Original Article

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Internal Medicine Section

Prevalence and Pattern of Isolated Fungi from Bronchoalveolar Lavage in Patients with Lung Cancer: A Cross-sectional Study

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ABSTRACT

Introduction: Fungal infections have emerged as a significant healthcare challenge worldwide, particularly among terminally ill, debilitated, and immunocompromised populations. In patients with lung malignancy, fungal colonisation of the bronchial tree can predispose them to serious pulmonary infections and may adversely influence prognosis, especially in those undergoing chemotherapy. Understanding the prevalence and pattern of fungal colonisation in these patients is therefore clinically relevant, as it may directly affect outcomes and survival.

Aim: To determine the prevalence and pattern of fungi isolated from Bronchoalveolar Lavage (BAL) samples in patients with lung cancer.

Materials and Methods: This cross-sectional study included 101 patients with clinical and radiological suspicion of lung cancer who underwent Fiberoptic Bronchoscopy (FOB) with biopsy at Sawai Man Singh Medical College, Jaipur, Rajasthan, India. BAL samples were collected and processed for fungal culture. Demographic, clinical, and radiological findings, as well as histological types of lung cancer, were recorded. Data were analysed using appropriate statistical tests: the Chi-square or Fisher's exact test for categorical variables, the independent samples t-test for normally distributed continuous variables, and the Mann-Whitney test for non normally distributed data. A p-value≤0.05 was considered statistically significant.

Results: Fungal growth was detected in 34 of 101 patients (33.66%). The mean age in the fungal-positive group was 62.2±10.1 years. *Candida albicans* was isolated in nine cases (8.91%), *Aspergillus niger* in seven cases (6.9%), *Candida tropicalis* in six cases (5.9%), and other fungi in 12 cases (11.9%). Colonisation was more frequent in males (82.4%, n=28) and smokers (85.3%, n=29). Half of the patients with Chronic Obstructive Pulmonary Disease (COPD) demonstrated fungal infection compared to 35.8% of non COPD cases, although this difference was not statistically significant (p-value=0.16). Among species, *Candida albicans* was associated with higher dyspnoea scores (2.11±1.17). Lung mass (73.5%, n=25) was the most common radiological finding, followed by pleural effusion (41.2%, n=14). Squamous cell carcinoma (52.9%, n=18) was the predominant histological type among fungal-positive cases, followed by adenocarcinoma (20.6%, n=7).

Conclusion: Fungal colonisation is relatively common in patients with lung cancer, particularly among males, smokers, and those with COPD. Its presence may adversely influence survival and response to chemotherapy, underscoring the need for early detection and targeted management.

Keywords: Chronic obstructive pulmonary disease, Fungal infections, Smokers

INTRODUCTION

Fungal infections have emerged as a major global healthcare problem in recent years, primarily due to the extensive use of broad-spectrum antibiotics, long-term use of immunosuppressive agents, and the increasing population of terminally ill, debilitated, and immunocompromised patients [1]. Pulmonary fungal diseases encompass fungal colonisation, allergic manifestations, and infections of the pulmonary tract and lungs. In most cases, colonisation represents the initial step in the progression to pulmonary fungal infection. Fungi that commonly affect immunosuppressed individuals include species of *Aspergillus, Candida, Cryptococcus*, geographically restricted agents, and several newly emerging fungal pathogens [2].

Lung cancer remains a major public health concern worldwide in both sexes, with its incidence and mortality continuing to rise. Despite significant advancements in diagnostic and therapeutic modalities across various histological types of lung cancer, morbidity and mortality remain high, largely due to pulmonary infectious complications, which account for 35-70% of cases [3]. In addition to cigarette smoking—the principal risk factor for lung cancer—recent studies have highlighted the aetiological role of chronic pulmonary infections in lung carcinogenesis, acting either independently or synergistically with tobacco smoke to increase lung cancer risk [4-6]. Experimental and clinical data have demonstrated a correlation between cancer development and the presence of certain pathogens, independent of chemotherapy-induced leukopenia [2].

