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Original Research Article

Microbiological Profile of Bronchoalveolar Lavage in Patients with Respiratory Tract Infections: A Retrospective Study at a Tertiary Care Center in Patna, Bihar

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Abstract:

Background: In India, respiratory tract infections (RTIs) are a leading cause of illness and death, because treating them is made more difficult by rising antibiotic resistance. By providing representative lower respiratory tract samples, bronchoalveolar lavage (BAL) is a useful testing technique, especially for individuals with immunocompromised conditions, a history of antibiotic use, or a nonproductive cough.

Methods: A retrospective study was conducted at Patna Medical College and Hospital, Bihar, over two years. Medical records of 200 patients with suspected RTIs who underwent BAL were reviewed. BAL samples were subjected to microscopy, culture, and antimicrobial susceptibility testing using standard microbiological procedures in accordance with CLSI guidelines. Data on patient demographics, microbial isolates, and resistance profiles were analyzed descriptively.

Results: Of 200 BAL specimens, 146 (73%) yielded significant growth. The predominant pathogens were Klebsiella pneumoniae (35.6%), Pseudomonas aeruginosa (23.3%), and Staphylococcus aureus (13.7%), including 40% methicillin-resistant S. aureus isolates. Other organisms included Escherichia coli, Acinetobacter spp., and Streptococcus pneumoniae. 5.5% of instances, primarily in immunocompromised individuals, involved the isolation of fungal infections. High rates of resistance were observed: K. pneumoniae exhibited 65% resistance to fluoroquinolones and 78% resistance to third-generation cephalosporins, despite the relative activity of carbapenems and amikacin. P. aeruginosa exhibited significant resistance to ceftazidime and piperacillin-tazobactam, while colistin retained 95% susceptibility. Nearly 42.5% of isolates qualified as multidrug-resistant organisms (MDROs).

Conclusion: BAL provides valuable diagnostic yield in RTIs, especially in detecting resistant Gram-negative organisms. The high prevalence of multidrug resistance highlights the urgent need for antimicrobial stewardship, rational empirical therapy, and strict infection control practices in tertiary care settings.

Introduction

Worldwide, RTIs remain a serious public health concern that greatly increases hospitalization and mortality, particularly in young people, the elderly, and people with weakened immune systems [1,2]. In India, the burden is particularly high due to factors such as environmental pollution, smoking, poor living conditions, and limited access to early medical care [3]. Lower respiratory tract infections such as pneumonia, bronchitis, and tuberculosis are among the leading causes of prolonged hospital stay and mortality, placing an additional strain on healthcare resources [4].

Accurate diagnosis of the causative organism in RTIs is essential because clinical symptoms and radiological findings often overlap, making it difficult to distinguish between bacterial, viral, or fungal infections [5]. Conventional diagnostic methods such as sputum examination are widely used but may suffer from contamination with upper airway flora, which limits their reliability [6]. In this context, BAL has emerged as a valuable diagnostic technique. BAL allows sampling of the distal airways and alveoli, providing a specimen that better represents the infective process in the lungs [7]. This method is particularly useful in patients with non-productive cough, those already on antibiotics, or immunocompromised individuals, where sputum or blood cultures often yield poor results [8].

Microbiological analysis of BAL samples helps identify the wide spectrum of pathogens responsible for respiratory infections, including bacteria, fungi, and occasionally viruses [9]. The identification of multidrug-resistant organisms (MDROs) has become increasingly common in hospital settings [10]. These organisms complicate management, as empirical treatment often fails, leading to prolonged illness, increased healthcare costs, and higher mortality [11]. Thus, studying the microbial profile and antibiotic sensitivity patterns of BAL samples is of immense clinical value.

Tertiary care hospitals cater to a large and diverse patient population, often including severely ill individuals referred from peripheral centers. Data from such settings provide important insights into the prevailing microbial spectrum and drug resistance trends of a particular region [12]. This information is essential not only for guiding patient-specific therapy but also for framing hospital antibiotic policies and implementing infection control strategies. This context led to the current retrospective investigation, which examined the microbiological profile of BAL samples taken from patients suffering from respiratory tract infections over a two-year period at Patna Medical College and Hospital, a significant tertiary care facility in Bihar. The study also focuses on the antimicrobial resistance patterns of the isolates, which can help clinicians make informed decisions regarding empirical therapy and contribute to better management of respiratory infections in this part of the country.

Materials and Methods

The research was carried out in Patna Medical College and Hospital, Patna, Bihar from Aug 2023 to Aug 2025. Case records of 200 patients with suspected respiratory tract infections who had undergone BAL were reviewed. Relevant demographic details, clinical presentations, and microbiological findings were collected from laboratory registers and patient files.

Inclusion criteria

- Patients of all age groups presenting with clinical or radiological evidence of lower respiratory tract infection (such as pneumonia, bronchitis, lung abscess, or suspected tuberculosis).
- Availability of BAL samples that were properly collected and processed during the study period.

Exclusion criteria

- BAL specimens showing inadequate cellular material or evidence of contamination with oropharyngeal flora.
- Cases with incomplete records or missing laboratory data.

