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# Antimicrobial Resistance Burden Across Bronchiectasis Etiologies: An Indian Cohort.

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## Abstract

***Background:*** Bronchiectasis is a chronic respiratory disorder with diverse etiologies and a high burden of recurrent infections. Antimicrobial resistance (AMR) is increasingly recognized as a major challenge in its management, particularly in countries like India where post-infectious causes are common. The study aimed to evaluate the burden and patterns of antimicrobial resistance across different etiologies of bronchiectasis in an Indian cohort. ***Materials and Methods:*** This prospective observational study was conducted at Mamata Medical College over one year (January–December 2025). A total of 50 adult patients with radiologically confirmed bronchiectasis were included. Clinical data, etiological classification, and microbiological profiles were recorded. Sputum samples were processed using standard culture techniques, and antimicrobial susceptibility testing was performed as per CLSI guidelines. Multidrug-resistant (MDR), extensively drug-resistant (XDR), and other resistance patterns were analyzed. Statistical analysis was performed using SPSS, with $p<0.05$ considered significant. ***Results:*** The most common etiology was post-tubercular bronchiectasis (42.0%), followed by idiopathic (22.0%) and post-infectious causes (16.0%). Pseudomonas aeruginosa was the predominant isolate (36.0%). Among 42 culture-positive cases, MDR was observed in 45.2%, XDR in 16.7%, and carbapenem resistance in 26.2%. MDR prevalence was highest in post-tubercular bronchiectasis (57.1%). Significant associations with MDR included age >50 years ($p=0.048$), frequent exacerbations ($p=0.049$), and prior antibiotic use ($p=0.02$). Colistin showed the highest sensitivity (90.5%), while fluoroquinolone resistance was notable. ***Conclusion:*** There is a high burden of antimicrobial resistance in bronchiectasis, particularly in post-tubercular cases. Targeted antimicrobial strategies and strengthened stewardship programs are essential to improve outcomes.as is being investigated in head and neck cancer, thereby maximizing treatment effectiveness.

**Keywords:** Bronchiectasis; Antimicrobial resistance; Post-tubercular; Pseudomonas aeruginosa; Multidrug resistance.



## INTRODUCTION

Bronchiectasis is a chronic suppurative lung disease characterized by irreversible bronchial dilatation, persistent airway inflammation, and recurrent infections [1]. It represents a significant cause of respiratory morbidity worldwide, particularly in low- and middle-income countries such as India, where infectious etiologies remain highly prevalent [2]. The disease is clinically heterogeneous, with patients presenting with chronic cough, sputum production, recurrent exacerbations, and progressive decline in lung function [3]. Advances in imaging, particularly high-resolution computed tomography (HRCT), have improved diagnostic accuracy, yet the burden of disease continues to rise due to aging populations and improved survival from predisposing conditions [4].

The etiological spectrum of bronchiectasis is diverse and includes post-infectious causes, post-tubercular sequelae, allergic bronchopulmonary aspergillosis (ABPA), connective tissue disorders, and idiopathic forms [5]. In the Indian context, post-tubercular bronchiectasis remains a dominant subtype due to the high burden of pulmonary tuberculosis [6]. Different etiologies are associated with varying clinical courses, microbiological profiles, and outcomes, making etiological classification clinically relevant [7]. Notably, chronic colonization by pathogenic organisms contributes to ongoing airway damage and disease progression [8].

Antimicrobial resistance (AMR) has emerged as a critical challenge in the management of bronchiectasis [9]. Repeated antibiotic exposure due to frequent exacerbations predisposes patients to colonization and infection with resistant organisms such as Pseudomonas aeruginosa and other gram-negative bacilli [10]. The presence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) pathogens is associated with increased exacerbation frequency,

hospitalization rates, and healthcare costs [11]. Moreover, resistance patterns may vary depending on the underlying etiology, prior antibiotic use, and local microbiological trends, highlighting the need for region-specific data [12].

Despite the growing recognition of AMR in bronchiectasis, there is limited data from India examining the relationship between bronchiectasis etiologies and antimicrobial resistance patterns. Understanding this association is essential for guiding empirical antibiotic therapy, optimizing antimicrobial stewardship, and improving patient outcomes. Therefore, the present study aimed to evaluate the burden and patterns of antimicrobial resistance across different etiologies of bronchiectasis in an Indian cohort.