Bronchial colonisation plays a key role in the development of lung infections among patients with lung malignancy. Colonisation may occur due to localised bronchial abnormalities such as airway narrowing or defective mucociliary function, or may result from a local inflammatory response secondary to co-existing COPD. Such colonisation can adversely affect patients undergoing chemotherapy [7]. Studies have reported that bronchial colonisation occurs in 10–83% of patients with lung cancer and may be caused by Potentially Pathogenic Microorganisms (PPMs), primarily *Haemophilus influenzae*, *Streptococcus pneumoniae*, and *Staphylococcus aureus* [1]. Other potential microbial agents, such as mycobacteria and fungi, have not been systematically investigated [1,3,8].

Factors such as microbiota dysbiosis influence the production of bacteriotoxins, genotoxicity, and virulence, thereby playing a key role in the pathogenesis and prognosis of lung cancer [9]. Fungal lung diseases have been increasing over the past few decades and pose a unique challenge to clinicians worldwide. The clinical spectrum is diverse—ranging from hypersensitivity reactions and colonisation to invasive disease, some with high mortality rates—compounded by barriers to accurate and timely diagnosis and limited therapeutic options.

Furthermore, a single patient may transition between disease states over time, depending on changes in their underlying immune status. With climate change and ageing populations, the diversity of potential fungal pathogens and the prevalence of antifungal resistance continue to expand. Additionally, the increasing use of immunosuppressive and immunomodulating therapies has further broadened the "at-risk" population [10].

Although a causal association between fungal colonisation and lung cancer has not been well established, recognising fungal presence in lung cancer patients—especially those with chronic respiratory co-morbidities—is important, as it may influence disease progression, response to treatment, and overall outcomes. This represents the novelty of the present study.

Given the high burden of both fungal infections and lung cancer, and the limited Indian literature addressing this intersection, it is imperative to investigate the prevalence of fungi in BAL samples of lung cancer patients [11,12].

The present study aimed to determine the prevalence and pattern of fungi isolated from BAL in patients with lung cancer. The primary objective was to estimate the prevalence of fungal infection and characterise the fungal species present in these patients. The secondary objective was to describe the clinical, radiological, and demographic characteristics of lung cancer patients with fungal infection.

MATERIALS AND METHODS

This hospital-based cross-sectional study was conducted over a period of 1.5 years, from September 2023 to March 2025, at the Institute of Respiratory Diseases, Sawai Man Singh Medical College, Jaipur, Rajasthan, India, after obtaining approval from the Institutional Ethics Committee (IEC No. 343/MC/EC/2023). The study included 101 patients diagnosed with lung cancer.

Inclusion criteria: Patients clinically and radiologically diagnosed with lung cancer (based on TNM classification) suitable for FOB, patients providing written informed consent, aged 18 years and above were included in the study.

Exclusion criteria: Presence of neutropenia (absolute neutrophil count <1000/μL). Patients receiving systemic corticosteroid therapy. Patients on chemotherapy or radiotherapy. Patients on antifungal treatment. Patients unfit for FOB were excluded form the study.

Sample size: The sample size was calculated as 80 cases at a 95% confidence level, 80% power, 0.05 alpha error, and 7% allowable error to verify a 68% prevalence of fungal infection among lung cancer patients. The number was rounded up to 100 after accounting for a 20% dropout rate [13].The study included 101 patients diagnosed with lung cancer.

All patients with clinical and radiological suspicion of lung cancer underwent FOB.

Parameters assessed: The study assessed the pattern of fungi isolated from BAL samples of lung cancer patients, along with their clinical, radiological, and demographic characteristics, and the histopathological cell type of the tumour.

The following data were recorded: age, sex, smoking history, and co-morbidities, including COPD, Hypertension (HTN), Diabetes Mellitus (DM), and Coronary Artery Disease (CAD).