Sample collection and transport: BAL samples were obtained by the treating pulmonologist using a fiberoptic bronchoscope under aseptic precautions. The lavage fluid was collected in sterile containers and promptly transported to the microbiology laboratory, usually within one hour of collection, to avoid loss of viability of pathogens.

Laboratory processing: Each sample underwent preliminary microscopic examination. Gram staining was done to identify bacterial morphology and the presence of pus cells. Ziehl–Neelsen staining was performed for acid-fast bacilli in cases with clinical suspicion of tuberculosis. A 10% potassium hydroxide (KOH) mount was examined when fungal infection was suspected.

Following inoculation on 5% sheep blood agar, MacConkey agar, and chocolate agar, samples were incubated under aerobic conditions at 37°C for 24 to 48 hours. Gram staining, typical biochemical responses, and colony features were used to identify growth. Sabouraud's dextrose agar (SDA) was utilized for fungal isolation, and it was cultured for up to two weeks at 25°C and 37°C.

Antimicrobial susceptibility testing: The Kirby-Bauer disc diffusion method on Mueller-Hinton agar was used to assess the antibiotic sensitivity of the bacterial isolates, and the results were interpreted in accordance with the criteria provided by the Clinical and Laboratory Standards Institute (CLSI). According to conventional protocols, methicillin resistance in Staphylococcus aureus (MRSA), carbapenem resistance, and extended-spectrum β-lactamase (ESBL) synthesis were screened for and verified.

Data collection and analysis: All microbiological findings, along with patient details, were entered in Microsoft Excel. The frequency of different pathogens, their distribution across age and sex, and their antibiotic resistance profiles were analyzed using descriptive statistics. Results were expressed as percentages and proportions.

Ethical considerations: Since this was a retrospective study using hospital records, patient identifiers were kept confidential. Institutional ethical approval was obtained before commencement of the study.

Result

A total of 200 BAL specimens were included in the study. Out of these, 146 samples (73%) yielded significant microbial growth, whereas 54 samples (27%) were sterile or showed only commensal flora.

Demographic profile: The mean age of the recruited patients was 46.3 years, with a range of 18 to 82 years. 38% of the patients were between the ages of 41 and 60, 32% were between the ages of 21 and 40, and 22% were above 60. Just 8% of the research sample consisted of patients under the age of twenty.

There was a definite male predominance in terms of gender distribution. There were 126 (63%) male patients and 74 (37%) female patients out of 200, yielding a male-to-female ratio of 1.7:1. The greater prevalence of respiratory illnesses in men, which may be linked to smoking and occupational exposures, was reflected in this statistically significant difference.

Table 1: Demographic Profile of Patients (n = 200)

Variable	**Category**	**Number (%)**
Age group (years)	<20	16 (8%)
	21–40	64 (32%)
	41–60	76 (38%)
	>60	44 (22%)
Mean age		**46.3 years**
Gender	Male	126 (63%)
	Female	74 (37%)
Male: Female ratio		**1.7:1**

Microbiological profile: Among the 146 culture-positive cases, bacterial pathogens were the most common isolates. The leading organism was Klebsiella pneumoniae (52 isolates, 35.6%), followed by Pseudomonas aeruginosa (34 isolates, 23.3%), and Staphylococcus aureus (20 isolates, 13.7%). Other notable bacterial pathogens included Escherichia coli (14 isolates, 9.6%), Acinetobacter species (12 isolates, 8.2%), and Streptococcus pneumoniae (6 isolates, 4.1%).

Fungal pathogens were identified in 8 cases (5.5%), with Candida albicans (5 cases) and Aspergillus species (3 cases) being the main isolates. These fungal infections were seen predominantly in immunocompromised patients, including those on prolonged corticosteroid therapy or with underlying diabetes mellitus.

No viral testing was routinely performed during the study, so viral etiologies could not be assessed.

Table 2: Microbiological Profile of BAL Cultures (n = 146 positive samples)

Pathogen	**Number of Isolates**	**Percentage (%)**
Klebsiella pneumoniae	52	35.6
Pseudomonas aeruginosa	34	23.3
Staphylococcus aureus	20 (8 MRSA)	13.7
Escherichia coli	14	9.6
Acinetobacter spp.	12	8.2
Streptococcus pneumoniae	6	4.1
Fungal pathogens (total)	8	5.5
– Candida albicans	5	—
– Aspergillus spp.	3	—

Antimicrobial resistance patterns

A worrisome degree of antimicrobial resistance was noted among both Gram-negative and Gram-positive isolates.

