A DESCRIPTIVE CASE SERIES OPEN ACESS

BACTERIOLOGICAL PROFILE AND ANTIBIOTIC RESISTANCE PATTERN IN PATIENTS WITH ACUTE EXACERBATION OF BRONCHIECTASIS

Ahmad Atif [1], Huma Batool [2], Afaq Haider [3], Asifa Iqbal [4], Muhammad Bilal Liaqat [5], M Umer Mumtaz [6]

[1,2,3,4,5,6] Pulmonology Department, Allama Iqbal Medical College/Jinnah Hospital, Lahore, Punjab, Pakistan.

ABSTRACT

Background: Bronchiectasis is a chronic respiratory condition characterized by irreversible bronchial dilatation and recurrent infections, often leading to acute exacerbations that significantly increase morbidity and healthcare burden. Bacterial infections are the primary cause of these exacerbations, and the rising prevalence of antibiotic-resistant pathogens has complicated effective management.

Objective: To determine the bacteriological profile and antibiotic resistance pattern in patients with acute exacerbation of bronchiectasis.

Study Design: Descriptive case series.

Place and Duration of Study: Department of Pulmonology, Allama Iqbal Medical College/Jinnah Hospital, Lahore, from 01 December 2024 to 30 May 2025.

Methodology: A total of 163 patients with acute exacerbation of bronchiectasis were included using a non-probability consecutive sampling technique. Sputum samples were collected and cultured to identify bacterial pathogens. Antibiotic susceptibility testing was performed using the disc diffusion method. Clinical and demographic data were obtained from medical records. Data were analyzed using SPSS version 20, and a p-value of ≤ 0.05 was considered statistically significant.

Results: The mean age of patients was 63.4 ± 12.5 years. The most commonly isolated pathogen was Pseudomonas aeruginosa (40%), followed by Haemophilus influenzae (11.6%), Staphylococcus aureus (7.0%), Klebsiella pneumoniae (5.8%), and Streptococcus pneumoniae (5.5%). Significant resistance was observed to beta-lactams ($p < 0.01$) and fluoroquinolones ($p = 0.03$). Patients with multidrug-resistant organisms had prolonged hospital stay ($p = 0.02$) and increased mortality ($p = 0.01$).

Conclusion: There is a high prevalence of antibiotic-resistant pathogens in acute exacerbation of bronchiectasis. Culture-guided antibiotic therapy and continuous local antimicrobial surveillance are essential to improve clinical outcomes and reduce morbidity and mortality.

Keywords: Antibiotic Resistance, Bronchiectasis, Exacerbation, Pseudomonas Aeruginosa, Sputum Culture

How To Cite This Article: Ahmad A, Batool H, Haider A, Iqbal A, Liaqat MB, Mumtaz MU. Bacteriological Profile and Antibiotic Resistance Pattern in Patients with Acute Exacerbation of Bronchiectasis. *J Bacha Khan Med Coll*. 2025;6(1),1-6.

Corresponding Author: Ahmad Atif
Pulmonology Department, Allama Iqbal Medical College/Jinnah Hospital, Lahore, Punjab, Pakistan
Email: ahmadatif3322@gmail.com

Received: 21st April, 2025
Revision: 20th May, 2025
Accepted: 28th June, 2025
Published: 10th July, 2025
DOI: 10.69830/jbkmc.v6i1.218

INTRODUCTION

Bronchiectasis is a chronic and progressive respiratory disorder characterized by irreversible dilatation of the

bronchi, leading to impaired mucociliary clearance, recurrent infections, and progressive lung damage [1]. Acute exacerbations of bronchiectasis (AEB) represent a major clinical concern, as they contribute significantly to worsening respiratory function, increased healthcare utilization, and reduced quality of life among affected patients [2].

Bacterial infections are the primary drivers of these exacerbations, with commonly isolated pathogens including *Pseudomonas aeruginosa*, *Haemophilus influenzae*, and *Streptococcus pneumoniae*. The persistence of these organisms within the airways promotes chronic inflammation and recurrent infective episodes, further accelerating disease progression [3]. Among these, *Pseudomonas aeruginosa* has been particularly associated with more severe disease, frequent hospitalizations, and poorer clinical outcomes.