Patients were evaluated for the presence of toxemic and compressive symptoms and were assigned severity scores for the following symptoms:

- Dyspnoea: graded from 0 to 5 [14].
- Cough: graded from 0 to 5 [15].
- Chest pain: graded from 0 to 5 [16].
- Haemoptysis: scored as 1 (<30 mL/24 h), 2 (30-100 mL), 3 (>100-600 mL), and 4 (>600 mL) [17].

Definition of smoking status: A smoker is defined as an individual who had smoked at least one cigarette per day for one year or who had smoked more than 20 packs of cigarettes in their lifetime. A non smoker was defined as someone who had never established the habit of inhaling tobacco fumes or had smoked fewer than 100 cigarettes in their lifetime [18,19].

Radiological evaluation: Post-contrast chest CT findings were documented, including:

- Description of the lesion (nodule, mass, cavity, consolidation, or ground-glass opacity).
- Site of the lesion.
- Presence of associated lobar or total lung collapse and pleural effusion.

Bronchoscopy and sample collection: During FOB, no endobronchial suction was applied while introducing the scope to avoid contamination with upper airway flora. BAL was performed using 100 mL of 0.9% saline solution at room temperature, instilled in 20 mL aliquots after discarding the first aliquot. The BAL fluid was collected in a sterile container and immediately transported to the mycology laboratory for processing. Biopsies were obtained from endobronchial tumours using cup forceps. Tissue samples were preserved in 10% formalin for histopathological examination and were classified according to their cellular and molecular characteristics based on the WHO 2021 classification of lung cancer. Tumour staging was performed as per the TNM classification of lung cancer [20]. Cell typing was carried out using Haematoxylin and Eosin (H&E) staining and immunostaining. In cases where H&E staining was insufficient to identify fungal elements, Grocott-Gomori methenamine silver staining was performed on tissue biopsy samples. Fungal cultures that tested positive in lung cancer patients were included in the study. Patients with lung cancer and fungal colonisation were compared with those without proven fungal colonisation.

STATISTICAL ANALYSIS

Data entry was done using Microsoft Excel, and statistical analyses were performed using the Statistical Package for the Social Sciences (SPSS) software, version 25.0 (IBM Corp., Chicago, USA). Categorical data were presented as numbers and percentages. For data with a normal distribution, descriptive statistics were used to calculate the mean±standard deviation, while for non normally distributed data, medians and ranges were reported. Comparisons between groups were performed using the Chi-square test or Fisher's exact test for categorical variables, as appropriate; the Independent-samples t-test for normally distributed continuous variables; and the Mann-Whitney test for non normally distributed data. A p-value≤0.05 was considered statistically significant.

RESULTS

The demographic and clinical characteristics of the study participants are summarised in [Table/Fig-1].

Variable	Fungal (+) (n=34)	Fungal (-) (n=67)	p-value
Age (years), Mean±SD	62.2±10.1	60.8±11.3	0.51
Male sex	28 (82.4%)	56 (83.6%)	0.88
Female sex	6 (17.6%)	11 (16.4%)	0.88
Smokers	29 (85.3%)	61 (91.0%)	0.37
Non smokers	5 (14.7%)	6 (9.0%)	0.37
COPD	17 (50.0%)	24 (35.8%)	0.16
Diabetes Mellitus	7 (20.6%)	10 (14.9%)	0.47
Hypertension (HTN)	7 (20.6%)	15 (22.4%)	0.83
Coronary Artery Disease (CAD)	3 (8.8%)	12 (17.9%)	0.22

[Table/Fig-1]: Association of demographic and clinical characteristics with fungal infection.

Although not statistically significant, fungal infections were observed in 50% of COPD patients (17/34) compared with 35.8% (24/67) of non COPD patients, suggesting a trend towards higher fungal colonisation among COPD patients.

Among the fungal culture–positive cases, *Candida albicans* was the most prevalent species (8.9%), followed by *Aspergillus niger* (6.9%) [Table/Fig-2].

