The Research of Medical Science Review
ISSN: 3007-1208 & 3007-1216 Volume 3, Issue 6, 2025

PATHOGENIC DIVERSITY IN PATIENTS ADMITTED WITH INFECTIVE EXACERBATION OF BRONCHIECTASIS IN LADY READING HOSPITAL CHEST WARD

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DOI: https://doi.org/10.5281/zenodo.15752836

Keywords
Bronchiectasis, Infective Exacerbation, Pathogenic Diversity, Haemophilus Influenzae, Pseudomonas Aeruginosa, Sputum Culture, Pakistan.

Article History
Received on 20 May 2025
Acceptsed on 20 June 2025
Published on 27 June 2025

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Abstract

BACKGROUND: *Bronchiectasis is a chronic airway disease characterized by irreversible bronchial dilatation and recurrent respiratory infections. Infective exacerbations significantly contribute to morbidity, often necessitating hospitalization and antibiotic therapy. Although microbial pathogens play a key role in these exacerbations, there is limited local data on their distribution in Pakistan.*

OBJECTIVE: *To determine the pathogenic diversity in patients presenting with infective exacerbation of bronchiectasis.*

METHODS: *This cross-sectional study was conducted over six months in the Department of Pulmonology, Lady Reading Hospital, Peshawar. A total of 381 patients aged 30–60 years with clinically defined infective exacerbation of bronchiectasis were included through non-probability consecutive sampling. Patients with recent antibiotic use, overlapping respiratory conditions, or immunocompromised states were excluded. Early morning sputum samples were collected and cultured using standard microbiological techniques. Microorganisms identified included Haemophilus influenzae, Pseudomonas aeruginosa, Moraxella catarrhalis, Streptococcus pneumoniae, Staphylococcus aureus, Aspergillus spp., and Escherichia coli. Demographic and clinical characteristics were recorded. Data were analyzed using SPSS* ***v26, with frequencies,*** *percentages, and chi-square/Fisher's exact tests applied for post-stratification. A p-value ≤0.05 was considered statistically significant.*

RESULTS: *Among the 381 patients, the most commonly isolated pathogen was Haemophilus influenzae (37.3%), followed by Pseudomonas aeruginosa (33.6%), Moraxella catarrhalis (17.6%), and Streptococcus pneumoniae (15.5%). Less frequently isolated organisms included Staphylococcus aureus (11%), Aspergillus spp. (9.4%), and Escherichia coli (7.3%). Statistically significant associations were found between pathogen distribution and patient age (p=0.041), presence of*

diabetes mellitus (p=0.021), and duration of bronchiectasis (p=0.032). No significant relationship was observed with gender, education, residential status, BMI, or hypertension.

CONCLUSION: *This study highlights a diverse microbial spectrum in patients with infective exacerbation of bronchiectasis, with Haemophilus influenzae and Pseudomonas aeruginosa being the predominant pathogens. The findings emphasize the importance of local microbial surveillance to guide targeted antibiotic therapy and reduce reliance on empirical treatment. Such data are vital for improving clinical outcomes and informing regional treatment guidelines.*

INTRODUCTION

Bronchiectasis is a chronic pulmonary disorder marked by irreversible dilation and damage of the bronchi, the air passages responsible for conducting air in and out of the lungs. This structural distortion impairs mucociliary clearance, resulting in mucus retention and promoting a cycle of recurrent infections and chronic inflammation.[1] Over time, this pathological process contributes to progressive airway remodeling, leading to persistent symptoms such as chronic productive cough, dyspnea, and frequent respiratory infections. The condition may develop secondary to various etiologies including previous pulmonary infections, immune system deficiencies, autoimmune diseases, and congenital disorders such as cystic fibrosis. In addition to its impact on pulmonary function, bronchiectasis significantly impairs quality of life and contributes to increased morbidity through recurrent infective exacerbations.[2]

Infective exacerbations of bronchiectasis are characterized by an acute worsening of respiratory symptoms, commonly indicated by increased cough, sputum volume or purulence, breathlessness, and systemic features such as fever. These episodes are clinically significant, often necessitating hospitalization and intensive antibiotic therapy.[3]The exacerbations result from heightened inflammation within already-damaged airways, creating a permissive environment for microbial colonization and infection. This cycle can accelerate lung function decline and increase the risk of long-term complications if not promptly and effectively managed.