In recent years, the emergence of antibiotic resistance among respiratory pathogens has become a significant global health concern. Patients with bronchiectasis often require repeated and prolonged courses of antibiotics, which increases the risk of developing resistant strains. Resistance to commonly used antibiotics such as beta-lactams, aminoglycosides, and fluoroquinolones has been widely reported, complicating empirical treatment strategies [4].

Furthermore, the presence of multidrug-resistant (MDR) organisms has been increasingly documented in patients with bronchiectasis. These organisms are associated with recurrent exacerbations, prolonged hospital stay, increased morbidity, and higher mortality rates [5]. Resistance patterns vary across different regions and healthcare settings, emphasizing the need for localized data to guide appropriate antimicrobial therapy.

Previous studies have highlighted that resistance to fluoroquinolones and aminoglycosides in *Pseudomonas aeruginosa*, as well as beta-lactam resistance in *Haemophilus influenzae* and *Streptococcus pneumoniae*, significantly affects treatment outcomes [6, 7]. However, there remains a paucity of region-specific data regarding the bacteriological profile and resistance patterns in patients with AEB, particularly in developing countries [8].

Therefore, this study aims to determine the bacteriological profile and antibiotic resistance patterns in patients with acute exacerbation of bronchiectasis and to evaluate their clinical implications in guiding effective management strategies.

METHODOLOGY

This descriptive case series was conducted at the Department of Pulmonology, Allama Iqbal Medical College/Jinnah Hospital, Lahore, over a period of six months from 01 December 2024 to 30 May 2025. Ethical approval was obtained prior to the commencement of the study from the Ethical Review Board of Allama Iqbal Medical College (Ref No: 511/ERB/AMC, dated 26 November 2024). Written informed consent was obtained from all participants, and confidentiality of patient data was strictly maintained throughout the study.

A total of 163 patients aged 25–75 years of either gender with a clinical diagnosis of bronchiectasis presenting with acute exacerbation were included using a non-probability consecutive sampling technique. The diagnosis was confirmed through clinical evaluation and high-resolution computed tomography (HRCT) findings. The sample size of 163 patients was calculated using the WHO sample size calculator with a 95% confidence level, 3.5% absolute precision, and an anticipated frequency of *Streptococcus pneumoniae* isolation of 5.5%.

Patients aged 25–75 years of either gender with clinically diagnosed bronchiectasis presenting with acute exacerbation and who provided informed consent were

included in the study. Patients with a history of HIV infection, cystic fibrosis, interstitial lung disease, asthma, active pulmonary tuberculosis, chronic obstructive pulmonary disease (COPD), or pneumonia were excluded. Medical records were reviewed to confirm these conditions.

Data were collected from medical records, including demographic characteristics, clinical presentation, microbiological culture results, and antibiotic resistance patterns. Sputum samples were obtained and cultured to identify bacterial pathogens, and antibiotic susceptibility testing was performed using the disc diffusion method.

Statistical analysis was performed using SPSS version 20.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics were used to summarize patient demographics, bacteriological profiles, and antibiotic resistance patterns. Associations between categorical variables were assessed using the Chi-square test, and a p-value of <0.05 was considered statistically significant.

RESULTS

A total of 163 patients diagnosed with acute exacerbation of bronchiectasis were included in the study. The most commonly isolated pathogen in sputum cultures was *Pseudomonas aeruginosa*, accounting for 65 (40.0%) cases. This was followed by *Haemophilus influenzae* in 19 (11.6%) cases, *Staphylococcus aureus* in 11 (7.0%) cases, *Klebsiella pneumoniae* in 9 (5.8%) cases, and *Streptococcus pneumoniae* in 9 (5.5%) cases, as shown in Table 1 and Figure 2.

The antibiotic resistance patterns varied among the isolated organisms. *Pseudomonas aeruginosa* demonstrated the highest resistance to aztreonam (32.0%), ciprofloxacin (27.1%), and gentamicin (25.6%). *Haemophilus influenzae* showed high resistance to cotrimoxazole (65.0%) and ciprofloxacin (64.1%), as presented in Table 2.

Staphylococcus aureus exhibited complete resistance to penicillin (100%), with high resistance to levofloxacin (83.3%) and erythromycin (75.0%). Isolates of *Klebsiella pneumoniae* were completely resistant to ampicillin and demonstrated more than 80% resistance to cefuroxime, ciprofloxacin, and cotrimoxazole. *Streptococcus pneumoniae* showed high resistance to cotrimoxazole (72.2%), tetracycline (52.9%), and erythromycin (50.0%), as summarized in Table 3 and Figure 1.