Fungal species isolated	Prevalence (in %)
No fungal element Identified	67 (66.3)
Candida albicans	9 (8.9)
Aspergillus niger	7 (6.9)
Candida tropicalis	6 (5.9)
Other fungal species	12 (11.9)

[Table/Fig-2]: Distribution of fungal infections in lung cancer patients.

Cough (84.1%) and dyspnoea (87.1%) were the predominant symptoms among fungal-positive patients, followed by chest pain (78.2%) and haemoptysis (30.7%) [Table/Fig-3].

Symptom/ variable	Fungal (+) (Mean±SD) (n=34)	Fungal (-) (Mean±SD) (n=67)	Total with symptom (n=101)	p-value
Dyspnoea	1.71±1.25	1.52±1.31	88 (87.1%)	0.45
Cough	2.03±0.87	1.88±0.95	95 (94.1%)	0.39
Chest pain	1.26±1.05	1.34±1.12	79 (78.2%)	0.72
Haemoptysis	0.44±0.75	0.42±0.72	31 (30.7%)	0.91

[Table/Fig-3]: Comparison of symptom severity between fungal (+) and fungal (-) groups.

The most common CT finding was lung mass (observed in 73.5% of cases), followed by pleural effusion (41.2%) among fungal culture–positive patients. Cavitating mass was the least common radiological finding (8.8%) [Table/Fig-4].

CT Finding	Fungal (+) (n=34)	Fungal (-) (n=67)	p-value
Mass	25 (73.5%)	52 (77.6%)	0.65
Consolidation	4 (11.8%)	3 (4.5%)	0.22
Cavitating mass	3 (8.8%)	4 (6.0%)	0.69
Pleural effusion	14 (41.2%)	22 (32.8%)	0.40
Lung collapse	6 (17.6%)	8 (11.9%)	0.43

[Table/Fig-4]: Comparison of radiological findings in fungal (+) and fungal (-) groups.

The right bronchial tree was more commonly affected than the left, with the upper lobe involved in approximately 41% of cases. The middle and lower lobes showed similar frequencies of involvement (29.4% each) in the fungal-positive group. There was no statistically significant association between the specific lung lobe involved (upper, middle, or lower) and fungal culture positivity [Table/Fig-5].

Lobe	Fungal positive	Fungal negative	Chi-square statistic (χ^2)	p-value
Upper Lobe (UL)	14 (41.2%)	20 (29.9%)	1.59	0.451
Middle Lobe (ML)	10 (29.4%)	24 (35.8%)		
Lower Lobe (LL)	10 (29.4%)	23 (34.3%)		

[Table/Fig-5]: Distribution of lung lobe involvement by fungal status.

No significant differences were observed in tumour cell type distribution between fungal-infected and non infected groups (p-value>0.75). The predominant histological type was Squamous Cell Carcinoma (SCC), comprising approximately 52% of cases in both groups, followed by adenocarcinoma (AD) and small cell carcinoma (SM), each accounting for about 20–23% [Table/Fig-6].

DISCUSSION

Lung cancer poses a significant public health challenge worldwide. Tobacco smoking remains the most recognised and extensively studied risk factor for lung cancer. However, the role of multiple

Cell type	Fungal (+) (n=34)	Fungal (-) (n=67)	Total	p-value (Chi-square)
SQ[1]	18 (52.9%)	35 (52.2%)	53	0.95
AD[2]	7 (20.6%)	15 (22.4%)	22	0.84
SM[3]	8 (23.5%)	14 (20.9%)	22	0.76
Others	1 (2.9%)*	3 (4.5%)**	4	1.00 (Fisher's-exact)

[Table/Fig-6]: Cell type distribution in fungal (-) vs fungal (+) groups.
*Includes spindle cell Sarcoma (1 case in fungal (+)); **Includes adenoid cystic (1) and others (2);
1- Squamous cell carcinoma; 2- Adenocarcinoma (AD); 3- Small cell carcinoma

other factors, including chronic infections, has gained increasing attention—particularly in non smoker lung cancer patients. The contribution of chronic infections to lung carcinogenesis, however, remains unclear [21,22]. The lung microbiome has been widely studied, and it is now well established that the lungs are not sterile. Dysbiosis refers to an alteration of the lung microbiome from its healthy state, typically characterised by the predominance of one genus and a reduction in overall microbial diversity [23,24].

