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# RETROSPECTIVE ANALYSIS OF MICROBIAL PROFILES IN BRONCHOALVEOLAR LAVAGE SAMPLES FROM PATIENTS WITH LOWER RESPIRATORY TRACT INFECTIONS

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Abstract: ***Background:*** Bronchoalveolar lavage (BAL) serves as an essential diagnostic technique for acquiring specimens from the lower respiratory tract, proving particularly useful in identifying pathogens responsible for lower respiratory tract infections (LRTI). This investigation aims to delineate the microbial spectrum present in BAL fluid from patients exhibiting respiratory symptoms and to assess antimicrobial susceptibility patterns to decide on therapeutic strategies in a tertiary care hospital setting. ***Materials and Methods:*** A prospective cohort study spanning six months was executed at Saveetha Hospital, Chennai, incorporating 93 patients presenting with lower respiratory tract infections. BAL fluid specimens were procured through bronchoscopy and cultured on diverse media. Microbial identification and antibiotic susceptibility testing was conducted employing standard microbiological procedures. ***Results:*** Microbial growth was detected in 51 out of 95 BAL samples (53.7%). Thirteen distinct microbial isolates were identified, with Klebsiella pneumoniae (23.53%), Acinetobacter baumannii (21.57%), and Pseudomonas aeruginosa (17.65%) emerging as the most prevalent. A significant majority of the infections were monomicrobial (96.08%). Antibiotic resistance was notably seen in Klebsiella pneumoniae and Acinetobacter baumannii. ***Conclusion:*** The findings underscore the dominance of Gram-negative bacteria in respiratory infections and the presence of multidrug-resistant organisms. These results emphasise the necessity for targeted antimicrobial therapies and ongoing surveillance of resistance trends to enhance patient outcomes and tackle antimicrobial resistance effectively.

Keywords: Bronchoalveolar lavage, microbial profile, antibiotic resistance, lower respiratory tract infections, tertiary care hospital.

## INTRODUCTION

In 1970, Bronchoalveolar lavage (BAL) was introduced as a method to obtain secretions and cellular substances from the lower respiratory tract (1). Initially used for diagnosing interstitial and occupational pulmonary diseases, it was first implemented in India in 1994 (2). BAL samples have proven effective in isolating various organisms causing lower respiratory tract infections (LRTI), such as bacteria and fungi (3). Unlike sputum samples, which have a low diagnostic yield of 24% due to contamination from oral flora, BAL avoids such contamination, providing higher quality samples for culture (4). The use of quantitative culture with a proper colony cut-off, further enhances the insight for therapy (5). BAL is particularly useful in diagnosing community-acquired pneumonia (CAP) and other infections, with studies from Western literature supporting its efficacy in increasing microbial isolation (6).

Accurate diagnosis of LRTI is essential for evidence-based management, considering that clinical features of respiratory diseases vary by gender, age, season, and other factors like environment and host (7). In India, there is a growing need for research on the use of BAL, for isolating microbes, but the number of studies available is currently limited (8). Chronic respiratory diseases, such as Pulmonary embolism, Asthma, Chronic obstructive pulmonary disease (COPD), Emphysema, Sarcoidosis, Pulmonary hypertension, Chronic pleural disease, Cystic fibrosis, Sleep apnoea syndrome, Pulmonary fibrosis, Cor pulmonale, Pulmonary eosinophilia, Bronchiectasis, Pulmonary heart diseases, Occupational lung diseases, Bronchitis, and Pneumoconiosis significantly impact global health (9, 10). These diseases account for approximately 4 million deaths annually, contributing to 5% of global deaths and leading to substantial disability-adjusted life years (DALYs) lost (9, 11). In India, chronic respiratory disease accounts for 7% of deaths and 3% of DALYs lost (12).