- Klebsiella pneumoniae: Resistance to third-generation cephalosporins was seen in 78% of isolates, while 65% were resistant to fluoroquinolones. Carbapenems retained relatively better activity, with imipenem and meropenem showing 72% and 70% sensitivity, respectively. Aminoglycosides, especially amikacin, also showed reasonable efficacy (68%).
- Pseudomonas aeruginosa: Resistance was common to ceftazidime (60%) and piperacillin–tazobactam (55%). Colistin remained the most effective agent (95% sensitivity), followed by meropenem (75%) and amikacin (70%).
- Staphylococcus aureus: Of the 20 isolates, 8 (40%) were methicillin-resistant (MRSA). These MRSA strains were resistant to most beta-lactams and fluoroquinolones but remained fully sensitive to vancomycin and linezolid. Methicillin-sensitive S. aureus (MSSA) strains also showed variable resistance to macrolides and tetracyclines.
- Acinetobacter species: These were highly resistant to almost all tested antibiotics, with resistance rates exceeding 70–80% for cephalosporins, fluoroquinolones, and carbapenems. Only colistin retained 100% sensitivity, underscoring the MDR nature of these isolates.
- Escherichia coli and Streptococcus pneumoniae showed moderate resistance, with ESBL production noted in nearly half of E. coli isolates.

Table 3: Antimicrobial Resistance Patterns of Major Isolates

Organism	Key Resistance Findings	Sensitive Agents (majority)
Klebsiella pneumoniae	78% resistant to cephalosporins; 65% to fluoroquinolones	Carbapenems (70–72%), Amikacin
Pseudomonas aeruginosa	60% to ceftazidime; 55% to piperacillin-tazobactam	Colistin (95%), Meropenem (75%)
Staphylococcus aureus	40% MRSA, resistant to beta-lactams, fluoroquinolones	Vancomycin, Linezolid
Acinetobacter spp.	70–80% to most agents; high carbapenem resistance	Colistin (100%)
Escherichia coli	~50% ESBL producers; variable fluoroquinolone resistance	Carbapenems, Amikacin
Streptococcus pneumoniae	Moderate penicillin resistance	Vancomycin, Linezolid

Multidrug-resistant organisms (MDROs): Overall, 62 isolates (42.5%) qualified as multidrug resistant (MDR). Extended-spectrum β-lactamase (ESBL) production was confirmed in 24 isolates (46%) of the Enterobacteriaceae family. Carbapenem resistance was detected in 8 isolates (24%) of Acinetobacter and 6 isolates (18%) of Pseudomonas.

The presence of such resistant organisms was associated with prolonged hospital stay and prior antibiotic exposure in most cases. MRSA isolates accounted for 40% of the Staphylococcus aureus infections, further emphasizing the challenge of resistance in respiratory pathogens.

Discussion

In the present study, BAL was used as a diagnostic tool to identify the etiological agents in patients with respiratory tract infections. A culture positivity rate of 73% was observed, which is in line with findings from other tertiary care centers across India [13,14]. The higher yield compared to sputum samples supports the role of BAL as a reliable specimen for microbiological evaluation, especially in patients with non-productive cough, prior antibiotic exposure, or immunocompromised status [15].

Gram-negative bacilli were the predominant pathogens in our study, with Klebsiella pneumoniae being the most common isolate, followed by Pseudomonas aeruginosa. This trend has been consistently reported in several Indian and international studies [16,17]. The predominance of these organisms may reflect both community-acquired and hospital-acquired infections, particularly in patients admitted to intensive care units.

The isolation of MDR organisms, particularly ESBL-producing Enterobacteriaceae, carbapenem-resistant Acinetobacter, and MRSA, poses a major therapeutic challenge. Similar resistance trends have been reported in studies from other parts of India [18,19]. The frequent use of broad-spectrum antibiotics, prolonged hospital stays, and invasive procedures are important contributing factors to the emergence of such resistance [20].

Fungal pathogens, though less common, were detected in a small subset of patients, mostly those with immunosuppression or comorbidities. This is consistent with earlier reports, which suggest that BAL is particularly useful in diagnosing fungal infections such as invasive aspergillosis, where conventional sputum cultures are often negative [21].

Our findings highlight the importance of continuous surveillance of the microbial spectrum and resistance patterns in respiratory infections. The data not only guide clinicians in choosing appropriate empirical therapy but also provide valuable input for the formulation of hospital antibiotic stewardship policies [7].

Conclusion

The significance of BAL in the precise identification of (RTIs) is highlighted by this retrospective study carried out in a tertiary care facility in Patna, Bihar. With a high diagnostic yield of 73% culture positivity, BAL samples outperformed traditional sputum techniques, particularly in patients who had previously used antibiotics or had a nonproductive cough. The microbial landscape typical of severe lower respiratory infections in this area is highlighted by the prevalence of Gram-negative bacteria, especially Klebsiella pneumoniae and Pseudomonas aeruginosa. Crucially, a sizable fraction of isolates exhibited multidrug resistance, with high rates of resistance to widely used medicines such fluoroquinolones and third-generation cephalosporins. The problem of antibiotic resistance in treating RTIs is further highlighted by the identification of carbapenem-resistant Gram-negative pathogens and methicillin-resistant Staphylococcus aureus (MRSA).

These results highlight the need for evidence-based empirical therapeutic procedures that are adapted to local resistance patterns and for careful antimicrobial stewardship. Limiting the spread of resistant infections and improving patient outcomes need constant monitoring of microbial profiles and resistance trends. Furthermore, in order to stop nosocomial transmission, infection control procedures need to be strengthened in tertiary care settings. All things considered, this study offers useful regional data that can guide clinical judgment and the creation of policies for improved respiratory infection management in Bihar and comparable healthcare environments.

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