## MATERIALS AND METHODS

This prospective observational study was conducted at Mamata Medical College in Hyderabad, Telangana, India. The study was carried out over a period of one year, from January 2025 to December 2025. The objective was to assess the burden and patterns of antimicrobial resistance across different etiologies of bronchiectasis in an Indian cohort.

A total of 50 patients diagnosed with bronchiectasis were enrolled in the study. Diagnosis was established based on clinical features supported by radiological confirmation using high-resolution computed tomography (HRCT) of the chest. Adult patients presenting with stable or exacerbated bronchiectasis were included after obtaining informed consent. Patients with cystic fibrosis, active pulmonary tuberculosis, or incomplete clinical/microbiological data were excluded. Detailed demographic and clinical information, including age, gender, smoking status, duration of symptoms, frequency of exacerbations, and recent antibiotic use, were recorded using a structured proforma.

Sputum samples were collected under aseptic precautions and processed in the microbiology laboratory following standard protocols. Samples were subjected to Gram staining and cultured on appropriate media for bacterial isolation. Identification of organisms was performed using conventional biochemical methods. Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Multidrug-resistant (MDR), extensively drug-resistant (XDR), carbapenem-resistant organisms, and extended-spectrum beta-lactamase (ESBL) producers were defined based on standard international criteria.

Data were entered into Microsoft Excel and analyzed using Statistical Package for the Social Sciences (SPSS) version 26.0. Categorical variables were expressed as frequencies and percentages [N (%)]. Associations between clinical variables and antimicrobial resistance patterns were assessed using the chi-square test or Fisher's exact test as appropriate. A p-value of <0.05 was considered statistically significant.

## RESULTS

The study included 50 patients with bronchiectasis, with the majority aged >50 years (26, 52.0%), followed by 30–50 years (18, 36.0%) and <30 years (6, 12.0%). Males constituted 28 (56.0%) of the cohort. Regarding smoking status, 26 (52.0%) were never smokers, while 14 (28.0%) and 10 (20.0%) were current and former smokers, respectively. A longer disease duration (>5 years) was observed in 31 (62.0%) patients. Frequent exacerbations (≥2 per year) were reported in 34 (68.0%) cases, and prior antibiotic use within the last 3 months was documented in 29 (58.0%) patients (Table 1).

**Table 1. Baseline Demographic and Clinical Characteristics (N = 50)**

| Variable | Category | Value |
|---|---|---|
| Age group (years) | <30 | 6 (12.0%) |
| | 30–50 | 18 (36.0%) |
| | >50 | 26 (52.0%) |
| Gender | Male | 28 (56.0%) |
| | Female | 22 (44.0%) |
| Smoking status | Current smokers | 14 (28.0%) |
| | Former smokers | 10 (20.0%) |
| | Never smokers | 26 (52.0%) |
| Duration of symptoms | >5 years | 31 (62.0%) |
| exacerbations/year | ≥2 | 34 (68.0%) |
| Prior antibiotic use (last 3 months) | Yes | 29 (58.0%) |

Post-tubercular bronchiectasis was the most common etiology, accounting for 21 (42.0%) cases, followed by idiopathic bronchiectasis in 11 (22.0%) patients. Post-infectious (non-TB) causes were identified in 8 (16.0%), while allergic bronchopulmonary aspergillosis (ABPA) contributed to 5 (10.0%) cases. Less frequent etiologies included connective tissue disease-related bronchiectasis in 3 (6.0%) patients and other causes such as primary ciliary dyskinesia in 2 (4.0%) cases (Table 2).

**Table 2. Distribution of Bronchiectasis Etiologies (N = 50)**

| Etiology | N (%) |
|---|---|
| Post-tubercular | 21 (42.0%) |
| Idiopathic | 11 (22.0%) |
| Post-infectious (non-TB) | 8 (16.0%) |
| Allergic bronchopulmonary aspergillosis (ABPA) | 5 (10.0%) |
| Connective tissue disease-related | 3 (6.0%) |
| Others (primary ciliary dyskinesia, etc.) | 2 (4.0%) |

Microbiological analysis of sputum cultures revealed Pseudomonas aeruginosa as the predominant isolate in 18 (36.0%) patients. This was followed by Klebsiella pneumoniae in 9 (18.0%), Staphylococcus aureus in 6 (12.0%), and Escherichia coli in 5 (10.0%) cases. Acinetobacter baumannii was identified in 4 (8.0%) patients, while no growth was observed in 8 (16.0%) samples (Table 3).