Acute respiratory infections (ARI) are prevalent and result in millions of emergency visits or hospitalizations annually (13). They are a significant global public health concern, contributing to high morbidity and mortality rates (14). Bacteria, fungi, viruses, and parasites are all responsible for pneumonia, an infection-related inflammation of one or both lungs' parenchyma (15). Identifying the specific pathogen causing pneumonia is critical for accurate diagnosis and effective treatment (13). The classification of pneumonia has been updated to include four subgroups: community-acquired pneumonia (CAP), hospital-acquired pneumonia (HAP), ventilator-associated pneumonia (VAP), and healthcare-associated pneumonia (HCAP) (16). Effective empirical antimicrobial therapy is essential for achieving

successful patient outcomes. Guidelines offer specific recommendations tailored to the care setting, pathogen-related risk factors, and the presence of multidrug resistance (17).

In Côte d'Ivoire, the mortality rate from pneumonia and severe acute respiratory infections (SARIs) has increased from 32.5% to 36% (18). Limited data is available on the microbial causes of SARI, with most information primarily focused on tuberculosis (19). Resistant genes from bacterial pathogens causing pneumonia, such as TEM, CTX-M for Extended-spectrum beta-lactamases (ESBLs) producers, NDM in *Pseudomonas aeruginosa*, OXA-48 in *Acinetobacter baumannii*, and mecAin Methicillin-resistant *Staphylococcus aureus* (MRSA), are detected using PCR technology (20). The increasing burden of multi-drug resistant gram-negative pathogens in severe pneumonia cases highlights the need for new antimicrobial stewardship and treatment strategies (21).

Exacerbations of chronic respiratory diseases, often triggered by infections, result in greater and irreversible declines in lung function, highlighting the importance of early diagnosis and appropriate antimicrobial therapy (22, 23). Common pathogens involved include viruses and bacteria, like Haemophilus influenzae, Streptococcus pneumoniae, and Moraxella catarrhalis frequently implicated in exacerbations (12). Non-smokers typically have a sterile lower respiratory tract, while patients with bronchiectasis or COPD often harbour pathogenic microorganisms (24-26). Bronchoscopy and quantitative invasive techniques like BAL have improved the sensitivity and specificity of diagnostic methods for pulmonary infections, surpassing traditional sputum culture (27).

This study aims to comprehensively characterise the microbial profile of BAL fluid in patients with radiological changes and evaluate the antimicrobial susceptibility patterns to guide effective treatment strategies in a tertiary care hospital setting at the Saveetha Hospital, Department of Respiratory Medicine, Chennai, India. Understanding the local microbial flora is essential for the effective and rational use of antimicrobial agents, crucial for managing the increasing burden of chronic respiratory diseases and improving patient outcomes. Identifying the specific pathogens causing infections can help tailor more precise antimicrobial therapies, reducing the risk of resistance and improving patient management.

# MATERIAL AND METHODS

**Study Framework:**

This retrospective study was conducted at Saveetha Hospital, Department of Respiratory Medicine, using medical records of patients treated between October 2023 and April 2024. Data were gathered from 93 patients diagnosed with lower respiratory tract infections who had undergone bronchoalveolar lavage (BAL) sampling as part of their clinical care.

**Inclusion Criteria:**

Patients aged 20-75 years, who presented with lower respiratory tract infection symptoms (e.g., fever, purulent sputum, dyspnoea, or radiological evidence of infection) and who had undergone bronchoalveolar lavage (BAL) sampling, were retrospectively included based on available records. Patients with unstable cardiac conditions, pregnant patients, and those who did not provide prior consent for retrospective use of their medical data were excluded.

**Exclusion Criteria:**

- Patients with unstable cardiac conditions (recent myocardial infarction, cardiac arrhythmias)
- Pregnant women.
- Patients who did not give consent for the procedure.

**Ethical clearance**

This retrospective study was approved by the Institutional Ethics Committee of Saveetha Medical College. Patient confidentiality was maintained by anonymizing all data used in the analysis.

**Data Collection**

**Obtaining Bronchoalveolar Lavage Fluid**

BAL fluid samples were previously collected as part of routine clinical procedures, conducted using Fibreoptic bronchoscopy at Saveetha Hospital's Respiratory Medicine Department. This retrospective study accessed pre-existing BAL results, including culture, microbial identification, and antibiotic susceptibility profiles from hospital laboratory records.