These findings highlight the substantial burden of antibiotic resistance among pathogens responsible for acute exacerbation of bronchiectasis and underscore the importance of local antimicrobial surveillance to guide effective empirical therapy.

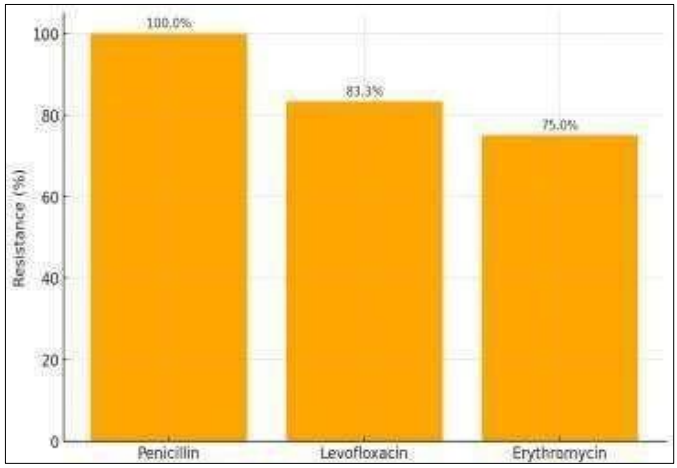

Figure 1: Antibiotic Resistance of Staphylococcus Aureus to Penicillin, Levofloxacin, and Erythromycin

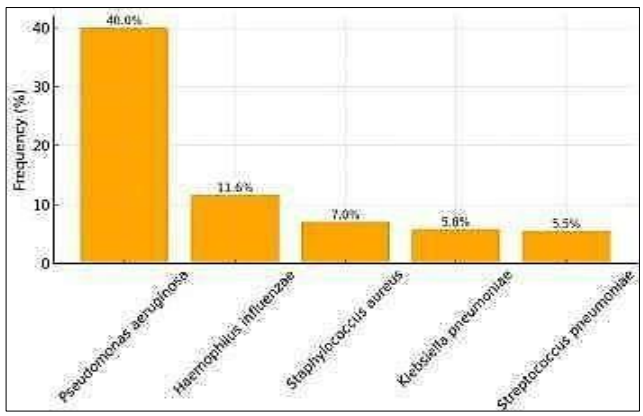

Figure 2: Frequency of pathogens in acute exacerbation of bronchiectasis

Table 1: Frequency of Pathogens

Pathogen	Frequency (%)
Pseudomonas aeruginosa	40.0
Haemophilus influenzae	11.6
Staphylococcus aureus	7.0
Klebsiella pneumoniae	5.8
Streptococcus pneumoniae	5.5

Table 2: Antibiotic Resistance - Pseudomonas & Haemophilus

Antibiotic	Pseudomonas Aeruginosa (%)	Haemophilus Influenzae (%)
Aztreonam	32.0	
Ciprofloxacin	27.1	
Gentamicin	25.6	
Cotrimoxazole		65.0
Ciprofloxacin (H. influenzae)		64.1

Table 3: Antibiotic Resistance - Other Pathogens

Antibiotic	Staphylococcus aureus (%)	Klebsiella pneumoniae (%)	Streptococcus pneumoniae (%)
Penicillin	100.0		
Levofloxacin	83.3		
Erythromycin	75.0		50.0
Ampicillin		100.0	
Cefuroxime		80.0	
Ciprofloxacin		80.0	

DISCUSSION

Acute exacerbations of bronchiectasis (AEB) are a significant cause of morbidity and healthcare burden in patients with chronic respiratory disease. These exacerbations are most commonly driven by bacterial infections, making the identification of causative pathogens and their antibiotic resistance patterns essential for effective clinical management. The present study evaluated the bacteriological profile and resistance patterns in patients with AEB and their implications for clinical outcomes.

In this study, *Pseudomonas aeruginosa* was identified as the most frequently isolated pathogen, accounting for 40% of cases. This finding is consistent with previous studies, which have reported *P. aeruginosa* as the predominant organism in patients with bronchiectasis exacerbations. The persistence of this pathogen is associated with disease progression, frequent exacerbations, and poorer clinical outcomes. Similarly, *Haemophilus influenzae* was the second most common pathogen, which aligns with existing literature indicating its role in chronic airway inflammation and recurrent infections in bronchiectasis.