The role of microorganisms in triggering exacerbations is well established, with several bacterial pathogens frequently isolated from sputum cultures of affected patients. Common organisms include Haemophilus influenzae, Pseudomonas aeruginosa, Staphylococcus aureus, Moraxella catarrhalis, and Streptococcus pneumoniae. Among these, Pseudomonas aeruginosa is particularly concerning due to its association with more severe disease, poorer prognosis, and resistance to multiple antibiotics. Its capacity to form biofilms further complicates treatment by shielding the bacteria from host immune responses and antimicrobial agents.[4] The identification of causative organisms during exacerbations is therefore essential in guiding appropriate and targeted antibiotic therapy. Tailoring treatment based on microbial profiling can reduce recurrence rates, limit the development of antimicrobial resistance, and improve long-term disease control.[5]

A study by King et al. reported that Haemophilus influenzae was the most frequently isolated pathogen in patients with infective exacerbation of bronchiectasis, accounting for 47% of cases, followed by Pseudomonas aeruginosa (12%), Moraxella catarrhalis (8%), Streptococcus pneumoniae (7%), Staphylococcus aureus (4%), and Aspergillus spp. and Escherichia coli each at 2% [9]. While international data provide valuable insight, local microbiological patterns may differ due to regional variations in environment, healthcare practices, and antibiotic resistance trends.[6]

Despite the clinical significance of infective exacerbations in bronchiectasis, there is a paucity of local studies exploring pathogen-specific trends in this population. Clinicians are often forced to rely on international data that may not accurately reflect regional microbial profiles. Given the potential geographic variability in infectious agents and resistance patterns, locally generated evidence is essential for formulating effective management

strategies. This study aims to address this gap by identifying the pathogenic spectrum associated with infective exacerbations of bronchiectasis in our local setting. These findings could inform more rational antibiotic use, reduce empirical reliance on broad-spectrum agents, and ultimately contribute to improved clinical outcomes. Moreover, the data may assist in guiding public health strategies and infection control policies by highlighting emerging or dominant pathogens within the community.

MATERIAL AND METHODS

This was a cross-sectional study conducted in the Department of Pulmonology at Lady Reading Hospital (LRH), Peshawar. The study duration was six months following approval of the research synopsis. The objective of this study was to determine the pathogenic diversity in patients presenting with infective exacerbation of bronchiectasis. Infective exacerbation was defined as a clinical condition in which patients presented with worsening respiratory symptoms including increased cough (exceeding 20% of baseline frequency), increased sputum volume (>10 ml/day), purulent sputum (darker yellow or green), and breathlessness persisting for more than 48 hours. The diagnosis was confirmed by the presence of fever >38°C and a reduction in FEV1 greater than 10% from the patient's baseline. Microbiological evaluation included identification of the following organisms: Haemophilus influenzae, Pseudomonas aeruginosa, Moraxella catarrhalis, Streptococcus pneumoniae, Staphylococcus aureus, Aspergillus spp., and Escherichia coli. Each organism was identified using standard culture methods with a diagnostic threshold of ≥1000 CFU/ml. Specific culture media and morphological characteristics were used to confirm each pathogen. For instance, Haemophilus influenzae appeared as grayish colonies with a musty odor on chocolate agar, whereas Pseudomonas aeruginosa formed greenish colonies on nutrient agar with a grape-like smell. A total of 381 patients were included using a non-probability consecutive sampling technique. The sample size was calculated using WHO sample size software, based on a 95% confidence level, 1% margin of error, and an expected frequency of Escherichia coli at 2% in patients with infective exacerbation of bronchiectasis. Inclusion criteria consisted of adult patients aged 30 to 60 years of both genders presenting with infective exacerbation of bronchiectasis as per operational definition. Exclusion criteria included a known history of asthma or overlapping respiratory conditions, recent antibiotic use (within the past four weeks), recent respiratory hospitalization (within the past month), immunocompromised status, coexisting respiratory infections such as tuberculosis or fungal infections, lung malignancy, pregnancy or lactation, and history of substance abuse.

Eligible patients were enrolled after obtaining ethical approval and written informed consent. Confidentiality and anonymity were ensured throughout the study. Baseline demographic and clinical information including age, gender, residential status, education level, BMI, diabetes mellitus, hypertension, and duration of bronchiectasis were documented. Sputum samples were collected as early-morning specimens to ensure optimal yield. Patients were instructed on how to produce deep, productive coughs for sample adequacy. Each specimen was collected in sterile containers, labeled with anonymized patient codes, and promptly transported to the laboratory within two hours while maintaining a cool chain to prevent overgrowth. A standardized laboratory form was included with each sample.