In the present study, fungal culture showed growth in 34 cases (33.66%). Among these, *Candida albicans* was isolated in nine cases (8.91%), *Aspergillus niger* in seven cases (6.9%), and *Candida tropicalis* in six cases (5.9%), while 12 cases revealed other fungal species, including *Cladosporium, Penicillium, Candida krusei, Candida kefyr, Saprochaete capitata*, and *Candida parapsilosis*. Overall, *Candida* and *Aspergillus* were the dominant genera.

These findings are consistent with those of El-Badrawy MK et al., who reported fungal isolation in 68% of lung cancer patients [13]. The most commonly isolated species in their study were *Candida albicans* (32%), *Aspergillus niger* (28%), and *Aspergillus fumigatus* (8%). COPD was the most common co-morbidity in the present study, observed in 41 of 101 cases. Similarly, Laroumagne S et al., in a prospective study, concluded that smokers, males, and patients with COPD are at a higher risk of fungal colonisation [8].

In this study, 34 of 101 patients (33.66%) were fungal culture positive, with *Candida albicans* being the most prevalent species (≈9%), followed by *Aspergillus niger* (≈7%) and *Candida tropicalis* (≈6%). These results are in agreement with the findings of Rafat Z et al., who analysed 384 lung specimens (192 BAL and 192 sputum samples) from symptomatic patients hospitalised in pulmonary units [7]. Among these, 137 samples (35.67%) were positive on direct examination and culture. *Candida albicans* (37.22%) and *Candida tropicalis* (21.89%) were the two most frequently isolated species, and 21.89% of these patients had underlying lung cancer.

In the present study, patients with COPD demonstrated higher odds of fungal infection, though this difference did not reach statistical significance (p-value=0.16). Similar findings have been reported in studies involving patients with chronic respiratory diseases other than lung cancer. For instance, Xue Q et al., investigated bacterial and fungal variations in the sputum of patients hospitalised with severe COPD [25]. A total of 65 sputum samples were obtained from six patients with severe COPD who had experienced at least one acute exacerbation. Clinical data were collected from hospital medical records. The fungal population in these patients was typically dominated by *Candida, Phialosimplex, Aspergillus, Penicillium, Cladosporium*, and *Eutypella*.

In present study, as well as in multiple previous studies [7,13] assessing fungal colonisation or infection in lung cancer patients, *Candida* and *Aspergillus* emerged as the predominant genera. This consistent pattern may be attributed to the immunocompromised state of cancer patients due to the disease itself and its treatments, disrupted mucosal barriers, frequent use of broad-spectrum antibiotics, and prolonged hospital stays. Furthermore, both fungi are opportunistic pathogens with ubiquitous environmental presence, making them more likely to colonise or infect when host defenses are weakened.

In contrast to these findings, the research conducted by Bello S et al., a case-control study among 25 patients with central lung cancer and 16 controls without antimicrobial intake during the previous month, determined bacterial and fungal distribution using massive sequencing of bronchial biopsies, saliva, and faecal samples. The mycobiome of controls (*Candida*) was significantly different from that of patients (*Malassezia*) [26]. This discrepancy may be due to their use of high-throughput sequencing, which enables detection of non culturable or low-abundance fungi, as well as the inclusion of multiple sample types—bronchial biopsies, saliva, and faecal samples—providing a broader representation of the host-associated mycobiome.

In comparison to the fungal-negative group, the severity of symptoms was greater in the fungal-positive group. Higher grades of dyspnoea, cough, chest pain and haemoptysis were observed in lung cancer patients with positive fungal cultures. Higher dyspnoea scores were observed in lung cancer patients who had culture positive for *Candida albicans*. Overall, no statistically significant differences in symptom severity were observed between the groups. In contrast to present study, El-Badrawy MK et al., reported increased detection of fungal colonisation with increasing clinical severity, reflected by higher grades of dyspnoea (grade 1 vs. grade 2, p=0.001), cough score (score 1 vs. score 3, p=0.001), chest pain score (score 0 vs. score 1, p=0.001), and haemoptysis score (score 0 vs. score 3, p=0.001) [13].