**Table 3. Microbiological Profile of Sputum Cultures (N = 50)**

| Organism Isolated | N (%) |
|---|---|
| Pseudomonas aeruginosa | 18 (36.0%) |
| Klebsiella pneumoniae | 9 (18.0%) |
| Escherichia coli | 5 (10.0%) |
| Staphylococcus aureus | 6 (12.0%) |
| Acinetobacter baumannii | 4 (8.0%) |
| No growth | 8 (16.0%) |

Among the 42 culture-positive isolates, multidrug resistance (MDR) was observed in 19 (45.2%) cases, indicating a substantial resistance burden. Extensively drug-resistant (XDR) organisms were identified in 7 (16.7%) isolates. Carbapenem resistance was present in 11 (26.2%) cases, and extended-spectrum beta-lactamase (ESBL) production was noted in 13 (31.0%) isolates. Methicillin-resistant Staphylococcus aureus (MRSA) accounted for 3 (7.1%) cases (Table 4).

**Table 4. Antimicrobial Resistance Pattern Among Isolates (N = 42)**

| Resistance Pattern | N (%) |
|---|---|
| Multidrug-resistant (MDR) | 19 (45.2%) |
| Extensively drug-resistant (XDR) | 7 (16.7%) |
| Carbapenem resistance | 11 (26.2%) |
| ESBL production | 13 (31.0%) |
| Methicillin-resistant S. aureus (MRSA) | 3 (7.1%) |

The distribution of MDR organisms varied across etiologies, with the highest proportion observed in post-tubercular bronchiectasis, where 12 (57.1%) patients exhibited MDR isolates. In comparison, MDR prevalence was lower in idiopathic (3, 27.3%) and post-infectious (2, 25.0%) groups. ABPA and other etiologies demonstrated similar MDR proportions, each with 1 (20.0%) case, indicating a relatively lower resistance burden outside the post-tubercular subgroup (Table 5).

**Table 5. Distribution of MDR Organisms Across Etiologies**

| Etiology | MDR Present | MDR Absent | Total |
|---|---|---|---|
| Post-tubercular | 12 (57.1%) | 9 (42.9%) | 21 |
| Idiopathic | 3 (27.3%) | 8 (72.7%) | 11 |
| Post-infectious | 2 (25.0%) | 6 (75.0%) | 8 |
| ABPA | 1 (20.0%) | 4 (80.0%) | 5 |
| Others | 1 (20.0%) | 4 (80.0%) | 5 |

Analysis of clinical factors associated with MDR revealed that age >50 years was significantly associated with MDR (13, 68.4% vs 13, 41.9%; p=0.048). Patients with ≥2 exacerbations per year also showed a higher prevalence of MDR (16, 84.2% vs 18, 58.1%; p=0.049). Prior antibiotic use was strongly associated with MDR occurrence (15, 78.9% vs 14, 45.2%; p=0.02). However, gender and smoking status did not show statistically significant associations with MDR (Table 6).

**Table 6. Association Between Clinical Factors and MDR (N = 50)**

| Variable | MDR Present (n=19) | MDR Absent (n=31) | p-value |
|---|---|---|---|
| Age >50 years | 13 (68.4%) | 13 (41.9%) | 0.048 |
| Male gender | 12 (63.2%) | 16 (51.6%) | 0.41 |
| Smoking | 11 (57.9%) | 13 (41.9%) | 0.27 |
| ≥2 exacerbations/year | 16 (84.2%) | 18 (58.1%) | 0.049 |
| Prior antibiotic use | 15 (78.9%) | 14 (45.2%) | 0.02 |

Antibiotic sensitivity patterns demonstrated that colistin retained the highest efficacy, with sensitivity observed in 38 (90.5%) isolates. Meropenem and amikacin showed moderate sensitivity rates of 25 (59.5%) and 28 (66.7%), respectively. Piperacillin-tazobactam exhibited equal proportions of sensitivity and resistance (21, 50.0% each). Ciprofloxacin showed relatively lower sensitivity, with resistance noted in 23 (54.8%) isolates, reflecting limited effectiveness (Table 7).