**Microbial Identification and Antibiotic Susceptibility Testing**

Microbial identification and antibiotic susceptibility testing were based on historical laboratory records of BAL fluid cultures. These records included data on initial microscopy, Gram staining results, and bacterial identification. Antibiotic susceptibility results, as performed per Clinical and Laboratory Standards Institute (CLSI) guidelines at the time of collection, were also extracted from existing records.

**Statistical Analysis:**

The data from the patient records were consolidated and anonymized in Microsoft Excel 2016, then transferred to SPSS for statistical analysis. Continuous data were analysed using unpaired t-tests, and categorical data were evaluated with Pearson's chi-squared test. Analysis was conducted at a 95% confidence level, with statistical significance set at $p < 0.05$. The statistical analysis was carried out using IBM SPSS Statistics, for Windows, version 28.0.1.0.

# RESULTS AND OBSERVATIONS:

The study involved 93 individuals with the most common age group being 51 to 60 years (24 participants) and the 61 to 70 years (18 participants). Male participants outnumbered females across most age groups, comprising 58 males and 35 females (Table 1). The gender distribution of microbial growth in bronchoalveolar lavage samples revealed that no growth was found in 34 samples (20 males and 14 females), minimal growth was observed in 10 samples (6 males and 4 females), and microbes were detected in 51 samples (33 males and 18 females), totalling 95 isolates examined (Table 2).

In the bronchoalveolar lavage samples, a total of 13 different types of microbial isolates were identified. Among them, *Klebsiella pneumoniae* was the most common accounting for 23.53% with 12 isolates, followed by *Pseudomonas aeruginosa* at 17.65% with 9 isolates and *Acinetobacter baumanii* (MDR) at 21.57% with 11 isolates. Additionally, Enterobacter cloacae and Escherichia coli were also identified with 4 isolates each making up 7.84% each of the population, in the samples (Table 3).

Microbial isolates were found to vary across age groups with *Enterobacter cloacae* and *Acinetobacter baumanii* (MDR) being the most common, among all age groups. *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Streptococcus pneumoniae* also appeared frequently in age groups whereas *Aspergillus fumigatus* was predominantly detected in the 41-50 age group (7.14%) (Table 4).

In terms of infection profile, the majority were monomicrobial infections accounting for 49 cases (96.08%) and 49 isolates (92.45%). On the hand, there were only 2 cases (3.92%) of polymicrobial infections involving a total of 4 isolates (7.55%). The overall data indicated a total of 51 cases and 53 isolates. The polymicrobial infections included combinations like *Klebsiella pneumoniae* + *Pseudomonas aeruginosa* and *Pseudomonas putida* + *Enterobacter cloacae*, each, with 2 isolates (3.775%) (Table 5 & 6).

The antibiotic resistance pattern observed in the study indicated significant resistance across various bacterial isolates. *Enterobacter cloacae* displayed resistance to Cefepime with 3 out of 4 isolates showing resistance (14.29%). *Pseudomonas aeruginosa* exhibited resistance to Amikacin in 2 out of 9 isolates (18.18%). *Klebsiella pneumoniae* showed resistance to Ceftriaxone in 6 out of 12 isolates (14.63%) and to Cefepime in 5 out of 12 isolates (12.20%). *Acinetobacter baumanii* (MDR) demonstrated resistance to Amikacin and Cefepime each with 7 out of 11 isolates (8.97%) and to Piperacillin/Tazobactam with 8 out of 11 isolates (10.26%). *Escherichia coli* showed resistance to Amikacin in one isolate (4.55%) to Cefepime in two isolates (9.09%) and to Imipenem in one isolate (4.55%) (Table-7).

**Authors contribution:**

Vijayalakshmi Sivasubramanian collected and interpreted the data. Vijayalakshmi Sivasubramanian and Swetha Sasikumar drafted the manuscript. Gangadharan Vadivelu critically reviewed and revised the manuscript. All authors contributed equally and agreed to be accountable for all aspects of the work.