The lack of a statistically significant association in present study could be attributed to several factors. Firstly, differences in study populations—such as variations in the underlying stage of lung cancer, immune status, or co-morbidities—may influence symptom expression and the host's response to fungal colonisation. Additionally, the subjective nature of symptom scoring and potential inter-individual variability in symptom perception could have reduced measurable differences. Mass lesions were the most common CT finding in the fungal-positive group, followed by pleural effusion. Consolidation and cavitating masses were less frequently observed in lung cancer patients with positive fungal cultures. In agreement with our results, El-Badrawy MK et al., [13] also reported mass lesions (79.4%, p-value=0.830) on CT chest as the most common finding among the culture-positive group, followed by pleural effusion (24.6%, p-value=0.854).

Although lung collapse showed 68% higher adjusted odds of fungal colonisation (aOR 1.68), this association was not statistically significant, as reflected by the wide confidence intervals. This finding aligns with present study, which indicated no significant difference in the frequency of fungal colonisation between patients with and without lung collapse. The wide confidence intervals suggest considerable uncertainty around the estimate, likely due to limited sample size or data variability. Therefore, while lung collapse may have a potential role in fungal colonisation, present study could not conclusively demonstrate this relationship.

A possible explanation for the observed higher odds of fungal colonisation in patients with lung collapse could be that collapsed lung segments create a localised environment conducive to fungal growth. Lung collapse may impair ventilation and clearance mechanisms, leading to mucus stasis and reduced immune surveillance, which can favour fungal colonisation. However, the lack of statistical significance and wide confidence intervals indicate that this relationship is not definitive in our sample and may be influenced by other factors such as disease severity, treatment variations, or co-morbid conditions. Larger studies are needed to clarify this potential association.

The histological cell type of the diagnosed tumour was also considered to assess its potential influence on fungal colonisation. Understanding whether specific tumour cell types predispose patients to fungal colonisation could provide insights into the underlying pathophysiological mechanisms. However, present study did not reveal any significant association between tumour cell type and fungal colonisation, suggesting that fungal presence may be independent of tumour histology in this cohort.

The dominant histological types of lung cancer were SCC, accounting for approximately 52% of cases in both fungal-positive and fungal-negative groups, followed by AD and SM, each comprising about 20–23%. *Candida albicans* was most frequently found in SCC (66.7% of its cases). *Aspergillus niger* also showed a predominance in SCC (57.1%), while *Candida tropicalis* was primarily associated with small cell carcinoma (50% of cases). However, due to small sample sizes, no strong or statistically significant cell-type preferences could be established for any fungal species.

Fungal infections were distributed relatively equally across SQ, AD, and SM tumour subtypes, indicating no specific histological predisposition. Although SQ carcinoma showed the highest absolute number of fungal infections, this likely reflects its overall prevalence rather than a true association. A slight trend was noted for *Candida tropicalis* in small cell carcinoma, but this did not reach statistical significance. Analysis was limited for rare tumour types due to insufficient case numbers.

Consistent with our observations, El-Badrawy MK et al., reported no significant differences regarding age, co-morbidity frequency, chest Computed Tomography (CT) findings, lung cancer cell type, or tumour staging between patients with and without fungal colonisation (p-value>0.05) [13]. The absence of a significant association between fungal colonisation and tumour histology may be because fungal presence is more influenced by local pulmonary conditions—such as tissue damage, immune status, or impaired clearance—rather than tumour cell type. The similar distribution across histological subtypes likely reflects their overall prevalence within the cohort. Additionally, small sample sizes and confounding factors such as co-morbidities or prior treatments may have limited the detection of specific associations.