The antibiotic resistance patterns observed in this study are of considerable clinical concern. *Pseudomonas aeruginosa* demonstrated significant resistance to commonly used antibiotics, including beta-lactams and fluoroquinolones. These findings are comparable to earlier studies that have reported increasing resistance rates in *P. aeruginosa*, particularly in patients with repeated antibiotic exposure. Such resistance complicates empirical therapy and necessitates the use of culture-guided treatment strategies [9,10].

Furthermore, *Haemophilus influenzae* exhibited high resistance to cotrimoxazole and ciprofloxacin, which may limit the effectiveness of commonly prescribed empirical regimens [11, 12]. Resistance among other pathogens, including *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Streptococcus pneumoniae*, was also notable, particularly against first-line antibiotics such as penicillin and ampicillin. These findings highlight the growing challenge of antimicrobial resistance in respiratory infections [13, 14].

The presence of multidrug-resistant (MDR) organisms was associated with adverse clinical outcomes, including prolonged hospital stay and increased mortality [15, 16]. This observation is in agreement with previous studies that have demonstrated a strong association between MDR infections and poor prognosis in

bronchiectasis patients [17, 18]. The need for alternative and often more toxic or expensive antibiotics further complicates the management of such cases [19, 20].

Overall, the findings of this study emphasize the importance of continuous local antimicrobial surveillance and individualized treatment approaches. Empirical antibiotic therapy should be guided by local resistance patterns, and susceptibility testing should be considered essential in the management of AEB. Implementation of antibiotic stewardship programs may also play a critical role in reducing the emergence and spread of resistant pathogens.

CONCLUSION

This study demonstrates a high prevalence of antibiotic-resistant pathogens in patients with acute exacerbation of bronchiectasis, with *Pseudomonas aeruginosa* being the most frequently isolated organism. Significant resistance to commonly used antibiotics highlights the growing challenge of multidrug-resistant infections in this population. The presence of resistant organisms was associated with adverse clinical outcomes, including prolonged hospital stay and increased mortality. These findings underscore the importance of culture-guided antibiotic therapy, regular antimicrobial surveillance, and implementation of antibiotic stewardship strategies to optimize treatment outcomes and reduce disease burden.

ACKNOWLEDGMENT: None

FUNDING STATEMENT: The authors received no financial support for this research

CONFLICT OF INTEREST: The authors declare no conflict of interest

AUTHOR CONTRIBUTIONS

Concept and Design of Study: Ahmad Atif
Drafting of Manuscript: Afaq Haider, Asifa Iqbal
Data Analysis: Muhammad Bilal Liaqat, M. Umer Mumtaz
Critical Review: Huma Batool
Final Approval of the Manuscript: All authors approved the final version of the manuscript.

REFERENCES

1. Khikmatov JS, Khudaibergenov SN, Khamdamov BZ, Ismatov JK. Bronchiectasis (literature review). Scientific progress. 2021;2:94–108.
2. Keir HR, Chalmers JD. Pathophysiology of bronchiectasis. InSeminars in respiratory and critical care medicine 2021 Aug. Vol. 42. Thieme Medical Publishers, Inc;
3. Leigh LY, Vannelli P, Crow HC, Desai S, Lepore M, Anolik R, et al. Diseases of the respiratory tract [Internet]. Burket's Oral Medicine. Wiley; 2021. p. 469–504. Available from: http://dx.doi.org/10.1002/9781119597797.ch13
4. Love ME, Proud D. Respiratory viral and bacterial exacerbations of COPD-the role of the airway epithelium. Cells [Internet]. 2022;11(9):1416. Available from: http://dx.doi.org/10.3390/cells11091416
5. Inchingolo R, Pierandrei C, Montemurro G, Smargiassi A, Lohmeyer FM, Rizzi A. Antimicrobial resistance in common respiratory pathogens of chronic bronchiectasis patients: A literature review. Antibiotics (Basel) [Internet]. 2021;10(3):326. Available from: http://dx.doi.org/10.3390/antibiotics10030326
6. Perikleous EP, Gkentzi D, Bertzouanis A, Paraskakis E, Sovtic A, Fouzas S. Antibiotic resistance in patients with cystic fibrosis: Past, present, and future. Antibiotics (Basel) [Internet]. 2023;12(2):217. Available from: http://dx.doi.org/10.3390/antibiotics12020217
7. Cabrera R, Fernández-Barat L, Vázquez N, Alcaraz-Serrano V, Bueno-Freire L, Amaro R, et al. Resistance mechanisms and molecular epidemiology of Pseudomonas aeruginosa strains from patients

with bronchiectasis. J Antimicrob Chemother [Internet]. 2022;77(6):1600–10. Available from: http://dx.doi.org/10.1093/jac/dkac084