**Tables:**

Table 1: Age sex distribution

| S. No | Age group | Male | Female | Total |
|---|---|---|---|---|
| 1 | 15-30 | 9 | 6 | 15 |
| 2 | 31-40 | 5 | 5 | 10 |
| 3 | 41-50 | 7 | 7 | 14 |
| 4 | 51-60 | 15 | 9 | 24 |
| 5 | 61-70 | 15 | 3 | 18 |
| 6 | <71 | 7 | 5 | 12 |
| **Total** | | 58 | 35 | 93 |

Table 2: Gender Distribution of Microbial Growth in Bronchoalveolar Lavage Samples

| | **Male** | **Female** | **Total** |
|---|---|---|---|
| **No growth** | 20 | 14 | 34 |
| **Insignificant growth** | 6 | 4 | 10 |
| **Presence of Microbes** | 33 | 18 | 51 |
| | 59 | 36 | 95 |

Table 3: Distribution of Microbial Isolates in Bronchoalveolar Lavage Samples with Percentage Analysis

| **S. No** | **Isolates** | **No. of isolates** | **Percentage %** |
|---|---|---|---|
| 1 | *Enterobacter cloacae* | 4 | 7.84 |
| 2 | *Aspergillus fumigatus* | 1 | 1.96 |
| 3 | *Pseudomonas aeruginosa* | 9 | 17.65 |
| 4 | *Pseudomonas putida* | 3 | 5.88 |
| 5 | *Nasopharyngeal flora* | 2 | 3.92 |
| 6 | *Klebsiella pneumoniae* | 12 | 23.53 |
| 7 | *Klebsiella oxytoca* | 1 | 1.96 |
| 8 | *Enterococcus faecalis* | 1 | 1.96 |
| 9 | *Acinetobacter baumanii (MDR)* | 11 | 21.57 |
| 10 | *Streptococcus pneumoniae* | 1 | 1.96 |
| 11 | *Escherichia coli* | 4 | 7.84 |
| 12 | *Stenotrophomonas maltophilia* | 1 | 1.96 |
| 13 | *Acinetobacter lwoffii* | 1 | 1.96 |
| Total | | 51 | 100 |

Table 4: Age-Wise Distribution of Microbial Isolates in Bronchoalveolar Lavage Fluid Samples

| **S. No** | **Isolate** | **15-30 (n=15)** | **31-40 (n=10)** | **41-50 (n=14)** | **51-60 (n=24)** | **61-70 (n=18)** | **<71 (n=12)** |
|---|---|---|---|---|---|---|---|
| 1 | *Enterobacter cloacae* | 0 | 0 | 0 | 1 (4.17%) | 2 (11.11%) | 1 (8.33%) |
| 2 | *Pseudomonas aeruginosa* | 2 (13.33%) | 0 | 1 (7.14%) | 4 (16.67%) | 2 (11.11%) | 0 |
| 3 | *pseudomonas putida* | 0 | 0 | 1 (7.14%) | 1 (4.17%) | 1 (5.56%) | 0 |
| 4 | *nasopharyngeal flora* | 0 | 1 (10%) | 0 | 1 (4.17%) | 0 | 0 |
| 5 | *Klebsiella pneumoniae* | 0 | 2 (20%) | 3 (21.43%) | 3 (12.5%) | 2 (11.11%) | 2 (16.67%) |
| 6 | *Klebsiella oxytoca* | 1 (6.67%) | 0 | 0 | 0 | 0 | 0 |
| 7 | *Acinetobacter baumanii (MDR)* | 2 (13.33%) | 1 (10%) | 1 (7.14%) | 3 (12.5%) | 1 (5.56%) | 3 (25%) |
| 8 | *streptococcus pneumoniae* | 1 (6.67%) | 0 | 0 | 0 | 0 | 0 |
| 9 | *Escherichia coli* | 0 | 0 | 0 | 3 (12.5%) | 1 (5.56%) | 0 |
| 10 | *Stenotrophomonas maltophilia* | 1 (6.67%) | 0 | 0 | 0 | 0 | 0 |
| 11 | *Acinetobacter lwoffii* | 0 | 0 | 0 | 1 (4.17%) | 0 | 0 |
| 12 | *Enterococcus faecalis* | 0 | 0 | 0 | 0 | 0 | 1 (8.33%) |
| 13 | *Aspergillus fumigatus* | 0 | 0 | 1 (7.14%) | 0 | 0 | 0 |

