and pulmonary fungal infections in hospitalisedand ventilated patients.

Candida albicans remained the most frequently isolated species; however, a considerable proportion of infections were due to non-*albicans* Candida species, notably *Candida auris* and *Candida tropicalis*. The emergence of *C. auris* as a significant pathogen, with high resistance to fluconazole and reduced susceptibility to echinocandins, underscores the growing challenge of antifungal resistance in healthcare settings.

The findings emphasisethe importance of routine fungal surveillance, early identification, and species-level antifungal susceptibility testing, especially in critically ill patients during pandemics. Strict infection control measures and antifungal stewardship programmesare essential to prevent the spread of multidrug-resistant fungal pathogens and reduce associated morbidity and mortality.

Author's Contribution: V S: Conceptualized and designed the study; supervised sample collection, microbiological processing, and fungal identification; performed data interpretation; and critically revised the manuscript for important intellectual content. M R: Assisted in study design and methodology; contributed to data collection, statistical analysis, and interpretation; and drafted the initial manuscript.

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