Microbiological analysis was performed for all target pathogens using specified culture techniques in accordance with the operational definitions. All observations were recorded on a specially designed proforma (Annexure-I). Patients were managed according to departmental protocols, independent of study findings.

Data were analyzed using IBM SPSS version 26. Categorical variables such as gender, residential status, education level, comorbidities (diabetes and hypertension), and organism types were reported as frequencies and percentages. Continuous variables including age, BMI, and duration of bronchiectasis were analyzed using means and standard deviations, or medians with interquartile ranges for non-normally distributed data as assessed by the Shapiro-Wilk test. Stratification of isolated pathogens was conducted against demographic and clinical variables. Chi-square or Fisher's exact test was

applied post-stratification, with a p-value ≤0.05 considered statistically significant. Results were presented in the form of tables and graphs.

RESULTS:

A total of 381 patients admitted with infective exacerbation of bronchiectasis were included in this analysis. The majority of the patients (41.2%) were in the 51–60 year age group, followed by 33.1% in the 41–50 age group and 25.7% in the 30–40 age group. Males constituted a slightly higher proportion of the sample (55.1%) compared to females (44.9%). Most patients were from rural areas (56.4%), while 43.6% belonged to urban settings. Educational background showed that 43% of patients were uneducated, 24.1% had primary education, 21% had secondary education, and only 11.8% had higher education. When assessed for BMI, nearly half the patients (49.3%) had normal weight (18.5–24.9 kg/m²), while 22% were overweight, 18.9% were underweight, and 9.7% were obese.

In terms of comorbidities, diabetes mellitus was present in 29.4% of patients and hypertension in 27.3%. A higher proportion (56.7%) had a bronchiectasis duration of more than 5 years, while 43.3% had been diagnosed within the past 5 years.

Microbiological analysis revealed that Haemophilus influenzae was the most commonly isolated pathogen, present in 37.3% of patients. This was followed by Pseudomonas aeruginosa in 33.6%, Moraxella catarrhalis in 17.6%, and Streptococcus pneumoniae in 15.5% of cases. Less frequent pathogens included Staphylococcus aureus (11%), Aspergillus spp. (9.4%), and Escherichia coli (7.3%). It is important to note that polymicrobial infections were observed in several patients.

Post-stratification analysis showed statistically significant associations between certain demographic and clinical factors and the presence of specific microorganisms. Age was significantly associated with microbial patterns ($p = 0.041$), with Haemophilus influenzae and Pseudomonas aeruginosa being more prevalent in older age groups. Diabetes mellitus was significantly associated with higher isolation rates of Pseudomonas aeruginosa and Haemophilus influenzae ($p = 0.021$), suggesting a potential link between glycemic status and pathogen susceptibility. Duration of bronchiectasis also showed a statistically significant relationship with pathogen distribution ($p = 0.032$), with chronic cases (>5 years) more likely to yield Pseudomonas aeruginosa and fungal organisms like Aspergillus spp. No statistically significant associations were observed between gender, residential status, education level, hypertension, or BMI and the distribution of specific microorganisms, although descriptive differences were noted. These findings highlight the need for tailored clinical management in patients with long-standing disease, diabetes, and advanced age, as they appear to have distinct microbiological profiles

Table 1: Demographic and Clinical Characteristics (n = 381)

Variable	Category	Frequency (n)	Percentage (%)
Age (years)	30–40	98	25.7%
	41–50	126	33.1%
	51–60	157	41.2%
Gender	Male	210	55.1%
	Female	171	44.9%
Residential Status	Rural	215	56.4%
	Urban	166	43.6%
Education Level	Uneducated	164	43.0%
	Primary	92	24.1%
	Secondary	80	21.0%
	Higher	45	11.8%
BMI (Kg/m²)	<18.5 (Underweight)	72	18.9%
	18.5–24.9 (Normal)	188	49.3%
	25–29.9 (Overweight)	84	22.0%

	≥30 (Obese)	37	9.7%
Diabetes Mellitus	Yes	112	29.4%
	No	269	70.6%
Hypertension	Yes	104	27.3%
	No	277	72.7%
Duration of Bronchiectasis (years)	≤5 years	165	43.3%
	>5 years	216	56.7%