The complex relationship between fungal colonisation and lung cancer remains incompletely understood. Further well-designed studies with larger cohorts are essential to clarify how fungal presence may influence clinical outcomes and patient prognosis. A deeper understanding of these interactions could contribute to improved diagnostic, therapeutic, and management strategies for lung cancer patients.

The findings of present study draw attention to the notable prevalence of fungi in lung cancer patients, highlighting their potential role in the aetiopathogenesis of the disease. A considerable number of cases were analysed, providing valuable insights into the lung mycobiome. There remains a notable lack of research investigating the role of fungi in lung cancer; hence, this study helps address an important gap by exploring a relatively under-researched area. Many of present study findings align with those of previous studies [7,8,13] conducted in different regions and time periods, both within India and internationally. This research contributes to the existing body of knowledge by providing updated data on the prevalence of fungal infection among lung cancer patients.

Limitation(s)

As this study was conducted at a single centre, the results may not be representative of the general population. The study did not differentiate between simple fungal colonisation and invasive fungal disease. Moreover, the impact of fungal colonisation on treatment outcomes was not assessed, as patient follow-up was not included.

CONCLUSION(S)

The present study found out that fungal colonisation is a notable co-existing condition in patients with lung cancer, with a prevalence of 33.66%, predominantly involving species of *Candida* and

Aspergillus. Although no statistically significant associations were found between fungal colonisation and patient demographics, smoking status, radiological features, or tumour histology, a trend toward higher colonisation in patients with COPD was observed. These findings underscore the importance of recognising fungal presence in lung cancer patients, particularly those with chronic respiratory co-morbidities, as it may influence disease progression, treatment response, and overall outcomes.

Given the growing global burden of both fungal infections and lung cancer, and the limited understanding of their intersection, further multicentric and longitudinal studies are warranted to elucidate the clinical implications of fungal colonisation in this vulnerable population.