Table 5: Infection Profile: Monomicrobial vs. Polymicrobial Cases in Bronchoalveolar Lavage Samples

| **Type of Organism** | **Number of cases (%)** | **Number of isolates (%)** |
|---|---|---|
| Monomicrobial | 49 (96.08%) | 49 (92.45%) |
| Polymicrobial | 2 (3.92%) | 4 (7.55%) |
| Total | 51 (100%) | 53 (100%) |

Table 6: Distribution and Prevalence of Polymicrobial Infections in Bronchoalveolar Lavage Samples

| **Type of Organism** | **Number of isolates** | **Percentage (%)** |
|---|---|---|
| Polymicrobial | 4 | 7.55 |
| *Klebsiella pneumoniae* + *Pseudomonas aeruginosa* | 2 | 3.775 |
| *Pseudomonas putida* + *Enterobacter cloacae* | 2 | 3.775 |

Table-7: Antibiotic resistance pattern

| **Antibiotics** | ***Enterobacter cloacae* (n=4)** | ***Pseudomonas aeruginosa* (n=9)** | ***pseudomonas putida* (n=3)** | ***Klebsiella pneumoniae* (n=12)** | ***Klebsiella oxytoca*( n=1)** | ***Enterococcus faecalis* (n=1)** | ***Acinetobacter baumanii*( n=11)** | ***Escherichia coli* (n=4)** | ***Stenotrophomonas melophilia* (n=1)** | ***Acinetobacter lwoffii*(n=1)** |
|---|---|---|---|---|---|---|---|---|---|---|
| Amikacin | 1 (4.76 %) | 2 (18.18 %) | 1 (6.25 %) | 3 (7.32 %) | - | - | 7 (8.97 %) | 1 (4.55 %) | 1 (12.50 %) | 1 (14.29 %) |
| Amoxicillin/Clavulanic acid | 2 (9.52 %) | - | - | 3 (7.32 %) | - | - | - | 2 (9.09 %) | - | - |
| Ampicillin | - | - | 1 (6.25 %) | 4 (9.76 %) | - | - | - | 2 (9.09 %) | - | - |
| Cefazolin | - | - | - | - | - | - | - | - | - | - |
| Cefepime | 3 (14.29 %) | 1 (9.09 %) | - | 5 (12.20 %) | - | - | 8 (10.26 %) | 2 (9.09 %) | - | - |
| Cefixime | - | - | - | 2 (4.88 %) | 1 (25.00 %) | - | - | - | - | - |
| Cefoperazone/Sulbactam | 1 (4.76 %) | 1 (9.09 %) | - | - | - | - | 6 (7.69 %) | 1 (4.55 %) | 1 (12.50 %) | 1 (14.29 %) |
| Cefotaxime | 1 (4.76 %) | - | - | - | - | - | 1 (1.28 %) | 1 (4.55 %) | 1 (12.50 %) | - |
| Cefoxitin | - | - | 1 (6.25 %) | - | 1 (25.00 %) | - | - | - | - | - |
| Ceftazidime | 1 (4.76 %) | 1 (9.09 %) | 1 (6.25 %) | - | 1 (25.00 %) | - | 4 (5.13 %) | - | - | - |
| ceftriaxone | 2 (9.52%) | - | 1 (6.25 %) | 6 (14.63 %) | 1 (25.00 %) | - | 3 (3.85 %) | 2 (9.09 %) | - | - |
| Cefuroxime | 1 (4.76 %) | - | 1 (6.25 %) | 5 (12.20 %) | - | - | - | 2 (9.09 %) | - | - |
| Ciprofloxacin | - | - | 2 (12.50 %) | 2 (4.88 %) | - | - | 11.54 | 2 (9.09 %) | - | 1 (14.29 %) |
| Clotrimazole | 1 (4.76 %) | - | - | - | - | - | 3 (3.85 %) | 1 (4.55 %) | - | - |
| Colistin | 1 (4.76 %) | - | - | - | - | - | - | - | - | - |
| Co-trimoxazole | - | - | 3 (18.75 %) | 3 (7.32 %) | - | - | 6 (7.69 %) | - | - | 1 (14.29 %) |