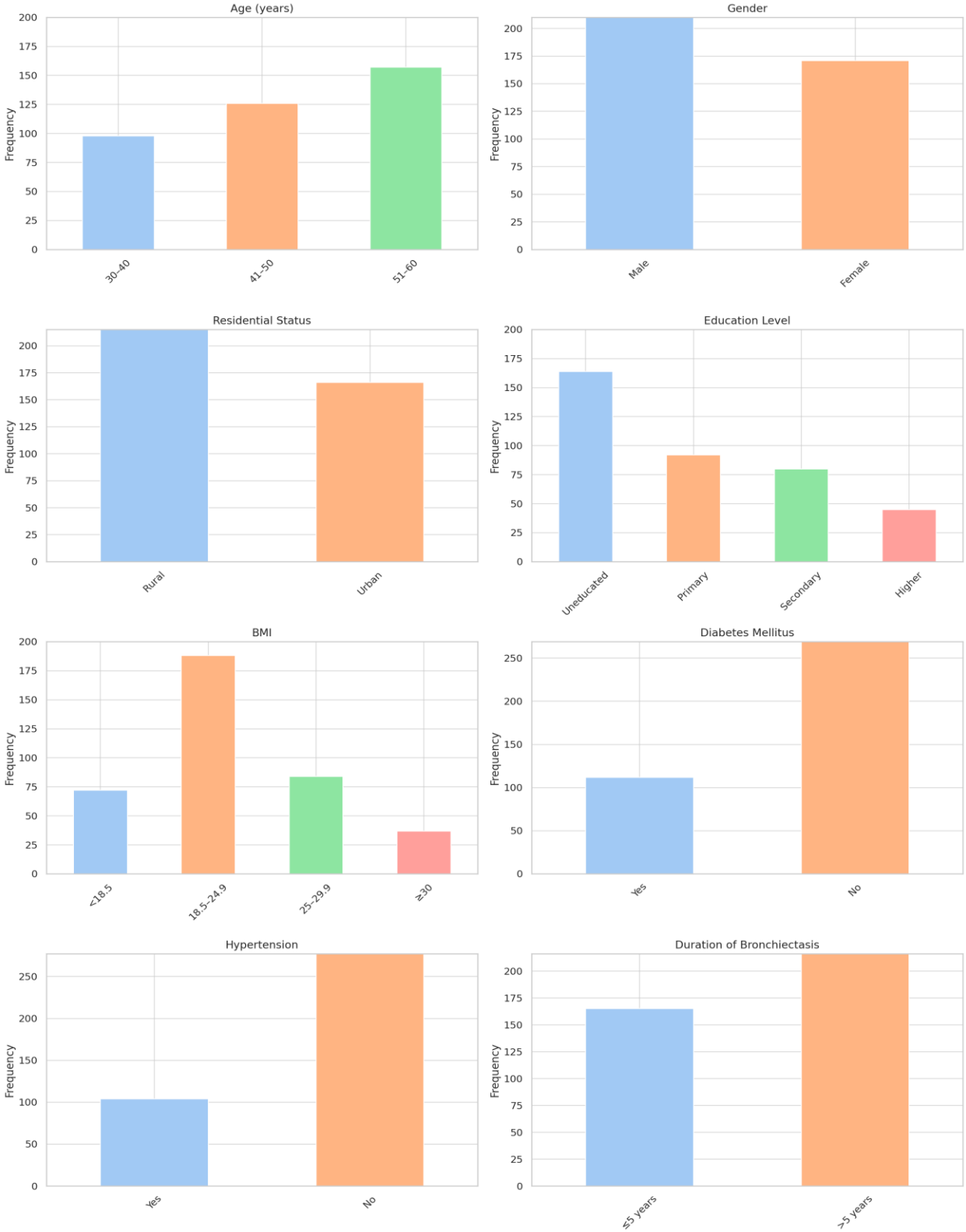
Table 2: Frequency of Pathogenic Microorganisms Isolated (n = 381)

Microorganism	Presence	Frequency (n)	Percentage (%)
Haemophilus influenzae	Yes	142	37.3%
Pseudomonas aeruginosa	Yes	128	33.6%
Moraxella catarrhalis	Yes	67	17.6%
Streptococcus pneumoniae	Yes	59	15.5%
Staphylococcus aureus	Yes	42	11.0%
Aspergillus spp.	Yes	36	9.4%
Escherichia coli	Yes	28	7.3%