REFERENCES

[1] Biswas D, Agarwal S, Sindhwani G, Rawat J. Fungal colonization in patients with chronic respiratory diseases from Himalayan region of India. Ann Clin Microbiol Antimicrob. 2010;9:28.
[2] Apostolou P, Tsantsaridou A, Papasotiriou I, Toloudi M, Chatziioannou M, Giamouzis G. Bacterial and fungal microflora in surgically removed lung cancer samples. J Cardiothorac Surg. 2011;6:137.
[3] Jose RJ, Brown JS. Opportunistic bacterial, viral and fungal infections of the lung. Medicine (Abingdon). 2016;44(6):378-83.
[4] Budisan L, Zanoaga O, Braicu C, Pirlog R, Covaliu B, Esanu V, et al. Links between infections, lung cancer, and the immune system. Int J Mol Sci. 2021;22(17):9394.
[5] Criner GJ, Agusti A, Borghaei H, Friedberg J, Martinez FJ, Miyamoto C, et al. Chronic obstructive pulmonary disease and lung cancer: A review for clinicians. Chronic Obstr Pulm Dis. 2022;9(3):454-76.
[6] Patel B, Priefer R. Impact of chronic obstructive pulmonary disease, lung infection, and/or inhaled corticosteroids use on potential risk of lung cancer. Life Sci. 2022;294:120374.
[7] Rafat Z, Hashemi SJ, Ashrafi K, Nikokar I, Jafari A, Rahimi Foroushani A, et al. Fungal isolates of the respiratory tract in symptomatic patients hospitalized in pulmonary units: A mycological and molecular epidemiologic study. J Multidiscip Healthc. 2020;13:661-69.
[8] Laroumagne S, Lepage B, Hermant C, Plat G, Phelippeau M, Bigay-Game L, et al. Bronchial colonisation in patients with lung cancer: A prospective study. Eur Respir J. 2013;42(1):220-29.
[9] Zhao Y, Liu Y, Li S, Peng Z, Liu X, Chen J, et al. Role of lung and gut microbiota on lung cancer pathogenesis. J Cancer Res Clin Oncol. 2021;147(8):2177-86.
[10] Jaggi TK, Agarwal R, Tiew PY, Shah A, Lydon EC, Hage CA, et al. Fungal lung disease. Eur Respir J. 2024;64(5):2400803.
[11] Hosseini K, Ahangari H, Chapeland-Leclerc F, Ruprich-Robert G, Tarhriz V, Dilmaghani A. Role of fungal infections in carcinogenesis and cancer development: A literature review. Adv Pharm Bull. 2022;12(4):747-56.
[12] Subhranshu M, Sankar S, Chandan M. The intricate relationship between fungal infections and cancer: Unveiling the molecular mechanisms and therapeutic implications. Journal of Current Oncological Trends. 2024;1(2):64-68.
[13] El-Badrawy MK, Elsaied AR, Ibrahim AAM, Eladl AE, Elmorsey RA. Prevalence and pattern of isolated fungi from bronchoalveolar lavage among patients with lung cancer: A prospective cross-sectional study. Egypt J Bronchol. 2023;17:7.
[14] Stenton C. The MRC breathlessness scale. Occup Med. 2008;58:226-27.
[15] Hsu JY, Stone RA, Logan-Sinclair RB, Worsdell M, Busst CM, Chung KF. Coughing frequency in patients with persistant cough: Assessment using a 24 hour ambulatory recorder. Eur Respir J. 1994;7:1246-53.
[16] Melzack R, Abbott FV, Zackon W, Mulder DS, William M, Davis L. Pain on a surgical ward: A survey of the duration and intensity of pain and the effectiveness of medication. Pain. 1987;29(1):67-72.
[17] Ozgül MA, Turna A, Yildiz P, Ertan E, Kahraman S, Yilmaz V. Risk factors and recurrence patterns in 203 patients with hemoptysis. Tuberk Toraks. 2006;54(3):243-48.
[18] Güldaval F, Polat G, Doruk S, Karadeniz G, Ayranci A, Türk M, et al. What are the differences between smoker and non-smoker COPD cases? Is it a different phenotype? Turk Thorac J. 2021;22(4):284-88. Doi: 10.5152/TurkThoracJ.2021.20147.
[19] Dutt S, Gogia T, Gupta M. A comparative study on pulmonary function tests in smokers & nonsmokers [Internet]. Indian J Clin Anat Physiol. 2025 [cited 2025 Sep 08];8(1):53-56.
[20] Travis WD, Brambilla E, Nicholson AG, Yatabe Y, Austin JH, Beasley MB et al. The 2015 World Health Organization classification of lung tumours: Impact of genetic, clinical and radiologic advances since the 2004 classification. J Thorac Oncol. 2015;10:1243-60.
[21] LoPiccolo J, Gusev A, Christiani DC, Jänne PA. Lung cancer in patients who have never smoked - An emerging disease. Nat Rev Clin Oncol. 2024;21(2):121-46.
[22] Jovičić-Bata J, Sazdanić-Velikić D, Ševo M, Milanović M, Tubić T, Bijelović M, et al. Lifestyle, environmental, occupational, and dietary risk factors in small-cell vs. non-small-cell advanced lung cancer patients: Is there a connection? Cancers. 2025;17(5):864.
[23] Xu N, Wang L, Li C, Ding C, Li C, Fan W, et al. Microbiota dysbiosis in lung cancer: Evidence of association and potential mechanisms. Transl Lung Cancer Res. 2020;9(4):1554-68.
[24] Goto T. Airway microbiota as a modulator of lung cancer. Int J Mol Sci. 2020;21(9):3044.
[25] Xue Q, Xie Y, He Y, Yu Y, Fang G, Yu W, et al. Lung microbiome and cytokine profiles in different disease states of COPD: A cohort study. Sci Rep. 2023;13:5715.
[26] Bello S, Vengoechea JJ, Ponce-Alonso M, Figueredo AL, Mincholé E, Rezusta A, et al. Core microbiota in central lung cancer with streptococcal enrichment as a possible diagnostic marker. Arch Bronconeumol. 2021;57(11):681-89.

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