| Ertapenem | 1 (4.76 %) | - | - | 1 (2.44 %) | - | - | 1 (1.28 %) | 1 (4.55 %) | - | - |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Gentamicin | 1 (4.76 %) | 2 (18.18 %) | - | 2 (4.88 %) | - | - | 7 (8.97 %) | 2 (9.09 %) | 1 (12.50 %) | 1 (14.29 %) |
| Imipenem | 2 (9.52 %) | 1 (9.09 %) | 1 (6.25 %) | 1 (2.44 %) | - | - | 7 (8.97 %) | 1 (4.55 %) | 1 (12.50 %) | - |
| Levofloxacin | - | - | 2 (12.50 %) | - | - | - | 1 (1.28 %) | - | 1 (12.50 %) | 1 (14.29 %) |
| Linezolid | - | - | - | - | - | - | - | - | - | 0.00 |
| Meropenem | 2 (9.52 %) | 1 (9.09 %) | 1 (6.25 %) | 1 (2.44 %) | - | - | 7 (8.97 %) | 1 (4.55 %) | 1 (12.50 %) | 0.00 |
| Minocycline | - | - | - | - | - | - | - | - | - | - |
| Ofloxacin | - | - | - | - | - | - | - | - | - | - |
| Penicillin | - | - | - | - | - | 1 (100.00 %) | - | - | - | - |
| Piperacillin/Tazobactam | 1 (4.76 %) | 1 (9.09 %) | 1 (6.25 %) | 3 (7.32 %) | - | - | 8 (10.26 %) | 1 (4.55 %) | 1 (12.50 %) | 1 (14.29 %) |
| Teicoplanin | - | - | - | - | - | - | - | - | - | - |
| Tetracycline | - | - | - | - | - | - | - | - | - | - |
| Tigecycline | - | 1 (9.09 %) | - | - | - | - | - | - | - | - |
| Vancomycin | - | - | - | - | - | - | - | - | - | - |
| Total | 21 (100 %) | 11 (100 %) | 16 (100 %) | 41 (100%) | 4 (100%) | 1 (100 %) | 78 (100 %) | 22 (100 %) | 8 (100 %) | 7 (100 %) |

# DISCUSSION

Bronchoalveolar lavage (BAL) has been instrumental in diagnosing and managing lower respiratory tract infections (LRTIs) since the 1970s. Initially used for interstitial and occupational pulmonary diseases, its application in India since 1994 has expanded to isolate pathogens causing LRTIs, including bacteria and fungi (28, 29). BAL's advantage over traditional sputum samples lies in providing uncontaminated samples from the lower respiratory tract, enhancing microbial isolation accuracy and guiding effective treatments (30, 31). This is crucial for chronic respiratory diseases like asthma, COPD, and bronchiectasis, which cause significant morbidity, mortality, and disability-adjusted life years (DALYs) lost (2, 32). Chronic respiratory diseases result in around 4 million deaths annually, accounting for 5% of global deaths and significant DALYs lost (33). In India, they account for 7% of deaths and 3% of DALYs lost (34). Infections often exacerbate these diseases, leading to irreversible lung function declines, emphasising the need for early diagnosis and appropriate antimicrobial therapy (2, 32). Common pathogens include viruses and bacteria, with Haemophilus influenzae, Streptococcus pneumoniae, and Moraxella catarrhalis frequently involved (34). Bronchoscopy and BAL have improved diagnostic sensitivity and specificity for pulmonary infections, surpassing traditional sputum culture (35).