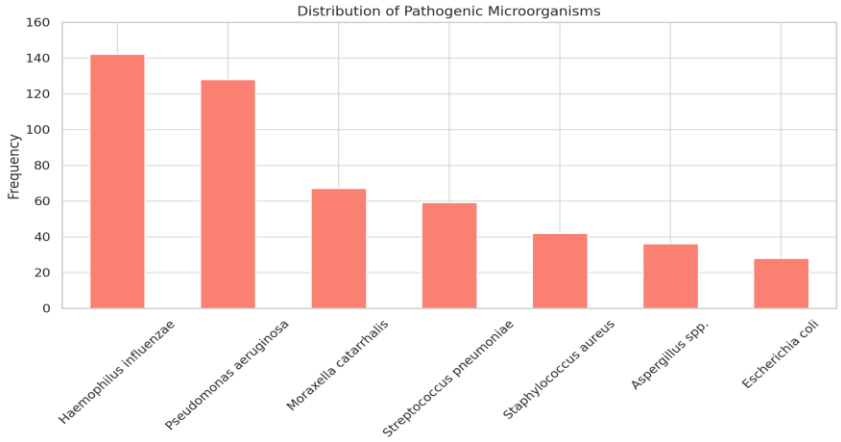
Table 3: Post-Stratification of Pathogenic microorganisms with Demographic and Clinical characteristics (n = 381)

Variable	Category	H. influenzae n (%)	P. aeruginosa n (%)	M. catarrhalis n (%)	S. pneumoniae n (%)	S. aureus n (%)	Aspergillus spp. n (%)	E. coli n (%)	p-value
Age (years)	30–40	42 (42.9%)	28 (28.6%)	16 (16.3%)	10 (10.2%)	6 (6.1%)	4 (4.1%)	4 (4.1%)	0.041*
	41–50	46 (36.5%)	46 (36.5%)	24 (19.0%)	18 (14.3%)	14 (11.1%)	12 (9.5%)	10 (7.9%)	
	51–60	54 (34.4%)	54 (34.4%)	27 (17.2%)	31 (19.7%)	22 (14.0%)	20 (12.7%)	14 (8.9%)	
Gender	Male	78 (37.1%)	84 (40.0%)	34 (16.2%)	26 (12.4%)	20 (9.5%)	18 (8.6%)	12 (5.7%)	0.148
	Female	64 (37.4%)	44 (25.7%)	33 (19.3%)	33 (19.3%)	22 (12.9%)	18 (10.5%)	16 (9.4%)	
Residential Status	Rural	86 (40.0%)	66 (30.7%)	39 (18.1%)	31 (14.4%)	25 (11.6%)	20 (9.3%)	14 (6.5%)	0.332
	Urban	56 (33.7%)	62 (37.3%)	28 (16.9%)	28 (16.9%)	17 (10.2%)	16 (9.6%)	14 (8.4%)	
Education Level	Uneducated	68 (41.5%)	58 (35.4%)	28 (17.1%)	23 (14.0%)	20 (12.2%)	18 (11.0%)	16 (9.8%)	0.063
	Primary	34 (37.0%)	28 (30.4%)	16 (17.4%)	14 (15.2%)	10 (10.9%)	6 (6.5%)	4 (4.3%)	
	Secondary+Higher	40 (33.6%)	42 (35.3%)	23 (19.3%)	22 (18.5%)	12 (10.1%)	12 (10.1%)	8 (6.7%)	
BMI (kg/m²)	<18.5	28 (38.9%)	18 (25.0%)	10 (13.9%)	8 (11.1%)	6 (8.3%)	6 (8.3%)	4 (5.6%)	0.090
	18.5–24.9	74 (39.4%)	66 (35.1%)	30 (16.0%)	26 (13.8%)	18 (9.6%)	18 (9.6%)	10 (5.3%)	
	≥25	40 (32.8%)	44 (36.1%)	27 (22.1%)	25 (20.5%)	18 (14.8%)	12 (9.8%)	14 (11.5%)	
Diabetes Mellitus	Yes	50 (44.6%)	54 (48.2%)	18 (16.1%)	20 (17.9%)	16 (14.3%)	16 (14.3%)	12 (10.7%)	0.021*
	No	92 (34.2%)	74 (27.5%)	49 (18.2%)	39 (14.5%)	26 (9.7%)	20 (7.4%)	16 (5.9%)	
Hypertension	Yes	38 (36.5%)	44 (42.3%)	18 (17.3%)	16 (15.4%)	14 (13.5%)	12 (11.5%)	10 (9.6%)	0.147
	No	104 (37.5%)	84 (30.3%)	49 (17.7%)	43 (15.5%)	28 (10.1%)	24 (8.7%)	18 (6.5%)	
Duration of Bronchiectasis	≤5 years	58 (35.2%)	48 (29.1%)	34 (20.6%)	28 (17.0%)	22 (13.3%)	12 (7.3%)	8 (4.8%)	0.032*
	>5 years	84 (38.9%)	80 (37.0%)	33 (15.3%)	31 (14.4%)	20 (9.3%)	24 (11.1%)	20 (9.3%)	