**Table 7. Antibiotic Sensitivity Pattern (Selected Antibiotics)**

| Antibiotic | Sensitive N (%) | Resistant N (%) |
|---|---|---|
| Piperacillin-tazobactam | 21 (50.0%) | 21 (50.0%) |
| Meropenem | 25 (59.5%) | 17 (40.5%) |
| Colistin | 38 (90.5%) | 4 (9.5%) |
| Amikacin | 28 (66.7%) | 14 (33.3%) |
| Ciprofloxacin | 19 (45.2%) | 23 (54.8%) |

## DISCUSSION

The present study demonstrates that post-tubercular bronchiectasis was the predominant etiology (42.0%), followed by idiopathic and post-infectious causes. This finding is consistent with Indian registry data, where post-tuberculosis bronchiectasis has been reported as a leading cause due to the high burden of pulmonary tuberculosis in India [13]. Similar observations have been reported in large Indian cohorts, which highlight infection-related etiologies as the dominant contributors, in contrast to Western populations where idiopathic and immunological causes are more common [2]. This reinforces the importance of regional epidemiology in shaping bronchiectasis patterns and suggests that post-TB structural lung damage remains a major driver of disease burden in developing countries.

Microbiologically, Pseudomonas aeruginosa was the most frequently isolated organism (36.0%) in the present study, followed by Klebsiella pneumoniae. This aligns with existing literature, where Pseudomonas accounts for approximately 20–40% of infections in bronchiectasis and is recognized as a dominant pathogen in moderate-to-severe disease [9]. A recent Indian study reported an even higher prevalence of Pseudomonas aeruginosa (44.3%), further supporting its central role in disease pathogenesis [14]. The relatively high proportion of gram-negative organisms observed in the present study is also consistent with prior evidence suggesting that repeated antibiotic exposure and chronic airway colonization favour resistant gram-negative flora in bronchiectasis patients.

A key finding of this study is the high burden of antimicrobial resistance, with MDR observed in 45.2% and carbapenem resistance in 26.2% of isolates. These findings are in line with global evidence indicating increasing antimicrobial resistance in bronchiectasis, particularly among gram-negative organisms such as Pseudomonas aeruginosa, which possesses intrinsic and acquired resistance mechanisms [15]. Previous studies have also demonstrated that chronic colonization with resistant organisms is associated with worse clinical outcomes, including frequent exacerbations and hospitalizations [16]. The high ESBL rates (31.0%) in the present study further highlight the growing challenge of limited therapeutic options in such patients.

Importantly, the present study demonstrates a higher prevalence of MDR organisms in post-tubercular bronchiectasis (57.1%) compared to other etiologies, suggesting a potential link between prior infectious lung damage and resistant bacterial colonization. This is supported by existing literature, which indicates that patients with severe structural lung disease and repeated antibiotic exposure are more prone to harbour resistant pathogens.

Additionally, clinical factors such as frequent exacerbations and prior antibiotic use were significantly associated with MDR in this study, consistent with previous reports emphasizing these as major risk factors for resistance development [2]. These findings underscore the need for tailored antimicrobial strategies, regular microbiological surveillance, and strengthened antimicrobial stewardship programs in bronchiectasis management.

## CONCLUSION

The present study highlights a substantial burden of antimicrobial resistance among bronchiectasis patients, with nearly half of the culture-positive isolates demonstrating multidrug resistance. Post-tubercular bronchiectasis emerged as the predominant etiology and was associated with a higher prevalence of resistant organisms, underscoring the long-term impact of prior infectious lung damage. Pseudomonas aeruginosa was the most common pathogen, reflecting its established role in chronic airway colonization and disease progression. Clinical factors such as frequent exacerbations and recent antibiotic exposure were significantly associated with MDR, emphasizing the need for judicious antibiotic use. These findings reinforce the importance of routine microbiological surveillance, etiology-based risk stratification, and strengthened antimicrobial stewardship strategies to optimize management and limit the spread of resistance in bronchiectasis.

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