This study aimed to characterise the microbial profile found in BAL fluid from patients with lung issues and analyse how well they respond to antibiotics at a hospital. Among the 93 people involved most were between the ages of 51 to 60 and 61 to 70 with a higher prevalence of male participants. Out of 93 BAL samples tested microbial growth was present in 51 samples showing 13 different kinds of microbial isolates. The common pathogens identified were Klebsiella pneumoniae, Pseudomonas aeruginosa and Acinetobacter baumanii (MDR) indicating that Gram-negative bacteria are predominant in respiratory infections. Monomicrobial infections were predominant making up over 96% of cases while polymicrobial infections were less frequent.

The study's key findings show that Klebsiella pneumoniae is highly prevalent making up 23.53% of the isolates followed by Pseudomonas aeruginosa at 17.65% and Acinetobacter baumanii (MDR) at 21.57%. These results are consistent with previous reports, such as the studies conducted by M. Priya et al., which highlighted the presence of significant multidrug resistant Gram-negative pathogens in pneumonia cases underscoring the importance of precise antimicrobial treatment (36). Similarly, a study by Inamdar et al. indicated a recovery rate of 43.3% in BAL samples from patients, with LRTI with a notable portion of isolates being multidrug resistant Gram-negative bacteria (2).

The resistance patterns observed in this study are concerning with significant resistance present among different types of bacteria. For example, Klebsiella pneumoniae displayed resistance to Ceftriaxone (14.63%). Cefepime (12.20%) while Acinetobacter baumanii(MDR) showed resistance to Amikacin and Cefepime (8.97%) as well as Piperacillin/Tazobactam

(10.26%). These results highlight the challenge of dealing with infections caused by multidrug resistant bacteria emphasising the need for specific antimicrobial treatments to enhance patient outcomes and combat the spread of resistance.

Comparing these results to previously published data, several studies have found a prevalence of Klebsiella pneumoniae and Pseudomonas aeruginosa in respiratory infections. For instance, Vivek KU et al. reported similar findings in their investigation of the microbiological profile of BAL fluid in individuals with chronic respiratory diseases. They emphasised the importance of these pathogens and their resistance patterns (33). Furthermore, the study conducted by Dhanashree P. Inamdar et al. on BAL samples from patients with respiratory tract infections revealed a significant number of Gram-negative bacterial isolates, with 59.2% showing multidrug resistance (2).
Identifying Enterobacter cloacae and Acinetobacter baumanii(MDR) as prevalent pathogens among different age groups in this study, underscores the importance of continuous monitoring and customised antimicrobial approaches. Previous studies conducted by Neha Patel and colleagues also pointed out the prevalence of Klebsiella pneumoniae and Pseudomonas aeruginosa in BAL samples showing significant resistance to cephalosporins. This highlights the need for regular monitoring of antimicrobial sensitivity to ensure effective treatment (32).

This study has inherent limitations due to its retrospective design, including potential data completeness issues, as it relies on historical records rather than active data collection. Additionally, the data reflect microbial profiles and resistance patterns specific to the retrospective period, which may differ from current trends. As a retrospective analysis, this study highlights associations rather than establishing causality, especially regarding resistance development. These findings suggest the need for future prospective studies to validate these results in real-time patient cohorts.

# CONCLUSION

This study offers valuable insights into the microbial profile of BAL fluid in patients with lower respiratory tract infections. It emphasises the prevalence of multidrug Gram-negative bacteria like Klebsiella pneumoniae, Pseudomonas aeruginosa and Acinetobacter baumanii(MDR). The resistance patterns observed highlights the urgent necessity for targeted treatments and ongoing monitoring to effectively address chronic respiratory conditions. These discoveries add to the growing body of evidence supporting the use of BAL, for diagnosing infections and guiding suitable treatment approaches. Ultimately, these efforts aim to enhance outcomes and tackle the escalating issue of antimicrobial resistance.

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