GRAPH:1: DEMOGRAPHIC AND CLINICAL CHARACTERISTICS: A SERIES OF BAR CHARTS



GRAPH:2: DISTRIBUTION OF PATHOGENIC MICROORGANISMS: A BAR CHART



DISCUSSION

The findings of this study provide insight into the demographic and microbiological patterns among patients with infective exacerbation of bronchiectasis in a tertiary care setting. The predominance of patients in the older age group (51–60 years) aligns with previous literature, where bronchiectasis is often described as a disease more common in the elderly due to cumulative exposure to infections and chronic lung conditions [1]. Similarly, the higher prevalence among males (55.1%) is supported by studies reporting male dominance in non-cystic fibrosis bronchiectasis, potentially due to higher exposure to environmental and occupational risk factors [7].

Rural predominance (56.4%) observed in this cohort may reflect limited healthcare access, delayed diagnosis, and chronic exposure to biomass fuels or poor sanitation—factors that have been associated with increased bronchiectasis risk in low- and middle-income settings [3]. The educational profile, with 43% uneducated, further highlights the potential role of socioeconomic disadvantage in disease burden, which has been described in South Asian populations with limited health literacy [8].

BMI distribution in this population indicated that nearly half had normal weight, while 22% were overweight and 18.9% underweight. Underweight status has previously been linked to poor prognosis in bronchiectasis due to malnutrition and frequent infections, whereas overweight individuals often exhibit different inflammatory profiles [9]. Comorbidities such as diabetes (29.4%) and hypertension (27.3%) were common, consistent with data suggesting that systemic inflammation and impaired immunity in chronic disease patients may predispose them to recurrent bronchial infections [10].

Microbiologically, Haemophilus influenzae (37.3%) was the most commonly isolated organism, which concurs with global reports indicating its dominance in stable and exacerbated bronchiectasis patients [11]. Pseudomonas aeruginosa, detected in 33.6% of patients, was especially prevalent in those with longer disease duration and comorbid diabetes. This is in line with previous studies identifying P. aeruginosa as a marker of disease severity, higher exacerbation frequency, and accelerated lung function decline [12]. A study from the UK bronchiectasis registry also noted that colonization with Pseudomonas was associated with higher mortality and hospital admissions [13].

Moraxella catarrhalis and Streptococcus pneumoniae were isolated in 17.6% and 15.5% of cases respectively, consistent with previous work identifying these as common secondary pathogens in exacerbations [14]. Less frequently isolated organisms included Staphylococcus aureus, Aspergillus spp., and Escherichia coli, similar to regional studies where these were often found in patients with structural lung disease or immunosuppression [15].

The post-stratification analysis revealed statistically significant associations between age, diabetes, and duration of bronchiectasis with specific pathogens. Notably, P. aeruginosa and Aspergillus spp. were more common in patients with longer disease

duration, consistent with the hypothesis that chronic airway remodeling promotes colonization by more resistant or opportunistic pathogens [16]. The higher rates of P. aeruginosa and H. influenzae in diabetic patients may be due to impaired mucociliary clearance and immune dysfunction, as described in prior clinical studies [17].

Overall, the findings reinforce the multifactorial nature of infective exacerbations in bronchiectasis, emphasizing the need for individualized antimicrobial therapy guided by local microbiological patterns and patient risk profiles. The observed trends also underscore the importance of early diagnosis, nutritional support, and chronic disease management to reduce recurrent exacerbations and pathogen colonization.

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