8. Rodríguez-Villodres Á, Martín-Gandul C, Peñalva G, Guisado-Gil AB, Crespo-Rivas JC, Pachón-Ibáñez ME, et al. Prevalence and risk factors for multidrug-resistant organisms colonization in long-term care facilities around the world: A review. Antibiotics (Basel) [Internet]. 2021;10(6):680. Available from: http://dx.doi.org/10.3390/antibiotics10060680
9. Sun J, Tong X, Wang D, Wang L, Zhang S, Liu S, et al. Multi-drug resistant Pseudomonas aeruginosa isolation is an independent risk factor for recurrent hemoptysis after bronchial artery embolization in patients with idiopathic bronchiectasis: a retrospective cohort study. Respir Res [Internet]. 2024;25(1):385. Available from: http://dx.doi.org/10.1186/s12931-024-03019-2
10. Ding F, Han L, Xue Y, Yang IT, Fan X, Tang R, et al. Multidrug-resistant Pseudomonas aeruginosa is predisposed to lasR mutation through up-regulated activity of efflux pumps in non-cystic fibrosis bronchiectasis patients. Front Cell Infect Microbiol [Internet]. 2022;12:934439. Available from: http://dx.doi.org/10.3389/fcimb.2022.934439
11. Rodrigo-Troyano A, Sibila O. The respiratory threat posed by multidrug resistant G ram-negative bacteria. Respirology. 2017;22(7):1288–99.
12. Chen Y-P, Tasi X-W, Chang K, Cao X-D, Chen J-R, Liao C-S. Multi-drug resistant organisms infection impact on patients length of stay in respiratory care ward. Antibiotics (Basel) [Internet]. 2021;10(5):608. Available from: http://dx.doi.org/10.3390/antibiotics10050608
13. Sibila O, Perea L, Cantó E, Shoemark A, Cassidy D, Smith AH, et al. Antimicrobial peptides, disease severity and exacerbations in bronchiectasis. Thorax [Internet]. 2019;74(9):835–42. Available from: http://dx.doi.org/10.1136/thoraxjnl-2018-212895
14. Vishwanath S, Chawla K, Gopinathan A. Multidrug resistant Gram-negative bacilli in lower respiratory tract infections. Iran J Microbiol. 2013;5(4):323–7.
15. Mood N, Katta SR, Badam AK, Chundru J. Clinico-bacteriological profile and antibiotic resistance pattern in patients with acute exacerbation of COPD. Egypt J Intern Med [Internet]. 2022;34(1). Available from: http://dx.doi.org/10.1186/s43162-021-00094-5
16. Reynolds D, Burnham JP, Vazquez Guillamet C, McCabe M, Yuenger V, Betthauser K, et al. The threat of multidrug-resistant/extensively drug-resistant Gram-negative respiratory infections: another pandemic. Eur Respir Rev [Internet]. 2022;31(166):220068. Available from: http://dx.doi.org/10.1183/16000617.0068-2022
17. Guitor AK, Wright GD. Antimicrobial resistance and respiratory infections. Chest. 2018;154(5):1202–12.
18. Georgakopoulou VE, Gkoufa A, Aravantinou-Fatorou A, Trakas I, Trakas N, Faropoulos K, et al. Lower respiratory tract infections due to multi-drug resistant pathogens in central nervous system injuries (Review). Biomed Rep [Internet]. 2023;18(4):30. Available from: http://dx.doi.org/10.3892/br.2023.1612
19. Cillóniz C, Dominedò C, Torres A. Multidrug resistant gram-negative bacteria in community-acquired pneumonia. Crit Care [Internet]. 2019;23(1):79. Available from: http://dx.doi.org/10.1186/s13054-019-2371-3
20. van Duin D, Paterson DL. Multidrug-resistant bacteria in the community: An update. Infect Dis Clin North Am [Internet]. 2020;34(4):709–22. Available from: http://dx.doi.org/10.1016/j.idc.2020.08.002